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SEQUENCE LISTING

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Olsen, Peter Bjarke  
Rasmussen, Michael Dolberg

<120> Improved Bacillus Host Cell

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<170> PatentIn version 3.3

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Arg	Ser	Lys	Gln	Ile	Leu	Asp	Pro	Lys	Ala	Ala	Phe	Ile	Thr	Ala	Asn		
		510					515					520					
atg	atg	agc	ggg	atg	ttc	gac	aaa	tca	ctc	aac	ggc	tat	aca	tct	gtt	2117	
Met	Met	Ser	Gly	Met	Phe	Asp	Lys	Ser	Leu	Asn	Gly	Tyr	Thr	Ser	Val		
		525				530					535						
acc	ggc	cgg	acg	atc	gca	gat	cag	ctg	acg	cgc	cga	tac	gcc	gga	aaa	2165	
Thr	Gly	Arg	Thr	Ile	Ala	Asp	Gln	Leu	Thr	Arg	Arg	Tyr	Ala	Gly	Lys		
540					545					550					555		
tcg	gga	acg	acc	agc	acc	gac	agc	tgg	atg	atc	ggc	ttt	tat	ccc	ggg	2213	
Ser	Gly	Thr	Thr	Ser	Thr	Asp	Ser	Trp	Met	Ile	Gly	Phe	Tyr	Pro	Gly		
				560					565					570			
ctt	gct	tca	ggc	gtg	tgg	acg	gga	tat	gac	aaa	gag	cgg	aca	atc	gat	2261	
Leu	Ala	Ser	Gly	Val	Trp	Thr	Gly	Tyr	Asp	Lys	Glu	Arg	Thr	Ile	Asp		
			575					580					585				
gcc	gtc	gca	gag	aaa	aac	tat	gcc	aaa	caa	att	tgg	gct	gag	ttt	atg	2309	
Ala	Val	Ala	Glu	Lys	Asn	Tyr	Ala	Lys	Gln	Ile	Trp	Ala	Glu	Phe	Met		
		590					595					600					
gaa	aaa	gcg	ctt	gaa	gac	gcg	ccc	gcc	gca	gct	tta	atg	ccg	cct	gaa	2357	
Glu	Lys	Ala	Leu	Glu	Asp	Ala	Pro	Ala	Ala	Ala	Leu	Met	Pro	Pro	Glu		
	605					610					615						
ggc	gtg	aaa	ggg	atg	tac	atc	gac	ccg	gct	aca	ggg	tat	gcg	gcg	gcg	2405	
Gly	Val	Lys	Gly	Met	Tyr	Ile	Asp	Pro	Ala	Thr	Gly	Tyr	Ala	Ala	Ala		
620					625					630					635		
ccc	agc	tgc	ccg	tcc	aaa	tat	ttc	gct	tat	ttt	atc	aaa	ggg	act	gaa	2453	
Pro	Ser	Cys	Pro	Ser	Lys	Tyr	Phe	Ala	Tyr	Phe	Ile	Lys	Gly	Thr	Glu		
				640					645					650			
ccc	gag	cag	gtt	tgc	tat	gga	aag	gaa	atc	tat	aag	gag	caa	aac	gcc	2501	
Pro	Glu	Gln	Val	Cys	Tyr	Gly	Lys	Glu	Ile	Tyr	Lys	Glu	Gln	Asn	Ala		
			655					660					665				
ggg	cac	gaa	aag	ccc	gcc	gct	ccc	ccc	cat	aag	cgg	caa	aag	tgg	tgg	2549	
Gly	His	Glu	Lys	Pro	Ala	Ala	Pro	Pro	His	Lys	Arg	Gln	Lys	Trp	Trp		
		670					675					680					
gaa	aaa	tgg	ttt	aaa	aaa	gga	gaa	taaaactttttt	aggggggatag	acgaaccccc	2603						
Glu	Lys	Trp	Phe	Lys	Lys	Gly	Glu										
		685				690											
cggacttcat	ggcagtc	ccgg	gggggtttttc	ctattgctgg	agcagtc	ccct	ttttcagctc	2663									
gtctgatgaa	cggtcccaaa	gcccttgatc	atgggtttttc	agaaaatcgg	caagaacgcg	2723											
cttagaacct	tcattccatat	gctcgacgat	aatcttccgc	ttcatcgact	tatccattaa	2783											



attgacgtgc tccggaagcg atttgtagcc gcggcggatg cttctgtcga ccgtcatttc 2843  
 gcatgccgtc acaccgcat aataagggcc ttcttcctg cggtcgatcg taaccacac 2903  
 aagccagtaa ggttt 2918

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Val Val Met Thr Val Val Leu Ala Ala Lys Trp Gln Gly Ala Pro Ser  
 35 40 45

Ile Gln Val Pro Arg Ser Thr Val Leu Tyr Asp Gly Ser Gly Lys Gln  
 50 55 60

Met Gly Glu Thr His Tyr Gly Gln Lys Arg Tyr Trp Val Ser Leu Lys  
 65 70 75 80

Asn Ile Asn Pro Ala Val Ile Asp Ala Thr Leu Ala Val Glu Asp Arg  
 85 90 95

Asn Phe Phe Arg His His Gly Phe Asp Tyr Met Arg Met Gly Gly Ala  
 100 105 110

Leu Ile Ala Asp Leu Lys Ala Met Ser Lys Val Gln Gly Ala Ser Thr  
 115 120 125

Ile Thr Gln Gln Tyr Ala Arg Asn Leu Tyr Leu Gly His Asp Lys Thr  
 130 135 140

Trp Lys Arg Lys Trp Asn Glu Ala Phe Tyr Thr Ile Arg Leu Glu Gln  
 145 150 155 160

Asn Tyr Thr Lys Lys Asp Ile Leu Glu Gly Tyr Leu Asn Thr Ile Tyr  
 165 170 175

Tyr Gly His Gly Ala Tyr Gly Ile Glu Ala Ala Ser Arg Leu Tyr Phe  
180 185 190

Gly Lys Arg Ala Lys Asp Ile Asn Thr Ala Glu Ala Ala Met Leu Ala  
195 200 205

Gly Ile Pro Lys Gly Pro Ser Val Tyr Ser Pro Phe Val Asn Glu Lys  
210 215 220

Lys Ala Lys Glu Arg Gln Glu Met Ile Leu Thr Met Met Glu Lys Gln  
225 230 235 240

Asn Lys Leu Thr Glu Met Gln Ala Ala Ala Leu Lys Lys Met Pro Leu  
245 250 255

Arg Phe Glu Lys Gln Asp Lys Gln Thr Thr Glu Lys Thr Ala Pro Tyr  
260 265 270

Phe Tyr Asp Glu Ala Val Lys Glu Ile Ser Arg Leu Leu Arg Leu Thr  
275 280 285

Pro Glu Gln Ala Glu Thr Gly Gly Tyr Asn Val Phe Thr Thr Leu Asn  
290 295 300

Pro Arg Leu Gln Lys Ile Ala Glu Asp Thr Ile Glu His Thr Ile Asp  
305 310 315 320

Ser Ser Ser Asp Ile Gln Ala Gly Phe Ala Ala Ile Asn Pro Ser Asp  
325 330 335

Gly Ser Val Leu Ala Leu Val Gly Gly Arg Asp Tyr Glu Lys Ser Pro  
340 345 350

Phe Asn Arg Val Thr Gln Ala Met Arg Gln Pro Gly Ser Thr Met Lys  
355 360 365

Pro Phe Leu Tyr Tyr Ser Ala Val Gln Asn Gly Phe Thr Pro Ala Thr  
370 375 380

Arg Met Arg Ser Ala Glu Thr Thr Phe Glu Leu Gly Gln Gly Ser Ala  
385 390 395 400

Tyr Ser Pro Ser Asn Tyr His Gly Tyr Tyr Ala Asp Gly Pro Ile Thr  
 405 410 415

Leu Leu Gln Ala Leu Ala Leu Ser Asp Asn Ile Tyr Ala Val Lys Thr  
 420 425 430

His Leu Phe Leu Gly Met Asp Lys Leu Ile Asp Ala Ala Lys Gln Phe  
 435 440 445

Gly Ile Asn Ser Pro Leu Gln Lys Val Pro Ser Leu Ala Leu Gly Thr  
 450 455 460

Ser Pro Val Lys Pro Ile Glu Met Val Asn Gly Tyr Ala Met Phe Ala  
 465 470 475 480

Asn Gly Gly Lys Lys Ile Glu Pro Ser Phe Ile Thr Lys Ile Thr Asp  
 485 490 495

Pro Asn Gly Lys Val Leu Tyr Glu Lys Pro Lys Arg Ser Lys Gln Ile  
 500 505 510

Leu Asp Pro Lys Ala Ala Phe Ile Thr Ala Asn Met Met Ser Gly Met  
 515 520 525

Phe Asp Lys Ser Leu Asn Gly Tyr Thr Ser Val Thr Gly Arg Thr Ile  
 530 535 540

Ala Asp Gln Leu Thr Arg Arg Tyr Ala Gly Lys Ser Gly Thr Thr Ser  
 545 550 555 560

Thr Asp Ser Trp Met Ile Gly Phe Tyr Pro Gly Leu Ala Ser Gly Val  
 565 570 575

Trp Thr Gly Tyr Asp Lys Glu Arg Thr Ile Asp Ala Val Ala Glu Lys  
 580 585 590

Asn Tyr Ala Lys Gln Ile Trp Ala Glu Phe Met Glu Lys Ala Leu Glu  
 595 600 605

Asp Ala Pro Ala Ala Ala Leu Met Pro Pro Glu Gly Val Lys Gly Met  
 610 615 620

Tyr Ile Asp Pro Ala Thr Gly Tyr Ala Ala Ala Pro Ser Cys Pro Ser

625

630

635

640

Lys Tyr Phe Ala Tyr Phe Ile Lys Gly Thr Glu Pro Glu Gln Val Cys  
 645 650 655

Tyr Gly Lys Glu Ile Tyr Lys Glu Gln Asn Ala Gly His Glu Lys Pro  
 660 665 670

Ala Ala Pro Pro His Lys Arg Gln Lys Trp Trp Glu Lys Trp Phe Lys  
 675 680 685

Lys Gly Glu  
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 tacgcaactg cagtcctctt tttcggcgga gcatgccttc tgatgttcca aaggtcccag 240  
 caaaaaaaaaat cagaggcgaa agcaagctga aatcggataa aaaaactgcc aatctatcaa 300  
 attatccttc tcgatatcca aaaagaatgg tacgatatgg ctagaattta gcgaaaagag 360  
 a gtg aca aag ttg cgt tca ttt ttt gga tgg att ttt ctg ttg atg tta 409  
 Val Thr Lys Leu Arg Ser Phe Phe Gly Trp Ile Phe Leu Leu Met Leu  
 1 5 10 15  
 ata cct ata ttt gtc ttt acc tta atg gcc tcc ggc cgg gaa gct cag 457  
 Ile Pro Ile Phe Val Phe Thr Leu Met Ala Ser Gly Arg Glu Ala Gln  
 20 25 30  
 aat atg aag cct ctc gat cag gtg ctc gat gag aag atc aat ata aag 505  
 Asn Met Lys Pro Leu Asp Gln Val Leu Asp Glu Lys Ile Asn Ile Lys  
 35 40 45  
 gat atc ggc ctt gta caa aac agc tac atg tat gac agg gac ggc gct 553  
 Asp Ile Gly Leu Val Gln Asn Ser Tyr Met Tyr Asp Arg Asp Gly Ala  
 50 55 60

ctg att tcc gaa atc gtt tca gat cac caa aac cgg gta ttc gtc ccc Leu Ile Ser Glu Ile Val Ser Asp His Gln Asn Arg Val Phe Val Pro 65 70 75 80	601
tat aaa gat atc cct gaa cat gtg aag cag ctg ttt ctg act tcg gag Tyr Lys Asp Ile Pro Glu His Val Lys Gln Leu Phe Leu Thr Ser Glu 85 90 95	649
gac cgt cat ttc ttt cag cat aaa ggc ttt gat ttt atc ggg atg gcc Asp Arg His Phe Phe Gln His Lys Gly Phe Asp Phe Ile Gly Met Ala 100 105 110	697
cgg gcc gcc gca gcc aat gtc aaa aaa ggc ggc att gat cag ggg gcc Arg Ala Ala Ala Ala Asn Val Lys Lys Gly Gly Ile Asp Gln Gly Ala 115 120 125	745
agc acg att aca cag cag ctt tcg aga aac ttg tat ttg aac cat gaa Ser Thr Ile Thr Gln Gln Leu Ser Arg Asn Leu Tyr Leu Asn His Glu 130 135 140	793
cga acc ttc gac cgc aag ttc act gag ctc ctg tat tcc tac cag ctg Arg Thr Phe Asp Arg Lys Phe Thr Glu Leu Leu Tyr Ser Tyr Gln Leu 145 150 155 160	841
gaa aaa aag ctt tca aaa gaa gaa att ttt gag aaa tac tta aac acc Glu Lys Lys Leu Ser Lys Glu Glu Ile Phe Glu Lys Tyr Leu Asn Thr 165 170 175	889
atc tat ttt aat cac ggg gtc tac gga att gga tcc gcg tct tct ttc Ile Tyr Phe Asn His Gly Val Tyr Gly Ile Gly Ser Ala Ser Ser Phe 180 185 190	937
tat ttc agc aag cct ttg aaa tct ctc agc ctt gcc gaa acg gcg ttt Tyr Phe Ser Lys Pro Leu Lys Ser Leu Ser Leu Ala Glu Thr Ala Phe 195 200 205	985
att tgc gcg atc cct aat aac cct aca tta tat gat cct ttg aaa cat Ile Cys Ala Ile Pro Asn Asn Pro Thr Leu Tyr Asp Pro Leu Lys His 210 215 220	1033
ttt gac tac aca aaa acc cgc caa aag cgg ctg ctt gaa ggg ctg aaa Phe Asp Tyr Thr Lys Thr Arg Gln Lys Arg Leu Leu Glu Gly Leu Lys 225 230 235 240	1081
aaa gcg ggc gtg atc acc gaa aaa gaa tac agc aaa gcc gtt aag caa Lys Ala Gly Val Ile Thr Glu Lys Glu Tyr Ser Lys Ala Val Lys Gln 245 250 255	1129
aaa att acg ctt aac gtg aaa gaa aag aaa gac gac tat ccc gac tat Lys Ile Thr Leu Asn Val Lys Glu Lys Lys Asp Asp Tyr Pro Asp Tyr 260 265 270	1177
acg acc tat gtc aac gag gaa ttc acc aaa ttg gtg tcc gct acg gaa Thr Thr Tyr Val Asn Glu Glu Phe Thr Lys Leu Val Ser Ala Thr Glu 275 280 285	1225

ggg ttt gac gaa cgg ctg aaa aag gca aaa aca aaa gaa gaa aag aaa Gly Phe Asp Glu Arg Leu Lys Lys Ala Lys Thr Lys Glu Glu Lys Lys 290 295 300	1273
aaa atc gaa aaa gag ctg tca aac cga atc agc tcc ctc acg aca agc Lys Ile Glu Lys Glu Leu Ser Asn Arg Ile Ser Ser Leu Thr Thr Ser 305 310 315 320	1321
gga atc aaa att tat acg gcg ctc gat acc agc atg caa aac cgt gtc Gly Ile Lys Ile Tyr Thr Ala Leu Asp Thr Ser Met Gln Asn Arg Val 325 330 335	1369
gtc cag caa gtg aag aac cgc ctc cct tat gaa ggc gta caa ggc gga Val Gln Gln Val Lys Asn Arg Leu Pro Tyr Glu Gly Val Gln Gly Gly 340 345 350	1417
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ggg aaa aac tat aaa aag tac gat tat aac ctg gca ttc caa gca tac Gly Lys Asn Tyr Lys Lys Tyr Asp Tyr Asn Leu Ala Phe Gln Ala Tyr 370 375 380	1513
agg cag ccg ggg tca tca att aag ccg ctc ctt gac tac ggg ccg tac Arg Gln Pro Gly Ser Ser Ile Lys Pro Leu Leu Asp Tyr Gly Pro Tyr 385 390 395 400	1561
att gaa gaa acg ggt gcg acg gca ggc agc atg att gac gca agc aaa Ile Glu Glu Thr Gly Ala Thr Ala Gly Ser Met Ile Asp Ala Ser Lys 405 410 415	1609
ttt tgc agc aag gaa tac tgt ccg aac aac ttc aac gaa aga aca tac Phe Cys Ser Lys Glu Tyr Cys Pro Asn Asn Phe Asn Glu Arg Thr Tyr 420 425 430	1657
gga acc gtg tcg atc aag aca gcc ttt aaa tat tcg tat aat aca cca Gly Thr Val Ser Ile Lys Thr Ala Phe Lys Tyr Ser Tyr Asn Thr Pro 435 440 445	1705
gcc gta cgt atg ctg aac cgg gtc ggc gtg caa aaa gga ttc agc tat Ala Val Arg Met Leu Asn Arg Val Gly Val Gln Lys Gly Phe Ser Tyr 450 455 460	1753
tta aaa ccg ttc gga ttc gat aaa atc gtt caa aac gac tac cgt ctt Leu Lys Pro Phe Gly Phe Asp Lys Ile Val Gln Asn Asp Tyr Arg Leu 465 470 475 480	1801
cct gct gcg ctg ggc gga ttt aca tgg ggc ttc tca ccg ctg gag atg Pro Ala Ala Leu Gly Gly Phe Thr Trp Gly Phe Ser Pro Leu Glu Met 485 490 495	1849
gct gat gcc tat acg acc ttc ggc aat aac gga agc tac aca tcc agc Ala Asp Ala Tyr Thr Thr Phe Gly Asn Asn Gly Ser Tyr Thr Ser Ser 500 505 510	1897
cat gca atc aca aag gtg acg gat tta aaa gga aaa acg cta tac aaa	1945

His	Ala	Ile	Thr	Lys	Val	Thr	Asp	Leu	Lys	Gly	Lys	Thr	Leu	Tyr	Lys		
		515					520					525					
tgg	aaa	gac	aag	ccg	cag	caa	gta	ttc	agc	atg	cgg	aca	aac	agc	caa	1993	
Trp	Lys	Asp	Lys	Pro	Gln	Gln	Val	Phe	Ser	Met	Arg	Thr	Asn	Ser	Gln		
	530					535					540						
atg	cgc	gaa	ctc	tta	gca	gcg	gtt	gtt	aaa	gaa	gga	acc	gga	aaa	aaa	2041	
Met	Arg	Glu	Leu	Leu	Ala	Ala	Val	Val	Lys	Glu	Gly	Thr	Gly	Lys	Lys		
	545				550					555					560		
gcg	aat	ttc	agc	ggc	gga	tat	gta	gga	gga	aaa	acc	gga	aca	tcc	aac	2089	
Ala	Asn	Phe	Ser	Gly	Gly	Tyr	Val	Gly	Gly	Lys	Thr	Gly	Thr	Ser	Asn		
			565						570					575			
ggg	tac	aga	gac	ctt	tgg	ttt	gtc	gga	ttg	acg	gat	aca	tac	aca	atg	2137	
Gly	Tyr	Arg	Asp	Leu	Trp	Phe	Val	Gly	Leu	Thr	Asp	Thr	Tyr	Thr	Met		
			580					585					590				
agt	gta	tgg	gtc	gga	aaa	gag	gca	aaa	ggc	act	gtc	gag	tac	ctg	cat	2185	
Ser	Val	Trp	Val	Gly	Lys	Glu	Ala	Lys	Gly	Thr	Val	Glu	Tyr	Leu	His		
		595					600					605					
cac	gcg	gga	cct	caa	ctt	tta	atc	tgg	aga	gga	acg	ctg	caa	tac	gca	2233	
His	Ala	Gly	Pro	Gln	Leu	Leu	Ile	Trp	Arg	Gly	Thr	Leu	Gln	Tyr	Ala		
	610					615					620						
tct	taaattaaaa	aaaggggtgg	atgaaagtgg	cggatatgcc	cgatcgaatc											2286	
Ser																	
625																	
gttctgtttg	acggcgtgtg	caactttttgc	gacggagccg	tgcaattcat	tatcaaacat											2346	
gacctgaag	gcttattttc	attcgcttcc	ctgcaatctg	acgccggagg	gaatctgtc											2406	
aagcaatata	acctcccttc	cgatcatttt	aacagcttta	ttttgatcga	aaacggcccg											2466	
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gccgcttccg	ccctcttgat	cattccccgg	ccgcttcggg	acgccgtcta	cagtgtcatt											2586	
gcgaaaaacc	gctacaaatg	gttcggggcaa	aaaagcgagt	gcaccgttcc	cggtcctgag											2646	
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 <212> PRT  
 <213> Bacillus licheniformis  
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Asn Met Lys Pro Leu Asp Gln Val Leu Asp Glu Lys Ile Asn Ile Lys  
35 40 45

Asp Ile Gly Leu Val Gln Asn Ser Tyr Met Tyr Asp Arg Asp Gly Ala  
50 55 60

Leu Ile Ser Glu Ile Val Ser Asp His Gln Asn Arg Val Phe Val Pro  
65 70 75 80

Tyr Lys Asp Ile Pro Glu His Val Lys Gln Leu Phe Leu Thr Ser Glu  
85 90 95

Asp Arg His Phe Phe Gln His Lys Gly Phe Asp Phe Ile Gly Met Ala  
100 105 110

Arg Ala Ala Ala Ala Asn Val Lys Lys Gly Gly Ile Asp Gln Gly Ala  
115 120 125

Ser Thr Ile Thr Gln Gln Leu Ser Arg Asn Leu Tyr Leu Asn His Glu  
130 135 140

Arg Thr Phe Asp Arg Lys Phe Thr Glu Leu Leu Tyr Ser Tyr Gln Leu  
145 150 155 160

Glu Lys Lys Leu Ser Lys Glu Glu Ile Phe Glu Lys Tyr Leu Asn Thr  
165 170 175

Ile Tyr Phe Asn His Gly Val Tyr Gly Ile Gly Ser Ala Ser Ser Phe  
180 185 190

Tyr Phe Ser Lys Pro Leu Lys Ser Leu Ser Leu Ala Glu Thr Ala Phe  
195 200 205

Ile Cys Ala Ile Pro Asn Asn Pro Thr Leu Tyr Asp Pro Leu Lys His  
210 215 220

Phe Asp Tyr Thr Lys Thr Arg Gln Lys Arg Leu Leu Glu Gly Leu Lys  
225 230 235 240



Lys Ala Gly Val Ile Thr Glu Lys Glu Tyr Ser Lys Ala Val Lys Gln  
245 250 255

Lys Ile Thr Leu Asn Val Lys Glu Lys Lys Asp Asp Tyr Pro Asp Tyr  
260 265 270

Thr Thr Tyr Val Asn Glu Glu Phe Thr Lys Leu Val Ser Ala Thr Glu  
275 280 285

Gly Phe Asp Glu Arg Leu Lys Lys Ala Lys Thr Lys Glu Glu Lys Lys  
290 295 300

Lys Ile Glu Lys Glu Leu Ser Asn Arg Ile Ser Ser Leu Thr Thr Ser  
305 310 315 320

Gly Ile Lys Ile Tyr Thr Ala Leu Asp Thr Ser Met Gln Asn Arg Val  
325 330 335

Val Gln Gln Val Lys Asn Arg Leu Pro Tyr Glu Gly Val Gln Gly Gly  
340 345 350

Ala Val Val Ile Asn His Gln Thr His Gln Ile Val Ala Met Ser Gly  
355 360 365

Gly Lys Asn Tyr Lys Lys Tyr Asp Tyr Asn Leu Ala Phe Gln Ala Tyr  
370 375 380

Arg Gln Pro Gly Ser Ser Ile Lys Pro Leu Leu Asp Tyr Gly Pro Tyr  
385 390 395 400

Ile Glu Glu Thr Gly Ala Thr Ala Gly Ser Met Ile Asp Ala Ser Lys  
405 410 415

Phe Cys Ser Lys Glu Tyr Cys Pro Asn Asn Phe Asn Glu Arg Thr Tyr  
420 425 430

Gly Thr Val Ser Ile Lys Thr Ala Phe Lys Tyr Ser Tyr Asn Thr Pro  
435 440 445

Ala Val Arg Met Leu Asn Arg Val Gly Val Gln Lys Gly Phe Ser Tyr  
450 455 460

Leu Lys Pro Phe Gly Phe Asp Lys Ile Val Gln Asn Asp Tyr Arg Leu  
 465 470 475 480

Pro Ala Ala Leu Gly Gly Phe Thr Trp Gly Phe Ser Pro Leu Glu Met  
 485 490 495

Ala Asp Ala Tyr Thr Thr Phe Gly Asn Asn Gly Ser Tyr Thr Ser Ser  
 500 505 510

His Ala Ile Thr Lys Val Thr Asp Leu Lys Gly Lys Thr Leu Tyr Lys  
 515 520 525

Trp Lys Asp Lys Pro Gln Gln Val Phe Ser Met Arg Thr Asn Ser Gln  
 530 535 540

Met Arg Glu Leu Leu Ala Ala Val Val Lys Glu Gly Thr Gly Lys Lys  
 545 550 555 560

Ala Asn Phe Ser Gly Gly Tyr Val Gly Gly Lys Thr Gly Thr Ser Asn  
 565 570 575

Gly Tyr Arg Asp Leu Trp Phe Val Gly Leu Thr Asp Thr Tyr Thr Met  
 580 585 590

Ser Val Trp Val Gly Lys Glu Ala Lys Gly Thr Val Glu Tyr Leu His  
 595 600 605

His Ala Gly Pro Gln Leu Leu Ile Trp Arg Gly Thr Leu Gln Tyr Ala  
 610 615 620

Ser  
 625

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aatttgcaac cggaaagtac ggcagcgtca ttacagctgt ttacgaggcg ttacatcacc	480
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Met Lys Arg Phe Leu Gln Cys Ala Leu Ile Ala	
1 5 10	
ttg ctg tta tgc tct ctc gct ttg cag ccg gcc gct cgc gaa gca gaa	581
Leu Leu Leu Ser Ser Leu Ala Leu Gln Pro Ala Ala Arg Glu Ala Glu	
15 20 25	
gca aaa cag cgt ccg gaa caa aac atc aaa caa atg gtc agc agc atg	629
Ala Lys Gln Arg Pro Glu Gln Asn Ile Lys Gln Met Val Ser Ser Met	
30 35 40	
tcg ctt gaa gag aaa atc ggg caa atg ctg atg cct gac ttt aga aac	677
Ser Leu Glu Glu Lys Ile Gly Gln Met Leu Met Pro Asp Phe Arg Asn	
45 50 55	
tgg aag aaa aaa ggg gaa tcg agc gcc aaa gga tta aca gaa atg aat	725
Trp Lys Lys Lys Gly Glu Ser Ser Ala Lys Gly Leu Thr Glu Met Asn	
60 65 70 75	
gac gaa gtt gct gga atc att gaa aaa tac cgg ctc ggg ggc gtc att	773
Asp Glu Val Ala Gly Ile Ile Glu Lys Tyr Arg Leu Gly Gly Val Ile	
80 85 90	
ctt ttt gct gaa aac gtc aca ggc aca gag cag act gta cgg tta acg	821
Leu Phe Ala Glu Asn Val Thr Gly Thr Glu Gln Thr Val Arg Leu Thr	
95 100 105	
gac ggc ctg caa caa gcg agc cct gac att ccg ctc ttt atc acg atc	869
Asp Gly Leu Gln Gln Ala Ser Pro Asp Ile Pro Leu Phe Ile Thr Ile	
110 115 120	
gat cag gaa ggc ggg att gtc acg aga ctc gaa tca ggc aca aac ctg	917
Asp Gln Glu Gly Gly Ile Val Thr Arg Leu Glu Ser Gly Thr Asn Leu	
125 130 135	
gcc ggc aat atg gca gtc gga gca tcg aga agc agc aaa aac gcc ttc	965
Ala Gly Asn Met Ala Val Gly Ala Ser Arg Ser Ser Lys Asn Ala Phe	
140 145 150 155	
aga tca gga aaa atc atc gga aaa gaa tta tca tca ctg ggc att aac	1013
Arg Ser Gly Lys Ile Ile Gly Lys Glu Leu Ser Ser Leu Gly Ile Asn	
160 165 170	

gtg aat ttc agt cct gta ctt gat gtc aac aac aat ccc gac aac cct	1061
Val Asn Phe Ser Pro Val Leu Asp Val Asn Asn Asn Pro Asp Asn Pro	
175 180 185	
gtc atc ggc gtc cgt tct ttc agt tcc aag cct gag ctg act tca aag	1109
Val Ile Gly Val Arg Ser Phe Ser Ser Lys Pro Glu Leu Thr Ser Lys	
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ctc ggc atc cag atg atg aag ggc ctt cag gac gag caa atg atc gcc	1157
Leu Gly Ile Gln Met Met Lys Gly Leu Gln Asp Glu Gln Met Ile Ala	
205 210 215	
aca gca aag cac ttt ccc gga cac ggc gat aca gcg gtt gac agt cat	1205
Thr Ala Lys His Phe Pro Gly His Gly Asp Thr Ala Val Asp Ser His	
220 225 230 235	
tac gga ttg ccg ctt gtt ccg cat aat gaa aaa agg ctg aga agt gtt	1253
Tyr Gly Leu Pro Leu Val Pro His Asn Glu Lys Arg Leu Arg Ser Val	
240 245 250	
gaa ctt gcg cca ttt caa aag gcg atc gat gca ggt att gac atg atc	1301
Glu Leu Ala Pro Phe Gln Lys Ala Ile Asp Ala Gly Ile Asp Met Ile	
255 260 265	
atg aca gcg cat gtc cag ttc ccc gcc ttt gac gat act acc tat aaa	1349
Met Thr Ala His Val Gln Phe Pro Ala Phe Asp Asp Thr Thr Tyr Lys	
270 275 280	
agc aaa aaa gac ggc gag gac atc atg gtg cct gct acg ctt tcc aaa	1397
Ser Lys Lys Asp Gly Glu Asp Ile Met Val Pro Ala Thr Leu Ser Lys	
285 290 295	
aaa gtc atg aca gac ctt ctc cgc aaa gat ctc agc ttt aag ggc gtt	1445
Lys Val Met Thr Asp Leu Leu Arg Lys Asp Leu Ser Phe Lys Gly Val	
300 305 310 315	
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Val Val Thr Asp Ala Leu Asn Met Lys Ala Ile Ser Asp Asn Phe Gly	
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cag gag gaa gcc gtc gtc atg gct gtt aaa gca gga gtc gac atc gca	1541
Gln Glu Glu Ala Val Val Met Ala Val Lys Ala Gly Val Asp Ile Ala	
335 340 345	
ctc atg ccc gcg caa gtc aca tcg ctt gag acc gaa aaa aat ctg gcg	1589
Leu Met Pro Ala Gln Val Thr Ser Leu Glu Thr Glu Lys Asn Leu Ala	
350 355 360	
cgt gta ttc gaa gct ctt ctg aca gcc gtt aaa aat ggg gat atc ccc	1637
Arg Val Phe Glu Ala Leu Leu Thr Ala Val Lys Asn Gly Asp Ile Pro	
365 370 375	
atg gaa caa atc gat cag tcg gtg gag cga atc ctt caa tta aaa ata	1685
Met Glu Gln Ile Asp Gln Ser Val Glu Arg Ile Leu Gln Leu Lys Ile	
380 385 390 395	

gac cga ggc atc ata gat cac acc ggc tcc gaa ccg ctt cag aaa aaa	1733
Asp Arg Gly Ile Ile Asp His Thr Gly Ser Glu Pro Leu Gln Lys Lys	
400 405 410	
atc aaa tac gcc ttg aaa acg gtc ggc agc agc aaa cac atg aaa tac	1781
Ile Lys Tyr Ala Leu Lys Thr Val Gly Ser Ser Lys His Met Lys Tyr	
415 420 425	
gaa aag aaa atg gca agg gat agc gcc act atc ctt aaa aac gac aaa	1829
Glu Lys Lys Met Ala Arg Asp Ser Ala Thr Ile Leu Lys Asn Asp Lys	
430 435 440	
agc acc ctg ccg ttt aaa ccg aaa aaa ggg gac acc gtc ctc att ctc	1877
Ser Thr Leu Pro Phe Lys Pro Lys Lys Gly Asp Thr Val Leu Ile Leu	
445 450 455	
gct cca tat gaa gag caa aca gca gca atc gca aag acc atc agc aaa	1925
Ala Pro Tyr Glu Glu Gln Thr Ala Ala Ile Ala Lys Thr Ile Ser Lys	
460 465 470 475	
ata agg aaa aac atc aag gta gtc gaa tac cgc ttt gca gaa aaa acg	1973
Ile Arg Lys Asn Ile Lys Val Val Glu Tyr Arg Phe Ala Glu Lys Thr	
480 485 490	
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Phe Glu Glu Glu Ile Gln Lys Lys Ile Asp Glu Ala Asp Tyr Val Ile	
495 500 505	
aca gga tca tac gtc atc aaa aac gat ccg gtt gtg aac gac ggt gtc	2069
Thr Gly Ser Tyr Val Ile Lys Asn Asp Pro Val Val Asn Asp Gly Val	
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Ile Asp Asp Ser Ile Gln Asp Ser Ser Lys Trp Ala Thr Ala Phe Pro	
525 530 535	
cgc gcc gcc atg aaa tac gcg cag gcc aac gga aaa aaa ttc gtc tta	2165
Arg Ala Ala Met Lys Tyr Ala Gln Ala Asn Gly Lys Lys Phe Val Leu	
540 545 550 555	
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Met Ser Leu Arg Asn Pro Tyr Asp Thr Ala Asn Phe Glu Glu Ala Glu	
560 565 570	
gcc gtg att gcg gta tac ggc ttt aaa ggc tat gca aac gga cgc ttc	2261
Ala Val Ile Ala Val Tyr Gly Phe Lys Gly Tyr Ala Asn Gly Arg Phe	
575 580 585	
agg cag ccg aat atc ccg gcc gga gtg gaa gcc att ttc gga aag gca	2309
Arg Gln Pro Asn Ile Pro Ala Gly Val Glu Ala Ile Phe Gly Lys Ala	
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aag cct aaa gga aca ttg ccc gta gac att cct tca gtc acg cgc ccc	2357
Lys Pro Lys Gly Thr Leu Pro Val Asp Ile Pro Ser Val Thr Arg Pro	
605 610 615	
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Gly Glu Thr Leu Tyr Pro Tyr Gly Tyr Gly Leu Asn Ile Lys Asn Gly  
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 aag ccg ctt cac aaa gga ggg tca tgatgggaaa aaaagcaatc tggctgcttg 2459  
 Lys Pro Leu His Lys Gly Gly Ser  
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Glu Gln Asn Ile Lys Gln Met Val Ser Ser Met Ser Leu Glu Glu Lys  
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Ile Gly Gln Met Leu Met Pro Asp Phe Arg Asn Trp Lys Lys Lys Gly  
 50 55 60

Glu Ser Ser Ala Lys Gly Leu Thr Glu Met Asn Asp Glu Val Ala Gly  
 65 70 75 80

Ile Ile Glu Lys Tyr Arg Leu Gly Gly Val Ile Leu Phe Ala Glu Asn  
 85 90 95

Val Thr Gly Thr Glu Gln Thr Val Arg Leu Thr Asp Gly Leu Gln Gln  
 100 105 110

Ala Ser Pro Asp Ile Pro Leu Phe Ile Thr Ile Asp Gln Glu Gly Gly  
 115 120 125

Ile Val Thr Arg Leu Glu Ser Gly Thr Asn Leu Ala Gly Asn Met Ala  
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Val Gly Ala Ser Arg Ser Ser Lys Asn Ala Phe Arg Ser Gly Lys Ile  
 145 150 155 160

Ile Gly Lys Glu Leu Ser Ser Leu Gly Ile Asn Val Asn Phe Ser Pro  
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Val Leu Asp Val Asn Asn Asn Pro Asp Asn Pro Val Ile Gly Val Arg  
 180 185 190

Ser Phe Ser Ser Lys Pro Glu Leu Thr Ser Lys Leu Gly Ile Gln Met  
 195 200 205

Met Lys Gly Leu Gln Asp Glu Gln Met Ile Ala Thr Ala Lys His Phe  
 210 215 220

Pro Gly His Gly Asp Thr Ala Val Asp Ser His Tyr Gly Leu Pro Leu  
 225 230 235 240

Val Pro His Asn Glu Lys Arg Leu Arg Ser Val Glu Leu Ala Pro Phe  
 245 250 255

Gln Lys Ala Ile Asp Ala Gly Ile Asp Met Ile Met Thr Ala His Val  
 260 265 270

Gln Phe Pro Ala Phe Asp Asp Thr Thr Tyr Lys Ser Lys Lys Asp Gly  
 275 280 285

Glu Asp Ile Met Val Pro Ala Thr Leu Ser Lys Lys Val Met Thr Asp  
 290 295 300

Leu Leu Arg Lys Asp Leu Ser Phe Lys Gly Val Val Val Thr Asp Ala  
 305 310 315 320

Leu Asn Met Lys Ala Ile Ser Asp Asn Phe Gly Gln Glu Glu Ala Val  
 325 330 335

Val Met Ala Val Lys Ala Gly Val Asp Ile Ala Leu Met Pro Ala Gln  
 340 345 350

Val Thr Ser Leu Glu Thr Glu Lys Asn Leu Ala Arg Val Phe Glu Ala  
 355 360 365

Leu Leu Thr Ala Val Lys Asn Gly Asp Ile Pro Met Glu Gln Ile Asp  
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Gln Ser Val Glu Arg Ile Leu Gln Leu Lys Ile Asp Arg Gly Ile Ile  
 385 390 395 400

Asp His Thr Gly Ser Glu Pro Leu Gln Lys Lys Ile Lys Tyr Ala Leu  
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Lys Thr Val Gly Ser Ser Lys His Met Lys Tyr Glu Lys Lys Met Ala  
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Arg Asp Ser Ala Thr Ile Leu Lys Asn Asp Lys Ser Thr Leu Pro Phe  
 435 440 445

Lys Pro Lys Lys Gly Asp Thr Val Leu Ile Leu Ala Pro Tyr Glu Glu  
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Gln Thr Ala Ala Ile Ala Lys Thr Ile Ser Lys Ile Arg Lys Asn Ile  
 465 470 475 480

Lys Val Val Glu Tyr Arg Phe Ala Glu Lys Thr Phe Glu Glu Glu Ile  
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Gln Lys Lys Ile Asp Glu Ala Asp Tyr Val Ile Thr Gly Ser Tyr Val  
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Ile Lys Asn Asp Pro Val Val Asn Asp Gly Val Ile Asp Asp Ser Ile  
 515 520 525

Gln Asp Ser Ser Lys Trp Ala Thr Ala Phe Pro Arg Ala Ala Met Lys  
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Tyr Ala Gln Ala Asn Gly Lys Lys Phe Val Leu Met Ser Leu Arg Asn  
 545 550 555 560



Pro Tyr Asp Thr Ala Asn Phe Glu Glu Ala Glu Ala Val Ile Ala Val  
 565 570 575

Tyr Gly Phe Lys Gly Tyr Ala Asn Gly Arg Phe Arg Gln Pro Asn Ile  
 580 585 590

Pro Ala Gly Val Glu Ala Ile Phe Gly Lys Ala Lys Pro Lys Gly Thr  
 595 600 605

Leu Pro Val Asp Ile Pro Ser Val Thr Arg Pro Gly Glu Thr Leu Tyr  
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 tacaatcaaa agaaaagcgg gtg act ttt ttg aaa tat atc atc ata tgt ctg 533  
 Val Thr Phe Leu Lys Tyr Ile Ile Ile Cys Leu  
 1 5 10  
 gca agc ttc ttg ctg atc acg gcg acg gga caa gcg gct gca gcc aaa 581  
 Ala Ser Phe Leu Leu Ile Thr Ala Thr Gly Gln Ala Ala Ala Ala Lys

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Asp Val Thr Val Asp Gly Ser Ile Leu Gly Glu Asn Ser Arg Glu Gln																				
30 35 40																				
gcc aag cag caa gtg ctc aca aac gat ctc ttg act tta tac ggg gca	677																			
Ala Lys Gln Gln Val Leu Thr Asn Asp Leu Leu Thr Leu Tyr Gly Ala																				
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aaa gac agc gcc gag ctg acg tat caa ata ccg gcg ggc gcc tcc tct	725																			
Lys Asp Ser Ala Glu Leu Thr Tyr Gln Ile Pro Ala Gly Ala Ser Ser																				
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acc cat cag cag ctt aca ctt aaa tac gag gcc tca gac ctt tta atc	773																			
Thr His Gln Gln Leu Thr Leu Lys Tyr Glu Ala Ser Asp Leu Leu Ile																				
80 85 90																				
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Ser Pro Ser Ser Leu Thr Ala Glu Ile Asp Gly Glu Pro Val Lys Thr																				
95 100 105																				
gtt aag ctt gaa ggg aat aac ggg aag aaa acg ctg aag ctc tcg ctg	869																			
Val Lys Leu Glu Gly Asn Asn Gly Lys Lys Thr Leu Lys Leu Ser Leu																				
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Tyr Gly Val Val His Glu Gly Val Cys Val Arg Gln Asp Ser Ser Gly																				
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Gln Ser Gly Ser Ser Val Glu Lys Thr Ala Ile Val Ile Pro Asp His																				
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Pro Ser Ser Ala Glu Ile Glu Ala Ala Val Lys Thr Glu Ala Tyr Leu																				
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Lys Thr Val Asp Asn Ser Ile Ser Thr Lys Ile Leu Gly Glu Ser Asp																				
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ctg gcg aag atc gac agg ccg acg att gtg atc ggc gtt cac cat cac	1253																			
Leu Ala Lys Ile Asp Arg Pro Thr Ile Val Ile Gly Val His His His																				
240 245 250																				

tgg agc ggc aaa gtg aaa aag ctg ttg aaa caa gcg aaa ctc gaa gca	1301
Trp Ser Gly Lys Val Lys Lys Leu Leu Lys Gln Ala Lys Leu Glu Ala	
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Lys Glu Asp Lys Leu Leu Leu Ala Lys Arg Met Leu Lys Ala Lys Asp	
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Lys Gln Gln Pro Val Leu Phe Ala Ala Ala Ser Asp Asp Val Leu	
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Gly Gly Ser Lys Leu Thr Leu Glu Asp Phe Gly Ala Gly Asp Leu Thr	
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Ile Gly Ser Gly Gln Thr Ser Ser Glu His Phe Tyr Tyr Pro Ala Pro	
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gct cta tta gac aag aat cag cct gca aag ctt tcg ctt gcg atg aaa	1637
Ala Leu Leu Asp Lys Asn Gln Pro Ala Lys Leu Ser Leu Ala Met Lys	
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Lys Ser Lys Thr Ile Gln Lys Gln Ala Gly Gln Ser Asp Leu Ala Ala	
380 385 390 395	
gaa cag gcg gag ctg aag gtc atg atc aat ggc cag cct cat tcc gtc	1733
Glu Gln Ala Glu Leu Lys Val Met Ile Asn Gly Gln Pro His Ser Val	
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gga ctt gac gat ata gga aaa gaa gac aaa aac ggc ttt tac cat gtt	1781
Gly Leu Asp Asp Ile Gly Lys Glu Asp Lys Asn Gly Phe Tyr His Val	
415 420 425	
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Ser Leu Lys Val Asp Pro Lys Leu Leu Gln Lys Ser Arg Tyr Ile Asp	
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Ile Gln Phe Ala Ala Ser Gly Leu Lys Glu Asn Asn Pro Cys Tyr Ala	
445 450 455	
gtg aac gag gac aaa tgg att ttt atc gat aaa caa agt gca ttg tct	1925
Val Asn Glu Asp Lys Trp Ile Phe Ile Asp Lys Gln Ser Ala Leu Ser	
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Lys Arg Lys Ala Asn Ala Gly Gly Gly Ile Asp Glu  
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Gly Ser Ile Leu Gly Glu Asn Ser Arg Glu Gln Ala Lys Gln Gln Val  
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Leu Thr Asn Asp Leu Leu Thr Leu Tyr Gly Ala Lys Asp Ser Ala Glu  
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Leu Thr Tyr Gln Ile Pro Ala Gly Ala Ser Ser Thr His Gln Gln Leu  
 65 70 75 80

Thr Leu Lys Tyr Glu Ala Ser Asp Leu Leu Ile Ser Pro Ser Ser Leu  
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Thr Ala Glu Ile Asp Gly Glu Pro Val Lys Thr Val Lys Leu Glu Gly  
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Asn Asn Gly Lys Lys Thr Leu Lys Leu Ser Leu Asn Lys Ser Gln Ser  
 115 120 125

Ser Pro Gly Phe His Ser Leu Ser Leu Lys Phe Tyr Gly Val Val His  
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Glu Gly Val Cys Val Arg Gln Asp Ser Ser Gly Asn Trp Ile Lys Ile  
 145 150 155 160

Tyr Pro Asp Ser Arg Leu Asn Ile Gly Glu Lys Asn Glu Ser Lys Gly  
165 170 175

Ala Ala Leu Glu His Tyr Pro Tyr Pro Phe Ala Gln Ser Gly Ser Ser  
180 185 190

Val Glu Lys Thr Ala Ile Val Ile Pro Asp His Pro Ser Ser Ala Glu  
195 200 205

Ile Glu Ala Ala Val Lys Thr Glu Ala Tyr Leu Lys Thr Val Asp Asn  
210 215 220

Ser Ile Ser Thr Lys Ile Leu Gly Glu Ser Asp Leu Ala Lys Ile Asp  
225 230 235 240

Arg Pro Thr Ile Val Ile Gly Val His His His Trp Ser Gly Lys Val  
245 250 255

Lys Lys Leu Leu Lys Gln Ala Lys Leu Glu Ala Lys Glu Asp Lys Leu  
260 265 270

Leu Leu Ala Lys Arg Met Leu Lys Ala Lys Asp Lys Gln Gln Pro Val  
275 280 285

Leu Phe Ala Ala Ala Ala Ser Asp Asp Val Leu Ser Glu Lys Ile Ser  
290 295 300

Val Ile Thr Asp Lys Thr Tyr Ala Ala Gln Leu Ser Gly Asp Thr Leu  
305 310 315 320

Ala Ile Gly Lys Leu Gln Gln His Ser Lys Arg Gly Gly Ser Lys Leu  
325 330 335

Thr Leu Glu Asp Phe Gly Ala Gly Asp Leu Thr Ile Gly Ser Gly Gln  
340 345 350

Thr Ser Ser Glu His Phe Tyr Tyr Pro Ala Pro Ala Leu Leu Asp Lys  
355 360 365

Asn Gln Pro Ala Lys Leu Ser Leu Ala Met Lys Lys Ser Lys Thr Ile  
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Gln Lys Gln Ala Gly Gln Ser Asp Leu Ala Ala Glu Gln Ala Glu Leu

385

390

395

400

Lys Val Met Ile Asn Gly Gln Pro His Ser Val Gly Leu Asp Asp Ile  
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Gly Lys Glu Asp Lys Asn Gly Phe Tyr His Val Ser Leu Lys Val Asp  
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Pro Lys Leu Leu Gln Lys Ser Arg Tyr Ile Asp Ile Gln Phe Ala Ala  
 435 440 445

Ser Gly Leu Lys Glu Asn Asn Pro Cys Tyr Ala Val Asn Glu Asp Lys  
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Trp Ile Phe Ile Asp Lys Gln Ser Ala Leu Ser Tyr His Val Ser Asp  
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Thr Ser Ala Ser Ala Asp Phe Gln Ala Trp Pro Leu Pro Tyr Ala Gly  
 485 490 495

Asp His Asn Asn Lys Thr Leu Met Ile Leu Pro Asp Asn Ala Asp Gln  
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Ser Lys Ile Asp Glu Leu Ser Leu Val Val Gly Ser Phe Gly Ser Glu  
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Ala Arg Gln Ala Phe Thr Val Lys Thr Ser Ser Glu Val Lys Pro Asp  
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Asp Val Lys Gly Arg Asn Val Ile Phe Ile Gly Ser Val Asp Gln Phe  
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Ser Leu Leu Lys Glu Lys Thr Ala Glu Leu Ala Val Pro Thr Ala Lys  
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Lys Gln Val Ala Phe Thr Gln Thr Ser Leu Trp Asp Ser Asn Tyr Ser  
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Met Ala Val Phe Ala Pro Phe Lys Gly Gln Gly Thr Ala Val Thr Lys  
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Glu Met Ile Asn Phe Leu Asn Ser Asn Asp Phe Ala Ala Thr Val Val  
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Asn Glu Thr Asp Ser His Gln Leu Phe Thr Asn His Gln Gln Leu Thr  
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Ala Lys Ser Ala Glu Thr Lys Thr Asp Asp Lys Gln Glu Ser Asn Gln  
 660 665 670

Gln His Val Leu Tyr Ile Ala Ile Leu Ile Val Ile Ile Ala Ala Ala  
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Val Ile Leu Ile Leu Thr Thr Ala Arg Arg Arg Lys Arg Lys Ala Asn  
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 atccatctat gtttgagcct gtgcacggct ctgctccgga catcatctga tagcgagtca 180  
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 Met Asn Gln Lys Ile Val  
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tct gtg ctc atc att gcg ctc agc ctg tta tgc ggc ttg gta aca ggc Ser Val Leu Ile Ile Ala Leu Ser Leu Leu Cys Gly Leu Val Thr Gly 10 15 20	584
gcc ggc ccg att ccg tta cat gat gtc gtt tca aaa gca tca gcg gct Ala Gly Pro Ile Pro Leu His Asp Val Val Ser Lys Ala Ser Ala Ala 25 30 35	632
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aat gac cca tac tcg gtc tat atg gat aaa cag acg gca aag cgg ttt Asn Asp Pro Tyr Ser Val Tyr Met Asp Lys Gln Thr Ala Lys Arg Phe 90 95 100	824
tca gat tcc ctt gat tcc tct ttt gaa gga atc ggt gca gaa atc gga Ser Asp Ser Leu Asp Ser Ser Phe Glu Gly Ile Gly Ala Glu Ile Gly 105 110 115	872
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aga ggc aaa aag gga tcg acg gtt aca ctg aaa gtt cac cga ccc gga Arg Gly Lys Lys Gly Ser Thr Val Thr Leu Lys Val His Arg Pro Gly 170 175 180	1064
atg aaa gac cag ctg aca ttt acg att aag cgc gat gaa atc ccg ctg Met Lys Asp Gln Leu Thr Phe Thr Ile Lys Arg Asp Glu Ile Pro Leu 185 190 195	1112
gaa acg gtg ttt gct tcc ata aag aaa gta cag gat aaa cct gtc ggc Glu Thr Val Phe Ala Ser Ile Lys Lys Val Gln Asp Lys Pro Val Gly 200 205 210	1160
tat atc gca ata tct tcc ttt tcc gaa cat acg gca aaa gat ttt act Tyr Ile Ala Ile Ser Ser Phe Ser Glu His Thr Ala Lys Asp Phe Thr 215 220 225 230	1208
gct gaa ctg aaa aag ctt gag aaa aag gga ata aaa ggg ctc gtt ttg	1256

Ala	Glu	Leu	Lys	Lys	Leu	Glu	Lys	Lys	Gly	Ile	Lys	Gly	Leu	Val	Leu		
				235					240					245			
gat	gta	aga	gga	aat	ccg	ggc	ggg	tac	ttg	caa	agc	gtg	gaa	gac	att	1304	
Asp	Val	Arg	Gly	Asn	Pro	Gly	Gly	Tyr	Leu	Gln	Ser	Val	Glu	Asp	Ile		
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Leu	Lys	His	Phe	Val	Thr	Lys	Asp	His	Pro	Tyr	Ile	Gln	Ile	Ala	Glu		
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cca	tac	cct	gtg	agc	gtg	atc	acg	gac	aag	ggc	agc	gct	tcg	gct	tcg	1448	
Pro	Tyr	Pro	Val	Ser	Val	Ile	Thr	Asp	Lys	Gly	Ser	Ala	Ser	Ala	Ser		
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Glu	Ile	Leu	Ala	Gly	Ala	Leu	Lys	Glu	Ala	Glu	Gly	Tyr	Asp	Val	Val		
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Gly	Asp	Pro	Ser	Phe	Gly	Lys	Gly	Thr	Val	Gln	Gln	Ala	Val	Pro	Met		
			330					335					340				
gga	gac	ggt	agc	aat	att	aag	ctg	acg	ctg	tac	aaa	tgg	ctg	aca	cct	1592	
Gly	Asp	Gly	Ser	Asn	Ile	Lys	Leu	Thr	Leu	Tyr	Lys	Trp	Leu	Thr	Pro		
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Lys	Gly	Asn	Trp	Ile	His	Lys	Gln	Gly	Ile	Gln	Pro	Thr	Val	Pro	Val		
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acg	cag	cct	gca	tat	ttc	tcg	gcg	ggg	cct	tta	cag	ctg	aaa	gaa	ccc	1688	
Thr	Gln	Pro	Ala	Tyr	Phe	Ser	Ala	Gly	Pro	Leu	Gln	Leu	Lys	Glu	Pro		
	375				380				385						390		
ctc	aag	ccg	gat	atg	aac	aac	aat	gaa	att	aag	cgg	gcg	cag	ttc	ctg	1736	
Leu	Lys	Pro	Asp	Met	Asn	Asn	Asn	Glu	Ile	Lys	Arg	Ala	Gln	Phe	Leu		
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ctg	aaa	gga	ctc	ggg	ttt	gtc	ccc	ggc	cgg	gaa	gac	ggc	tat	tac	aat	1784	
Leu	Lys	Gly	Leu	Gly	Phe	Val	Pro	Gly	Arg	Glu	Asp	Gly	Tyr	Tyr	Asn		
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gaa	agc	aca	aaa	aaa	gcc	gtc	atg	gcg	ttt	cag	gca	gca	aac	aag	ctg	1832	
Glu	Ser	Thr	Lys	Lys	Ala	Val	Met	Ala	Phe	Gln	Ala	Ala	Asn	Lys	Leu		
		425					430					435					
aag	caa	aca	ggg	atc	att	gac	caa	aaa	acg	gca	aat	aca	atg	aac	ctg	1880	
Lys	Gln	Thr	Gly	Ile	Ile	Asp	Gln	Lys	Thr	Ala	Asn	Thr	Met	Asn	Leu		
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cgg	att	gag	gag	aaa	aag	atg	gat	gaa	aag	aac	gat	ctt	cag	ctg	caa	1928	
Arg	Ile	Glu	Glu	Lys	Lys	Met	Asp	Glu	Lys	Asn	Asp	Leu	Gln	Leu	Gln		

455                      460                      465                      470  
 gcc gca tta aaa gtg ctg ttt aac aaa aag tgagggcacg ggatgtcctc 1978  
 Ala Ala Leu Lys Val Leu Phe Asn Lys Lys  
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 ataaaaaaaa cattcataat gaatagaatt gacccgataa cataagtata tgggagactt 2098  
 tataaggatg taaagatgca gtaaaaatgt aacttttgca agttgtataa cataggaaaa 2158  
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 gaatgttagc gctgtttgcg ttcttcgtct ctgttggtgg agtcgtctga cgcttgcgct 2278  
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 Ser Lys Ala Ser Ala Ala Glu Glu Ala Ala Ala Lys Ser Thr Ala Arg  
                     35                      40                      45  
  
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 Tyr Val Glu Gln Val Asp Arg Glu Lys Leu Leu Glu Gly Ala Ile Gln  
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 Gly Met Leu Ser Thr Leu Asn Asp Pro Tyr Ser Val Tyr Met Asp Lys  
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Ile Gly Ala Glu Ile Gly Met Glu Asp Arg Lys Ile Ile Ile Val Ser  
115 120 125

Pro Phe Lys Gln Ser Pro Ala Glu Lys Ala Gly Leu Lys Pro Asn Asp  
130 135 140

Glu Ile Ile Ser Ile Asp Gly Asp Ser Met Ser Gly Met Asp Leu Asn  
145 150 155 160

Asp Ala Val Leu Lys Ile Arg Gly Lys Lys Gly Ser Thr Val Thr Leu  
165 170 175

Lys Val His Arg Pro Gly Met Lys Asp Gln Leu Thr Phe Thr Ile Lys  
180 185 190

Arg Asp Glu Ile Pro Leu Glu Thr Val Phe Ala Ser Ile Lys Lys Val  
195 200 205

Gln Asp Lys Pro Val Gly Tyr Ile Ala Ile Ser Ser Phe Ser Glu His  
210 215 220

Thr Ala Lys Asp Phe Thr Ala Glu Leu Lys Lys Leu Glu Lys Lys Gly  
225 230 235 240

Ile Lys Gly Leu Val Leu Asp Val Arg Gly Asn Pro Gly Gly Tyr Leu  
245 250 255

Gln Ser Val Glu Asp Ile Leu Lys His Phe Val Thr Lys Asp His Pro  
260 265 270

Tyr Ile Gln Ile Ala Glu Arg Asn Gly Asn Lys Lys Gln Tyr Phe Ser  
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Lys Leu Lys Glu Lys Lys Pro Tyr Pro Val Ser Val Ile Thr Asp Lys  
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Gly Ser Ala Ser Ala Ser Glu Ile Leu Ala Gly Ala Leu Lys Glu Ala  
305 310 315 320

Glu Gly Tyr Asp Val Val Gly Asp Pro Ser Phe Gly Lys Gly Thr Val  
325 330 335

Gln Gln Ala Val Pro Met Gly Asp Gly Ser Asn Ile Lys Leu Thr Leu  
 340 345 350

Tyr Lys Trp Leu Thr Pro Lys Gly Asn Trp Ile His Lys Gln Gly Ile  
 355 360 365

Gln Pro Thr Val Pro Val Thr Gln Pro Ala Tyr Phe Ser Ala Gly Pro  
 370 375 380

Leu Gln Leu Lys Glu Pro Leu Lys Pro Asp Met Asn Asn Asn Glu Ile  
 385 390 395 400

Lys Arg Ala Gln Phe Leu Leu Lys Gly Leu Gly Phe Val Pro Gly Arg  
 405 410 415

Glu Asp Gly Tyr Tyr Asn Glu Ser Thr Lys Lys Ala Val Met Ala Phe  
 420 425 430

Gln Ala Ala Asn Lys Leu Lys Gln Thr Gly Ile Ile Asp Gln Lys Thr  
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Ala Asn Thr Met Asn Leu Arg Ile Glu Glu Lys Lys Met Asp Glu Lys  
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 aaaagccgct cggcattacg attttgagaa agcgtgaagt gccccggatt ctttggccca 180  
 tggacatcag cgagatgtac ggagtcggcc ggaaaaccgc cgaaaagctt aagacgctcg 240  
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gcatcaacgg cccccgttta aaaagaaggg caaacggcat cgacacagga gaagtgaatc	360
ccgacagaat atacgaattc aaaagcgtcg gcaattcctc gaccctccc catgacagca	420
cagatgagaa agagctgttc ggactgattg acaagctttc aatctcagta agcgacaggc	480
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agaagggagc ttagac atg gca aaa caa caa ata ggt gta gtt ggt tta gca	1012
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gta atg gga aaa aac ttg gct tta aac att gaa agc cgc ggg ttt tca	1060
Val Met Gly Lys Asn Leu Ala Leu Asn Ile Glu Ser Arg Gly Phe Ser	
15 20 25	
gtt tct gtc tac aac aga tca agc gag aaa acc gaa gag ttt ctg aaa	1108
Val Ser Val Tyr Asn Arg Ser Ser Glu Lys Thr Glu Glu Phe Leu Lys	
30 35 40	
gaa gcc gaa ggc aaa aac gtt gtc ggt aca tac agc att gaa gag ttt	1156
Glu Ala Glu Gly Lys Asn Val Val Gly Thr Tyr Ser Ile Glu Glu Phe	
45 50 55 60	
gtt gaa tct ctt gaa aaa ccg cgc aaa att ctt tta atg gtc aaa gct	1204
Val Glu Ser Leu Glu Lys Pro Arg Lys Ile Leu Leu Met Val Lys Ala	
65 70 75	
gga aca ccg aca gac gca acg att caa tcg ctt ctg cct cat ctt gaa	1252
Gly Thr Pro Thr Asp Ala Thr Ile Gln Ser Leu Leu Pro His Leu Glu	
80 85 90	
aaa ggc gac att ttg att gac ggc gga aat aca tat tat aaa gat acg	1300
Lys Gly Asp Ile Leu Ile Asp Gly Gly Asn Thr Tyr Tyr Lys Asp Thr	
95 100 105	
cag aga aga aac agg gag ctg gcc gaa agc ggc att cac ttc atc ggc	1348
Gln Arg Arg Asn Arg Glu Leu Ala Glu Ser Gly Ile His Phe Ile Gly	
110 115 120	
acc ggc gtt tcc ggc ggt gaa gaa ggc gct ctg aaa ggg ccg tct atc	1396
Thr Gly Val Ser Gly Gly Glu Glu Gly Ala Leu Lys Gly Pro Ser Ile	
125 130 135 140	

atg cca ggc gga caa aag gaa gcc cat gag ctt gtc aag ccg att ctt	1444
Met Pro Gly Gly Gln Lys Glu Ala His Glu Leu Val Lys Pro Ile Leu	
145 150 155	
gaa gct att tct gcc aag gtg gac ggc gaa ccg tgt acg aca tac atc	1492
Glu Ala Ile Ser Ala Lys Val Asp Gly Glu Pro Cys Thr Thr Tyr Ile	
160 165 170	
ggc cct gac ggc gcc ggc cat tat gta aaa atg gtt cat aac ggc atc	1540
Gly Pro Asp Gly Ala Gly His Tyr Val Lys Met Val His Asn Gly Ile	
175 180 185	
gaa tac ggc gat atg cag ctg atc tca gaa tcc tac ttt att ttg aaa	1588
Glu Tyr Gly Asp Met Gln Leu Ile Ser Glu Ser Tyr Phe Ile Leu Lys	
190 195 200	
cac att gtc ggt ctg tca tca gat gag ctt cac gaa gtc ttt tcc gag	1636
His Ile Val Gly Leu Ser Ser Asp Glu Leu His Glu Val Phe Ser Glu	
205 210 215 220	
tgg aat aag gga gag ctt gac agc tat ctg atc gaa atc acg gct gat	1684
Trp Asn Lys Gly Glu Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Asp	
225 230 235	
att ttc acg aaa aaa gac gag gaa acc ggc aag ccg ctt gtt gac gtc	1732
Ile Phe Thr Lys Lys Asp Glu Glu Thr Gly Lys Pro Leu Val Asp Val	
240 245 250	
atc ctc gat aaa gca ggt caa aaa ggc aca gga aaa tgg aca agc caa	1780
Ile Leu Asp Lys Ala Gly Gln Lys Gly Thr Gly Lys Trp Thr Ser Gln	
255 260 265	
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Ser Ala Leu Asp Leu Gly Val Pro Leu Pro Ile Ile Thr Glu Ser Val	
270 275 280	
ttc gcc cgc ttc atc tct tcc atg aaa gag gag cgc gtc aaa gcg agc	1876
Phe Ala Arg Phe Ile Ser Ser Met Lys Glu Glu Arg Val Lys Ala Ser	
285 290 295 300	
aag ctt ctg gca gga cct gaa gcg aaa cct gcc gct gag aac aaa gaa	1924
Lys Leu Leu Ala Gly Pro Glu Ala Lys Pro Ala Ala Glu Asn Lys Glu	
305 310 315	
gag ctg atc gaa gcg gtc aga aaa gcg ctc ttc atg agc aaa atc tgt	1972
Glu Leu Ile Glu Ala Val Arg Lys Ala Leu Phe Met Ser Lys Ile Cys	
320 325 330	
tct tac gcc caa ggc ttt gct caa atg aaa gcc gca tca gaa gaa tac	2020
Ser Tyr Ala Gln Gly Phe Ala Gln Met Lys Ala Ala Ser Glu Glu Tyr	
335 340 345	
ggc tgg gat ttg aaa tac ggc gat atc gcg atg att ttc cgc gga gga	2068
Gly Trp Asp Leu Lys Tyr Gly Asp Ile Ala Met Ile Phe Arg Gly Gly	
350 355 360	

tgc atc atc cgc gcg gcg ttc ctg caa aaa atc aaa gaa gcg tat gac	2116
Cys Ile Ile Arg Ala Ala Phe Leu Gln Lys Ile Lys Glu Ala Tyr Asp	
365 370 375 380	
cgc gat cca gag ctt gac aac ctg ctt ctt gac ccg tac ttc aaa aat	2164
Arg Asp Pro Glu Leu Asp Asn Leu Leu Leu Asp Pro Tyr Phe Lys Asn	
385 390 395	
atc gtt gaa agc tat cag gga gcc ctc cgc aaa acg att tct ctt gcg	2212
Ile Val Glu Ser Tyr Gln Gly Ala Leu Arg Lys Thr Ile Ser Leu Ala	
400 405 410	
gtt gaa caa gga att cct gta cct tgc ttc tca agc gct ctc gct tac	2260
Val Glu Gln Gly Ile Pro Val Pro Cys Phe Ser Ser Ala Leu Ala Tyr	
415 420 425	
ttt gac agc tac cgc act gca acc ctg ccg gcc aac ctg att cag gcg	2308
Phe Asp Ser Tyr Arg Thr Ala Thr Leu Pro Ala Asn Leu Ile Gln Ala	
430 435 440	
cag cgc gac tac ttt ggc gcc cat acg tat gag cgt aca gat aaa gaa	2356
Gln Arg Asp Tyr Phe Gly Ala His Thr Tyr Glu Arg Thr Asp Lys Glu	
445 450 455 460	
ggc att ttc cac act gag tgg atg aaa taagatgtaa aaccgcaagc	2403
Gly Ile Phe His Thr Glu Trp Met Lys	
465	
tgaaaagctt gcggtttttt tgattttcgg aaggatgcat gtttaagcgg ttgtgtggaa	2463
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35 40 45

Lys Asn Val Val Gly Thr Tyr Ser Ile Glu Glu Phe Val Glu Ser Leu
50 55 60



Glu Lys Pro Arg Lys Ile Leu Leu Met Val Lys Ala Gly Thr Pro Thr  
65 70 75 80

Asp Ala Thr Ile Gln Ser Leu Leu Pro His Leu Glu Lys Gly Asp Ile  
85 90 95

Leu Ile Asp Gly Gly Asn Thr Tyr Tyr Lys Asp Thr Gln Arg Arg Asn  
100 105 110

Arg Glu Leu Ala Glu Ser Gly Ile His Phe Ile Gly Thr Gly Val Ser  
115 120 125

Gly Gly Glu Glu Gly Ala Leu Lys Gly Pro Ser Ile Met Pro Gly Gly  
130 135 140

Gln Lys Glu Ala His Glu Leu Val Lys Pro Ile Leu Glu Ala Ile Ser  
145 150 155 160

Ala Lys Val Asp Gly Glu Pro Cys Thr Thr Tyr Ile Gly Pro Asp Gly  
165 170 175

Ala Gly His Tyr Val Lys Met Val His Asn Gly Ile Glu Tyr Gly Asp  
180 185 190

Met Gln Leu Ile Ser Glu Ser Tyr Phe Ile Leu Lys His Ile Val Gly  
195 200 205

Leu Ser Ser Asp Glu Leu His Glu Val Phe Ser Glu Trp Asn Lys Gly  
210 215 220

Glu Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Asp Ile Phe Thr Lys  
225 230 235 240

Lys Asp Glu Glu Thr Gly Lys Pro Leu Val Asp Val Ile Leu Asp Lys  
245 250 255

Ala Gly Gln Lys Gly Thr Gly Lys Trp Thr Ser Gln Ser Ala Leu Asp  
260 265 270

Leu Gly Val Pro Leu Pro Ile Ile Thr Glu Ser Val Phe Ala Arg Phe  
275 280 285

Ile Ser Ser Met Lys Glu Glu Arg Val Lys Ala Ser Lys Leu Leu Ala  
 290 295 300

Gly Pro Glu Ala Lys Pro Ala Ala Glu Asn Lys Glu Glu Leu Ile Glu  
 305 310 315 320

Ala Val Arg Lys Ala Leu Phe Met Ser Lys Ile Cys Ser Tyr Ala Gln  
 325 330 335

Gly Phe Ala Gln Met Lys Ala Ala Ser Glu Glu Tyr Gly Trp Asp Leu  
 340 345 350

Lys Tyr Gly Asp Ile Ala Met Ile Phe Arg Gly Gly Cys Ile Ile Arg  
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Ala Ala Phe Leu Gln Lys Ile Lys Glu Ala Tyr Asp Arg Asp Pro Glu  
 370 375 380

Leu Asp Asn Leu Leu Leu Asp Pro Tyr Phe Lys Asn Ile Val Glu Ser  
 385 390 395 400

Tyr Gln Gly Ala Leu Arg Lys Thr Ile Ser Leu Ala Val Glu Gln Gly  
 405 410 415

Ile Pro Val Pro Cys Phe Ser Ser Ala Leu Ala Tyr Phe Asp Ser Tyr  
 420 425 430

Arg Thr Ala Thr Leu Pro Ala Asn Leu Ile Gln Ala Gln Arg Asp Tyr  
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gctaaatgat caggaaacct atcttaaaag ataggtttct ttatttttaa aatcctgttg 300  
acagcgcttc catttttgat atgataggaa agaagttaat acaagtgacg gagaatggga 360  
gattcacaat aagaccctct tgtgccaggg gtttttttgt ggatctcttt ttcttcgtca 420  
tctaagaggg ggcgaaagca atcgtaatga atagacggca cttttattct gtataacagc 480  
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Met Lys Arg Leu Val Arg Ser Ile Phe Leu Ile  
1 5 10  
acg gcc gca atc gct gct ttt ggt ttt gga ttc agc ggg cat gcg gag 581  
Thr Ala Ala Ile Ala Ala Phe Gly Phe Gly Phe Ser Gly His Ala Glu  
15 20 25  
gcg gca agc cat tcc cag ccg cag ctc aat ccg aac aag cta cta aat 629  
Ala Ala Ser His Ser Gln Pro Gln Leu Asn Pro Asn Lys Leu Leu Asn  
30 35 40  
gtc gcg cac cgc ggc gca tcg ggg cat gct ccc gag cac acg ctt ttg 677  
Val Ala His Arg Gly Ala Ser Gly His Ala Pro Glu His Thr Leu Leu  
45 50 55  
gct tat aag ctt gga caa aaa atg aaa ggc gat tac ata gaa atc gat 725  
Ala Tyr Lys Leu Gly Gln Lys Met Lys Gly Asp Tyr Ile Glu Ile Asp  
60 65 70 75  
ctt caa atg aca aaa gac ggc cac ttg gtc gcc atg cac gat gag aca 773  
Leu Gln Met Thr Lys Asp Gly His Leu Val Ala Met His Asp Glu Thr  
80 85 90  
ttg gat cgt acg act aat ggt acg ggt ttt gtc aaa gac tat acg ctg 821  
Leu Asp Arg Thr Thr Asn Gly Thr Gly Phe Val Lys Asp Tyr Thr Leu  
95 100 105  
aaa gaa atc aaa gag ctt gat gca ggc tcc tgg ttt aac gaa gca tat 869  
Lys Glu Ile Lys Glu Leu Asp Ala Gly Ser Trp Phe Asn Glu Ala Tyr  
110 115 120  
cct gag cgg gca aaa ccg gag tac gcc ggg ctg aaa gtg ccc acc ctt 917  
Pro Glu Arg Ala Lys Pro Glu Tyr Ala Gly Leu Lys Val Pro Thr Leu  
125 130 135  
gaa gaa atc atc caa aca ttc ggg aga agc gcg cgc tac tat atc gaa 965  
Glu Glu Ile Ile Gln Thr Phe Gly Arg Ser Ala Arg Tyr Tyr Ile Glu  
140 145 150 155

aca aaa tca ccg gaa gac tat gat cat atg gaa gaa aag ctc ctg gac	1013
Thr Lys Ser Pro Glu Asp Tyr Asp His Met Glu Glu Lys Leu Leu Asp	
160 165 170	
atc ctg aag caa tac aaa ttg acc gga gca gac att cat tca agc aaa	1061
Ile Leu Lys Gln Tyr Lys Leu Thr Gly Ala Asp Ile His Ser Ser Lys	
175 180 185	
gtc atc att caa tct ttt agt cct gaa agc tta aaa atc att cat aac	1109
Val Ile Ile Gln Ser Phe Ser Pro Glu Ser Leu Lys Ile Ile His Asn	
190 195 200	
gct aat cca aac att ccg cta gtg caa tta tta tgg tac gac aaa cct	1157
Ala Asn Pro Asn Ile Pro Leu Val Gln Leu Leu Trp Tyr Asp Lys Pro	
205 210 215	
gct gcc att act gac gcc gaa tta aaa caa tat caa tct tac agc gtc	1205
Ala Ala Ile Thr Asp Ala Glu Leu Lys Gln Tyr Gln Ser Tyr Ser Val	
220 225 230 235	
gga ctc ggc atg aac ttt gac cgc att ggc cgg gca tac gtg caa aag	1253
Gly Leu Gly Met Asn Phe Asp Arg Ile Gly Arg Ala Tyr Val Gln Lys	
240 245 250	
att cga cgc acc ggc atg ctg gtc cat cct tat act gtg aat aaa aaa	1301
Ile Arg Arg Thr Gly Met Leu Val His Pro Tyr Thr Val Asn Lys Lys	
255 260 265	
gaa gat atg aag cgg ctg ctc gat tgg gga gcg acc gga atg ttc acc	1349
Glu Asp Met Lys Arg Leu Leu Asp Trp Gly Ala Thr Gly Met Phe Thr	
270 275 280	
aac ttt ccg gac cgg ctg cgc gat gtt ttg cgc gaa aag aag	1391
Asn Phe Pro Asp Arg Leu Arg Asp Val Leu Arg Glu Lys Lys	
285 290 295	
taaatgaata aagaagggga ataccatggtt aaaactgttt aagccagcac cgccgattga	1451
gcggctgccg gaagatcaaa ttgattcgga atataagaaa ttcagactgc aagtttttct	1511
cggcattcttc atcggttatg cggcatacta ttttaattcgc aaaaatttct cgcttgccat	1571
gccttatttg atcgaagagg gctttttcaaa gtcggcgctc ggctttgcct tgtccgctct	1631
atccatctct tacgggctga gcaagttcgt gatggccacg atatcggacc ggagcaatcc	1691
gaggatgttc ctgcccgcg gtttgatcct ttccgctgtc atcagcctct tgatgggggt	1751
tgttcctttt ttcacctcat cgatcgccat tatgtttatc atgctgttct taaacggctg	1811
gttccagggc atgggatggc cgccgtcagg gcgtgtcctt gtccactggt tcagcgtcag	1871
cgaaagggga aataaaaccg ccatatggaa tgtcgcccac aatgtcggcg ggggactgat	1931
ggcgccgatt gccgttgccg gcgtcgccat cttctcaggc ataacgggat ctgctacagg	1991

ctatgaaggt gtgtttattt tgccggcctt ggtcgcat

2030

<210> 16  
<211> 297  
<212> PRT  
<213> *Bacillus licheniformis*

<400> 16

Met Lys Arg Leu Val Arg Ser Ile Phe Leu Ile Thr Ala Ala Ile Ala  
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Ala Phe Gly Phe Gly Phe Ser Gly His Ala Glu Ala Ala Ser His Ser  
20 25 30

Gln Pro Gln Leu Asn Pro Asn Lys Leu Leu Asn Val Ala His Arg Gly  
35 40 45

Ala Ser Gly His Ala Pro Glu His Thr Leu Leu Ala Tyr Lys Leu Gly  
50 55 60

Gln Lys Met Lys Gly Asp Tyr Ile Glu Ile Asp Leu Gln Met Thr Lys  
65 70 75 80

Asp Gly His Leu Val Ala Met His Asp Glu Thr Leu Asp Arg Thr Thr  
85 90 95

Asn Gly Thr Gly Phe Val Lys Asp Tyr Thr Leu Lys Glu Ile Lys Glu  
100 105 110

Leu Asp Ala Gly Ser Trp Phe Asn Glu Ala Tyr Pro Glu Arg Ala Lys  
115 120 125

Pro Glu Tyr Ala Gly Leu Lys Val Pro Thr Leu Glu Glu Ile Ile Gln  
130 135 140

Thr Phe Gly Arg Ser Ala Arg Tyr Tyr Ile Glu Thr Lys Ser Pro Glu  
145 150 155 160

Asp Tyr Asp His Met Glu Glu Lys Leu Leu Asp Ile Leu Lys Gln Tyr  
165 170 175

Lys Leu Thr Gly Ala Asp Ile His Ser Ser Lys Val Ile Ile Gln Ser  
180 185 190

Phe Ser Pro Glu Ser Leu Lys Ile Ile His Asn Ala Asn Pro Asn Ile  
 195 200 205

Pro Leu Val Gln Leu Leu Trp Tyr Asp Lys Pro Ala Ala Ile Thr Asp  
 210 215 220

Ala Glu Leu Lys Gln Tyr Gln Ser Tyr Ser Val Gly Leu Gly Met Asn  
 225 230 235 240

Phe Asp Arg Ile Gly Arg Ala Tyr Val Gln Lys Ile Arg Arg Thr Gly  
 245 250 255

Met Leu Val His Pro Tyr Thr Val Asn Lys Lys Glu Asp Met Lys Arg  
 260 265 270

Leu Leu Asp Trp Gly Ala Thr Gly Met Phe Thr Asn Phe Pro Asp Arg  
 275 280 285

Leu Arg Asp Val Leu Arg Glu Lys Lys  
 290 295

<210> 17  
 <211> 2308  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1814)

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 acgccggatt ggcgcgcttc tgacaattga acgggagacg ggaatgggcg attacataga 120  
 aacggggatc cctttgaatg caaaggtcag ctctgagcta ttgatcaaca tctttattcc 180  
 gaacactccg cttcatgacg gagccgtgat tatgaaaaac gatgaggttg ctgcagctgc 240  
 ctgctacctt ccgctttctg aaagcccttt tatttcaaaa gagcttggaa cgaggcacag 300  
 agcagcagtg ggaatcagtg aagtgaccga cagtctgacg gttgttgtat ccgaagagac 360  
 gggcggcatc agcgtcgcca aaaacggaga ccttcaccgt gatttatcgg aagaggcatt 420  
 gaaaaatatg cttgaagcgg aatttaagaa aaattcgcg gaaacttcct caaatcgctg 480  
 gtattggagg gcgaagaaaa atg gat aag ttc tta aac aat ccc tgg gct gtc 533

Met Asp Lys Phe Leu Asn Asn Pro Trp Ala Val  
 1 5 10

aaa gtt gtc gcg tta ttg ttc gcg ttt ctt ctt tac ttt gcg gtc cac	581
Lys Val Val Ala Leu Leu Phe Ala Phe Leu Leu Tyr Phe Ala Val His	
15 20 25	
agc gct cag gcg ccg act ccg aag aaa cca ggt gaa tcg ttt ttc ccg	629
Ser Ala Gln Ala Pro Thr Pro Lys Lys Pro Gly Glu Ser Phe Phe Pro	
30 35 40	
aca tcg aca aca gac gaa gcg acg ctc acc gat ata ccg gtc aaa tcg	677
Thr Ser Thr Thr Asp Glu Ala Thr Leu Thr Asp Ile Pro Val Lys Ser	
45 50 55	
ttt tat gat gat gaa aac tac gtc gta aca ggc gtg ccg cag acg gtg	725
Phe Tyr Asp Asp Glu Asn Tyr Val Val Thr Gly Val Pro Gln Thr Val	
60 65 70 75	
aat gtc acg att aaa ggc ccg acc gga acc gtc aag aag gtc aga caa	773
Asn Val Thr Ile Lys Gly Pro Thr Gly Thr Val Lys Lys Val Arg Gln	
80 85 90	
gtg aag gat ttt gag att tat gcc gac atg caa aac ctg aaa aca ggc	821
Val Lys Asp Phe Glu Ile Tyr Ala Asp Met Gln Asn Leu Lys Thr Gly	
95 100 105	
agg cat aaa gtc gag ctg aag gcc aga aat gtt gcc gac ggc ctc act	869
Arg His Lys Val Glu Leu Lys Ala Arg Asn Val Ala Asp Gly Leu Thr	
110 115 120	
ctg acc atc aat cca tcg gtg aca acc gtg acg atc gaa gaa aaa acg	917
Leu Thr Ile Asn Pro Ser Val Thr Thr Val Thr Ile Glu Glu Lys Thr	
125 130 135	
acg aag gaa ttc ccg gtc gag gtt gat ttt tat aat aaa aac aaa atg	965
Thr Lys Glu Phe Pro Val Glu Val Asp Phe Tyr Asn Lys Asn Lys Met	
140 145 150 155	
aaa gac ggc tac acg ccg gag ctg ccg atc atc aac ccg aaa aac gtc	1013
Lys Asp Gly Tyr Thr Pro Glu Leu Pro Ile Ile Asn Pro Lys Asn Val	
160 165 170	
agc gtc acc ggc tca aaa gcc gtg atc gac aga atc cag aac atc aag	1061
Ser Val Thr Gly Ser Lys Ala Val Ile Asp Arg Ile Gln Asn Ile Lys	
175 180 185	
gcg acg atc aat tta gag ggc gtc gac cag acg gtt gaa aaa gaa gcc	1109
Ala Thr Ile Asn Leu Glu Gly Val Asp Gln Thr Val Glu Lys Glu Ala	
190 195 200	
aag ctt aca gta tac gac aag gac gga aat gtc ctg ccg gtt gaa gtc	1157
Lys Leu Thr Val Tyr Asp Lys Asp Gly Asn Val Leu Pro Val Glu Val	
205 210 215	
agc cct tcc gtc gtt aaa atc acc gtt ccg gtg acg agc ccg agc aaa	1205
Ser Pro Ser Val Val Lys Ile Thr Val Pro Val Thr Ser Pro Ser Lys	

220	225	230	235	
aag att ccg gtc aaa gtt gac cgg aaa ggc agc ctt ccg gac ggc atc				1253
Lys Ile Pro Val Lys Val Asp Arg Lys Gly Ser Leu Pro Asp Gly Ile				
240	245	250		
agc att tcc agc ctc gat ata agt ccg gga gag gtg acc gtc tac ggg				1301
Ser Ile Ser Ser Leu Asp Ile Ser Pro Gly Glu Val Thr Val Tyr Gly				
255	260	265		
ccg caa aat gtt ctt gat tcg tta gaa ttt gtc gag gcc gac gag att				1349
Pro Gln Asn Val Leu Asp Ser Leu Glu Phe Val Glu Ala Asp Glu Ile				
270	275	280		
gat tta agt aaa ata aag gat gat act gaa ttg gaa gcc ggc att aaa				1397
Asp Leu Ser Lys Ile Lys Asp Asp Thr Glu Leu Glu Ala Gly Ile Lys				
285	290	295		
gtg ccg gac ggc gct aaa aag gtg tca ccc gaa aaa gtg aaa atc aag				1445
Val Pro Asp Gly Ala Lys Lys Val Ser Pro Glu Lys Val Lys Ile Lys				
300	305	310	315	
gtg aaa gtt gac aag gaa gaa gag aaa aaa ctg aaa aac gtt tca att				1493
Val Lys Val Asp Lys Glu Glu Glu Lys Lys Leu Lys Asn Val Ser Ile				
320	325	330		
aaa acc gcg ggg ctg aat gac agc cgg gat ctt gaa ttt ctc gat ccg				1541
Lys Thr Ala Gly Leu Asn Asp Ser Arg Asp Leu Glu Phe Leu Asp Pro				
335	340	345		
aag tca ggc aag ctg gat atc acg gca aag ggc tcg aca gcc gcg atc				1589
Lys Ser Gly Lys Leu Asp Ile Thr Ala Lys Gly Ser Thr Ala Ala Ile				
350	355	360		
gaa aaa ctc cag cct tcc gac gtc gag ctc tat gtc aat gtg gcg gat				1637
Glu Lys Leu Gln Pro Ser Asp Val Glu Leu Tyr Val Asn Val Ala Asp				
365	370	375		
ctc gat gac ggc gag cac aat gta aag ctg gaa gta aac ggt ccg cag				1685
Leu Asp Asp Gly Glu His Asn Val Lys Leu Glu Val Asn Gly Pro Gln				
380	385	390	395	
aac atg aca tgg tcg ctg ccg cgg caa agc att cga gtg aaa atc tca				1733
Asn Met Thr Trp Ser Leu Pro Arg Gln Ser Ile Arg Val Lys Ile Ser				
400	405	410		
tct caa aca acc caa aac gaa aaa aac aat ggt cag gat gaa gaa gaa				1781
Ser Gln Thr Thr Gln Asn Glu Lys Asn Asn Gly Gln Asp Glu Glu Glu				
415	420	425		
gag aat cat tct gaa aag gat tca caa cct tca tgaatcaaaa aggagcgata				1834
Glu Asn His Ser Glu Lys Asp Ser Gln Pro Ser				
430	435			
ttaatgggca agtatttttg tacagacggt gtaagaggcg tggcaaacag tgaacttaca				1894
cctgagctgg cctttaagt cggacgcttt ggcggatatg tcctaacaaa agataaggag				1954



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 cttgtagcag gccttctttc gataggagca gaagtcatgc gtctcggcgt gatttcgacg 2074  
 cccggagtcg catatttgac gaaggctatg gacgcggagg cgggtgtgat gatttccgct 2134  
 tcccacaacc ctgtccagga caacggaatt aagtttttcg gcggcgacgg ctttaagctt 2194  
 tccgatgaac aggagcttga aatcgagcgt ctgatggatc agccggaaga tcacctgcca 2254  
 aggctgtag gcgctgatct gggcatgggtg aacgactact ttgaaggcgg acag 2308

<210> 18  
 <211> 438  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 18

Met Asp Lys Phe Leu Asn Asn Pro Trp Ala Val Lys Val Val Ala Leu  
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Leu Phe Ala Phe Leu Leu Tyr Phe Ala Val His Ser Ala Gln Ala Pro  
 20 25 30

Thr Pro Lys Lys Pro Gly Glu Ser Phe Phe Pro Thr Ser Thr Thr Asp  
 35 40 45

Glu Ala Thr Leu Thr Asp Ile Pro Val Lys Ser Phe Tyr Asp Asp Glu  
 50 55 60

Asn Tyr Val Val Thr Gly Val Pro Gln Thr Val Asn Val Thr Ile Lys  
 65 70 75 80

Gly Pro Thr Gly Thr Val Lys Lys Val Arg Gln Val Lys Asp Phe Glu  
 85 90 95

Ile Tyr Ala Asp Met Gln Asn Leu Lys Thr Gly Arg His Lys Val Glu  
 100 105 110

Leu Lys Ala Arg Asn Val Ala Asp Gly Leu Thr Leu Thr Ile Asn Pro  
 115 120 125

Ser Val Thr Thr Val Thr Ile Glu Glu Lys Thr Thr Lys Glu Phe Pro  
 130 135 140

Val Glu Val Asp Phe Tyr Asn Lys Asn Lys Met Lys Asp Gly Tyr Thr  
 145 150 155 160

Pro Glu Leu Pro Ile Ile Asn Pro Lys Asn Val Ser Val Thr Gly Ser  
 165 170 175

Lys Ala Val Ile Asp Arg Ile Gln Asn Ile Lys Ala Thr Ile Asn Leu  
 180 185 190

Glu Gly Val Asp Gln Thr Val Glu Lys Glu Ala Lys Leu Thr Val Tyr  
 195 200 205

Asp Lys Asp Gly Asn Val Leu Pro Val Glu Val Ser Pro Ser Val Val  
 210 215 220

Lys Ile Thr Val Pro Val Thr Ser Pro Ser Lys Lys Ile Pro Val Lys  
 225 230 235 240

Val Asp Arg Lys Gly Ser Leu Pro Asp Gly Ile Ser Ile Ser Ser Leu  
 245 250 255

Asp Ile Ser Pro Gly Glu Val Thr Val Tyr Gly Pro Gln Asn Val Leu  
 260 265 270

Asp Ser Leu Glu Phe Val Glu Ala Asp Glu Ile Asp Leu Ser Lys Ile  
 275 280 285

Lys Asp Asp Thr Glu Leu Glu Ala Gly Ile Lys Val Pro Asp Gly Ala  
 290 295 300

Lys Lys Val Ser Pro Glu Lys Val Lys Ile Lys Val Lys Val Asp Lys  
 305 310 315 320

Glu Glu Glu Lys Lys Leu Lys Asn Val Ser Ile Lys Thr Ala Gly Leu  
 325 330 335

Asn Asp Ser Arg Asp Leu Glu Phe Leu Asp Pro Lys Ser Gly Lys Leu  
 340 345 350

Asp Ile Thr Ala Lys Gly Ser Thr Ala Ala Ile Glu Lys Leu Gln Pro  
 355 360 365

Ser Asp Val Glu Leu Tyr Val Asn Val Ala Asp Leu Asp Asp Gly Glu

370

375

380

His Asn Val Lys Leu Glu Val Asn Gly Pro Gln Asn Met Thr Trp Ser  
 385 390 395 400

Leu Pro Arg Gln Ser Ile Arg Val Lys Ile Ser Ser Gln Thr Thr Gln  
 405 410 415

Asn Glu Lys Asn Asn Gly Gln Asp Glu Glu Glu Glu Asn His Ser Glu  
 420 425 430

Lys Asp Ser Gln Pro Ser  
 435

<210> 19  
 <211> 2632  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (852)..(2606)

<400> 19  
 atatgtttta atgaagaaaa tctccaggcc gctcttcggt ttcagatata aatgtcagcg 60  
 cgtcgccagc ctggcggttc gatttattgt gagttgaaac atcgccgagc gtaatgatgc 120  
 cggcaagcgt ttttccccgt gtaaccggga cccttctgat ctgataatct cccatgagat 180  
 cgaccgcttt tcaatgaatg tttacactta ccgtaatgat agaagggccc tttggatatg 240  
 aacgattcat cgaagcgatc ccgtcttata aagaagtgtt tggcacagac gaaaagggtgt 300  
 ggacaaaagc atcgccgctc tcatacataa acaactcaaa attgccgccg gcctatcttg 360  
 tgaccgcgtg ggaagaccct gccgtttaca agttcgcgga aaccgcaaac aaagcgaagg 420  
 caacggaatt tgtgtatcaa gtcaacagct tatctcacag tgatttaaac aagatgttcg 480  
 gctctccaga tgcaccggca gaagcgcaga atctgacaaa agcggttatg gcgttttttag 540  
 agaaggaaaa taaatagatc aaacggccga ctcggttcc tacatgtact tgctgaaagg 600  
 atataaacag ctgttaaact agcagagaaa ggccgaaaat gttaaattcg gcctcttctc 660  
 acacttgga ccccttact cataagacat cgatctgaaa attcccaaaa tataaacaaa 720  
 acattaataa aatcaagcca tttgattaac aaatttacga tacgatcata tagaacttga 780  
 tgattgggaa aagcattttg agagaagatt aagagcaagg gagatatgat gtgagaatga 840

aacgattaag g atg agg aag cat tta ctg ata gct gtc tgt act ttg gca	890
Met Arg Lys His Leu Leu Ile Ala Val Cys Thr Leu Ala	
1 5 10	
ctt ctt cta agt tcc ccg att gta agc gat gcg agc ccg gca act aaa	938
Leu Leu Leu Ser Ser Pro Ile Val Ser Asp Ala Ser Pro Ala Thr Lys	
15 20 25	
cca aca act gca gat tcg ccg caa tct tcc gga ttt ttc gta gac cat	986
Pro Thr Thr Ala Asp Ser Pro Gln Ser Ser Gly Phe Phe Val Asp His	
30 35 40 45	
tac aaa aat aat atc tct gcc aat acg acg gcg gaa tcc aat cct gtc	1034
Tyr Lys Asn Asn Ile Ser Ala Asn Thr Thr Ala Glu Ser Asn Pro Val	
50 55 60	
atc ggc ctg ctt tcc gaa ttt aat aaa ctt tgg act ccc gga aag aca	1082
Ile Gly Leu Leu Ser Glu Phe Asn Lys Leu Trp Thr Pro Gly Lys Thr	
65 70 75	
tgg aat acc ggt act aaa ctg aac agc agg gtg ctg gat gcc aac att	1130
Trp Asn Thr Gly Thr Lys Leu Asn Ser Arg Val Leu Asp Ala Asn Ile	
80 85 90	
caa aaa gtc gtg gat att gct gaa cgc cgc acg atg ctt gag gaa aat	1178
Gln Lys Val Val Asp Ile Ala Glu Arg Arg Thr Met Leu Glu Glu Asn	
95 100 105	
gct gcc tat ttt gat gat cgg cgg agc cag agc tac agt ata att gac	1226
Ala Ala Tyr Phe Asp Asp Arg Arg Ser Gln Ser Tyr Ser Ile Ile Asp	
110 115 120 125	
ggc ctc ggc aag ctt gcc ggc gtc tat cga atg aac gcg gga gcg acg	1274
Gly Leu Gly Lys Leu Ala Gly Val Tyr Arg Met Asn Ala Gly Ala Thr	
130 135 140	
aca acg atc acc agc att ccg gca gat gcc tcg att aga aaa tac aat	1322
Thr Thr Ile Thr Ser Ile Pro Ala Asp Ala Ser Ile Arg Lys Tyr Asn	
145 150 155	
gat gaa gga acc aat tcg ggc agc acc agc tct gaa ctt gga aat gtc	1370
Asp Glu Gly Thr Asn Ser Gly Ser Thr Ser Ser Glu Leu Gly Asn Val	
160 165 170	
gta agt ttg gtc aat act tta cgc ggc aac tat tct tca tcg aat ccg	1418
Val Ser Leu Val Asn Thr Leu Arg Gly Asn Tyr Ser Ser Ser Asn Pro	
175 180 185	
gct aaa agc tat ttc aac tat ccc cgc ccg ttt cgc tgg aaa gac aat	1466
Ala Lys Ser Tyr Phe Asn Tyr Pro Arg Pro Phe Arg Trp Lys Asp Asn	
190 195 200 205	
tcg atc att gtt cca acg ctt atc ccc gtc atc aat cct gat ccg aac	1514
Ser Ile Ile Val Pro Thr Leu Ile Pro Val Ile Asn Pro Asp Pro Asn	
210 215 220	

aaa gac gga ggt ttt cca agc gga cac acg aac gcc gca tat ctc agc Lys Asp Gly Gly Phe Pro Ser Gly His Thr Asn Ala Ala Tyr Leu Ser 225 230 235	1562
gct ttt gct atg gcc tat gcg ata ccg gag cgt tat cag gag ctg ctg Ala Phe Ala Met Ala Tyr Ala Ile Pro Glu Arg Tyr Gln Glu Leu Leu 240 245 250	1610
act cgc gct tca gaa ctc ggt cat aac cgg att gtt gcc ggt atg cat Thr Arg Ala Ser Glu Leu Gly His Asn Arg Ile Val Ala Gly Met His 255 260 265	1658
tcc ccg ctg gac gtc atg ggg gga cga gta atg gca aca gct ttg tct Ser Pro Leu Asp Val Met Gly Gly Arg Val Met Ala Thr Ala Leu Ser 270 275 280 285	1706
gca gca atc ctg tct gac ccc gca aat gaa aga ttg aag aaa acg gct Ala Ala Ile Leu Ser Asp Pro Ala Asn Glu Arg Leu Lys Lys Thr Ala 290 295 300	1754
ttt gat gaa gcc cgc cgt aaa tta tta acg caa acc ggt aca gct gaa Phe Asp Glu Ala Arg Arg Lys Leu Leu Thr Gln Thr Gly Thr Ala Glu 305 310 315	1802
gac aga tac agc gat tat gag aag aat aaa aaa caa tat acg gaa cga Asp Arg Tyr Ser Asp Tyr Glu Lys Asn Lys Lys Gln Tyr Thr Glu Arg 320 325 330	1850
ttg aca tat gga ttt cga caa atg aac aaa acc gcc aaa cca atg gca Leu Thr Tyr Gly Phe Arg Gln Met Asn Lys Thr Ala Lys Pro Met Ala 335 340 345	1898
gtt cca aag gga gcc gaa gtc ctg ctg gaa aca cgt ttt cct tac ctt Val Pro Lys Gly Ala Glu Val Leu Leu Glu Thr Arg Phe Pro Tyr Leu 350 355 360 365	1946
gac aaa aag cag cgc cgt tcg gtt tta gcc act acc ggt ctt ccg gcc Asp Lys Lys Gln Arg Arg Ser Val Leu Ala Thr Thr Gly Leu Pro Ala 370 375 380	1994
ggc tac cct gtt ctt gat gat cga gaa gga tgg gga agg ctt aat ctc Gly Tyr Pro Val Leu Asp Asp Arg Glu Gly Trp Gly Arg Leu Asn Leu 385 390 395	2042
ttt tcc gcg gca gat ggg tat ggg gct ttt acc aaa aat gtt acc gtg Phe Ser Ala Ala Asp Gly Tyr Gly Ala Phe Thr Lys Asn Val Thr Val 400 405 410	2090
acc atg gat tcc gca aaa ggc ggc ttc cat aca gcc gat cgc tgg cgc Thr Met Asp Ser Ala Lys Gly Gly Phe His Thr Ala Asp Arg Trp Arg 415 420 425	2138
aac gac atc tcc ggc acc gga aag ctg acc aaa aaa ggg aca ggc gct Asn Asp Ile Ser Gly Thr Gly Lys Leu Thr Lys Lys Gly Thr Gly Ala 430 435 440 445	2186
ttg aag ctg gaa ggg gat aat aca tat tcc ggc ggt aca cgg att gat	2234

Leu	Lys	Leu	Glu	Gly	Asp	Asn	Thr	Tyr	Ser	Gly	Gly	Thr	Arg	Ile	Asp	
				450					455					460		
caa	gga	aca	ctt	gag	ggc	ggg	tcg	gag	aca	gct	ttc	ggg	aga	ggg	gat	2282
Gln	Gly	Thr	Leu	Glu	Gly	Gly	Ser	Glu	Thr	Ala	Phe	Gly	Arg	Gly	Asp	
			465					470					475			
gtt	gca	cta	aac	gga	ggc	atc	ctt	aag	gaa	gat	gcg	ccg	gga	aaa	ctg	2330
Val	Ala	Leu	Asn	Gly	Gly	Ile	Leu	Lys	Glu	Asp	Ala	Pro	Gly	Lys	Leu	
			480					485					490			
atc	atc	gaa	gga	gac	tac	aaa	caa	tct	gct	aaa	gga	ata	ctt	gaa	ctt	2378
Ile	Ile	Glu	Gly	Asp	Tyr	Lys	Gln	Ser	Ala	Lys	Gly	Ile	Leu	Glu	Leu	
			495				500					505				
cag	ctc	agc	ggc	aaa	aaa	gat	cag	ttg	aaa	att	aag	gga	aaa	gca	aga	2426
Gln	Leu	Ser	Gly	Lys	Lys	Asp	Gln	Leu	Lys	Ile	Lys	Gly	Lys	Ala	Arg	
					515					520					525	
ttg	aaa	ggg	aca	ttg	cgt	ctc	aat	ttt	acg	gac	aat	tac	gta	ccg	gct	2474
Leu	Lys	Gly	Thr	Leu	Arg	Leu	Asn	Phe	Thr	Asp	Asn	Tyr	Val	Pro	Ala	
				530						535					540	
gac	gga	tcg	gcg	atc	ata	acc	ttc	cgc	aag	cgt	cat	gga	tca	ttt	tct	2522
Asp	Gly	Ser	Ala	Ile	Ile	Thr	Phe	Arg	Lys	Arg	His	Gly	Ser	Phe	Ser	
				545					550					555		
tcc	gtc	gag	acc	agt	gga	ttg	cca	agc	aag	tat	aaa	gtg	aag	atc	atc	2570
Ser	Val	Glu	Thr	Ser	Gly	Leu	Pro	Ser	Lys	Tyr	Lys	Val	Lys	Ile	Ile	
			560					565					570			
tat	aaa	tcc	aac	agt	att	cag	ttg	aaa	gtt	gag	caa	aaggggagaa				2616
Tyr	Lys	Ser	Asn	Ser	Ile	Gln	Leu	Lys	Val	Glu	Gln					
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Ser	Ser	Pro	Ile	Val	Ser	Asp	Ala	Ser	Pro	Ala	Thr	Lys	Pro	Thr	Thr
			20					25					30		

Ala	Asp	Ser	Pro	Gln	Ser	Ser	Gly	Phe	Phe	Val	Asp	His	Tyr	Lys	Asn
			35				40						45		

Asn Ile Ser Ala Asn Thr Thr Ala Glu Ser Asn Pro Val Ile Gly Leu  
 50 55 60

Leu Ser Glu Phe Asn Lys Leu Trp Thr Pro Gly Lys Thr Trp Asn Thr  
 65 70 75 80

Gly Thr Lys Leu Asn Ser Arg Val Leu Asp Ala Asn Ile Gln Lys Val  
 85 90 95

Val Asp Ile Ala Glu Arg Arg Thr Met Leu Glu Glu Asn Ala Ala Tyr  
 100 105 110

Phe Asp Asp Arg Arg Ser Gln Ser Tyr Ser Ile Ile Asp Gly Leu Gly  
 115 120 125

Lys Leu Ala Gly Val Tyr Arg Met Asn Ala Gly Ala Thr Thr Thr Ile  
 130 135 140

Thr Ser Ile Pro Ala Asp Ala Ser Ile Arg Lys Tyr Asn Asp Glu Gly  
 145 150 155 160

Thr Asn Ser Gly Ser Thr Ser Ser Glu Leu Gly Asn Val Val Ser Leu  
 165 170 175

Val Asn Thr Leu Arg Gly Asn Tyr Ser Ser Ser Asn Pro Ala Lys Ser  
 180 185 190

Tyr Phe Asn Tyr Pro Arg Pro Phe Arg Trp Lys Asp Asn Ser Ile Ile  
 195 200 205

Val Pro Thr Leu Ile Pro Val Ile Asn Pro Asp Pro Asn Lys Asp Gly  
 210 215 220

Gly Phe Pro Ser Gly His Thr Asn Ala Ala Tyr Leu Ser Ala Phe Ala  
 225 230 235 240

Met Ala Tyr Ala Ile Pro Glu Arg Tyr Gln Glu Leu Leu Thr Arg Ala  
 245 250 255

Ser Glu Leu Gly His Asn Arg Ile Val Ala Gly Met His Ser Pro Leu  
 260 265 270

Asp Val Met Gly Gly Arg Val Met Ala Thr Ala Leu Ser Ala Ala Ile

275

280

285

Leu Ser Asp Pro Ala Asn Glu Arg Leu Lys Lys Thr Ala Phe Asp Glu  
 290 295 300

Ala Arg Arg Lys Leu Leu Thr Gln Thr Gly Thr Ala Glu Asp Arg Tyr  
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Ser Asp Tyr Glu Lys Asn Lys Lys Gln Tyr Thr Glu Arg Leu Thr Tyr  
 325 330 335

Gly Phe Arg Gln Met Asn Lys Thr Ala Lys Pro Met Ala Val Pro Lys  
 340 345 350

Gly Ala Glu Val Leu Leu Glu Thr Arg Phe Pro Tyr Leu Asp Lys Lys  
 355 360 365

Gln Arg Arg Ser Val Leu Ala Thr Thr Gly Leu Pro Ala Gly Tyr Pro  
 370 375 380

Val Leu Asp Asp Arg Glu Gly Trp Gly Arg Leu Asn Leu Phe Ser Ala  
 385 390 395 400

Ala Asp Gly Tyr Gly Ala Phe Thr Lys Asn Val Thr Val Thr Met Asp  
 405 410 415

Ser Ala Lys Gly Gly Phe His Thr Ala Asp Arg Trp Arg Asn Asp Ile  
 420 425 430

Ser Gly Thr Gly Lys Leu Thr Lys Lys Gly Thr Gly Ala Leu Lys Leu  
 435 440 445

Glu Gly Asp Asn Thr Tyr Ser Gly Gly Thr Arg Ile Asp Gln Gly Thr  
 450 455 460

Leu Glu Gly Gly Ser Glu Thr Ala Phe Gly Arg Gly Asp Val Ala Leu  
 465 470 475 480

Asn Gly Gly Ile Leu Lys Glu Asp Ala Pro Gly Lys Leu Ile Ile Glu  
 485 490 495

Gly Asp Tyr Lys Gln Ser Ala Lys Gly Ile Leu Glu Leu Gln Leu Ser  
 500 505 510



Gly Lys Lys Asp Gln Leu Lys Ile Lys Gly Lys Ala Arg Leu Lys Gly  
 515 520 525

Thr Leu Arg Leu Asn Phe Thr Asp Asn Tyr Val Pro Ala Asp Gly Ser  
 530 535 540

Ala Ile Ile Thr Phe Arg Lys Arg His Gly Ser Phe Ser Ser Val Glu  
 545 550 555 560

Thr Ser Gly Leu Pro Ser Lys Tyr Lys Val Lys Ile Ile Tyr Lys Ser  
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Asn Ser Ile Gln Leu Lys Val Glu Gln  
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 ttccacggta tgagaacgct cccttctttt aatctatttt ttattttaatt aaattgtagg 180  
 ttgtaagcca gtcaataaca ttgttcactt tcaacaaaaa caaaagtaac attatacatt 240  
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 tttaaaacta acttggagta cccaatttaa cttcccgaat aaacaggaag cttcacaat 360  
 gttgatataa cagtgttttt aacgttttaa aaactaaagg tgcattgacaa ggcaccttaa 420  
 gataagcttt ctttctcttt gaaaattcaa aaatcctccg atatatatag cgaacgccgc 480  
 taaaaaagga ggagagccgg atg aaa aag tta tgg aaa atc gcg gtt tcg gct 533  
 Met Lys Lys Leu Trp Lys Ile Ala Val Ser Ala  
 1 5 10  
 gca atg ttc gtc ggt ttt ttc gca aat tca ccc cgc att caa gcg gaa 581  
 Ala Met Phe Val Gly Phe Phe Ala Asn Ser Pro Arg Ile Gln Ala Glu  
 15 20 25

agc aat aag cag gaa aac gag gtc att gtt gta tat aaa aat acc agc Ser Asn Lys Gln Glu Asn Glu Val Ile Val Val Tyr Lys Asn Thr Ser 30 35 40	629
gga aaa gaa acc gtc atc gaa cag gca gac acg gta gaa cac gtt tac Gly Lys Glu Thr Val Ile Glu Gln Ala Asp Thr Val Glu His Val Tyr 45 50 55	677
cgg cac att ccc gca gcc gct gtc act gcg gac gac aaa aca gtg cgc Arg His Ile Pro Ala Ala Ala Val Thr Ala Asp Asp Lys Thr Val Arg 60 65 70 75	725
gaa ctt gaa cac gat ccc gac gtc ctg tat gtc gaa gac aac ctc ccg Glu Leu Glu His Asp Pro Asp Val Leu Tyr Val Glu Asp Asn Leu Pro 80 85 90	773
gta gct gct gcc gac agc acc gct cta aaa gct ttc tcc agc agc aca Val Ala Ala Ala Asp Ser Thr Ala Leu Lys Ala Phe Ser Ser Ser Thr 95 100 105	821
gcg caa aac gcc tcc gcg ttt tca cag tgg aac atc aag ctg att caa Ala Gln Asn Ala Ser Ala Phe Ser Gln Trp Asn Ile Lys Leu Ile Gln 110 115 120	869
gcc gca ctg gct tgg aat aaa ggt ttg acc gga aaa cag gtg aag atc Ala Ala Leu Ala Trp Asn Lys Gly Leu Thr Gly Lys Gln Val Lys Ile 125 130 135	917
gcg gtt att gac agc ggg att tcc ccc cat gag gag ctg tcg atc gcc Ala Val Ile Asp Ser Gly Ile Ser Pro His Glu Glu Leu Ser Ile Ala 140 145 150 155	965
ggc ggt gca tcg atg gtc ggc tat acc gct tca tac cgt gac gat aat Gly Gly Ala Ser Met Val Gly Tyr Thr Ala Ser Tyr Arg Asp Asp Asn 160 165 170	1013
ggc cac gga acc cat gtt gcc gga atc atc gga gcg aag cat aac gga Gly His Gly Thr His Val Ala Gly Ile Ile Gly Ala Lys His Asn Gly 175 180 185	1061
cgg ggg atc gac ggc atc gcg ccc ggc gcg cag ctg tat gcc gta aaa Arg Gly Ile Asp Gly Ile Ala Pro Gly Ala Gln Leu Tyr Ala Val Lys 190 195 200	1109
gcg ctg gac cgg aat ggt gcg ggg gat ctg aaa ggt atc tta caa ggc Ala Leu Asp Arg Asn Gly Ala Gly Asp Leu Lys Gly Ile Leu Gln Gly 205 210 215	1157
atc gat tgg tcg atc caa cac gga atc gat atc atc aat atg agc ctc Ile Asp Trp Ser Ile Gln His Gly Ile Asp Ile Ile Asn Met Ser Leu 220 225 230 235	1205
gtc gtt tca ggc gac agt caa gtt ctc cac gat gcg gta gat aaa gca Val Val Ser Gly Asp Ser Gln Val Leu His Asp Ala Val Asp Lys Ala 240 245 250	1253
tac aaa cgg gga atc att tta gtc gga gcg agc gga aat gcc gga aac	1301

Tyr	Lys	Arg	Gly	Ile	Ile	Leu	Val	Gly	Ala	Ser	Gly	Asn	Ala	Gly	Asn	
			255					260					265			
gga	aaa	tcc	gtt	tat	tac	ccg	gcc	gcc	tac	agc	agc	gtc	att	gcc	gtc	1349
Gly	Lys	Ser	Val	Tyr	Tyr	Pro	Ala	Ala	Tyr	Ser	Ser	Val	Ile	Ala	Val	
		270					275					280				
tcg	gca	acc	aat	gaa	aaa	aat	cag	atc	gcc	tca	ttt	acc	aac	acc	cgg	1397
Ser	Ala	Thr	Asn	Glu	Lys	Asn	Gln	Ile	Ala	Ser	Phe	Thr	Asn	Thr	Arg	
	285					290					295					
agc	gcc	gta	tcg	tat	tcc	gct	ccg	agc	aca	tct	att	atc	aat	aca	tcg	1445
Ser	Ala	Val	Ser	Tyr	Ser	Ala	Pro	Ser	Thr	Ser	Ile	Ile	Asn	Thr	Ser	
300					305					310					315	
ggc	aat	cgc	gga	tat	gca	atc	gga	agc	tgc	act	gca	caa	ggg	aca	ccc	1493
Gly	Asn	Arg	Gly	Tyr	Ala	Ile	Gly	Ser	Cys	Thr	Ala	Gln	Gly	Thr	Pro	
			320					325					330			
gac	gtc	acc	tgc	gtg	atc	gca	ctt	atg	aaa	cag	ctg	cac	cca	acc	gct	1541
Asp	Val	Thr	Cys	Val	Ile	Ala	Leu	Met	Lys	Gln	Leu	His	Pro	Thr	Ala	
			335					340					345			
tca	aat	gct	gag	ctg	cgc	aag	aaa	atg	cag	ttt	tat	aca	agc	gat	ttg	1589
Ser	Asn	Ala	Glu	Leu	Arg	Lys	Lys	Met	Gln	Phe	Tyr	Thr	Ser	Asp	Leu	
		350					355					360				
ggc	gct	ccc	ggg	cgt	gat	cat	ttg	ttc	ggc	tac	cga	tta	atc	cgc	ttc	1637
Gly	Ala	Pro	Gly	Arg	Asp	His	Leu	Phe	Gly	Tyr	Arg	Leu	Ile	Arg	Phe	
	365					370					375					
aaa	gag	gtc	aca	cag	cca	ttg	gaa	aaa	gcg	caa	aaa	gcc	gtc	gga	caa	1685
Lys	Glu	Val	Thr	Gln	Pro	Leu	Glu	Lys	Ala	Gln	Lys	Ala	Val	Gly	Gln	
380					385					390					395	
gcg	gaa	aag	aca	aag	aaa	aaa	gcg	gac	att	caa	acc	gca	caa	aaa	gcg	1733
Ala	Glu	Lys	Thr	Lys	Lys	Lys	Ala	Asp	Ile	Gln	Thr	Ala	Gln	Lys	Ala	
			400					405					410			
atc	gaa	ccg	ctc	cct	gca	gac	gca	gat	aaa	ccc	gct	ttg	aaa	aag	aga	1781
Ile	Glu	Pro	Leu	Pro	Ala	Asp	Ala	Asp	Lys	Pro	Ala	Leu	Lys	Lys	Arg	
			415					420					425			
ctc	aat	act	gtt	aaa	gag	cag	ctt	aaa	aaa	aca	gcc	gaa	agc	aaa	gtg	1829
Leu	Asn	Thr	Val	Lys	Glu	Gln	Leu	Lys	Lys	Thr	Ala	Glu	Ser	Lys	Val	
		430					435					440				
aaa	ctc	gct	gag	aag	caa	aaa	aag	aaa	acc	aat	gcc	gac	tcc	gcc	caa	1877
Lys	Leu	Ala	Glu	Lys	Gln	Lys	Lys	Lys	Thr	Asn	Ala	Asp	Ser	Ala	Gln	
	445					450					455					
aaa	gcg	gtc	aac	gaa	ctc	gac	agc	ggc	act	ttc	aaa	acg	aat	ttg	caa	1925
Lys	Ala	Val	Asn	Glu	Leu	Asp	Ser	Gly	Thr	Phe	Lys	Thr	Asn	Leu	Gln	
460					465					470					475	
aaa	cgg	atc	aac	gcg	gtc	cgt	tca	agc	ctc	ttg	aag	acc	gca	aag	cag	1973
Lys	Arg	Ile	Asn	Ala	Val	Arg	Ser	Ser	Leu	Leu	Lys	Thr	Ala	Lys	Gln	

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gcc gtt gcc aaa gct gaa aaa gcg gca aca gac tca aac ctc ggc aaa			2021
Ala Val Ala Lys Ala Glu Lys Ala Ala Thr Asp Ser Asn Leu Gly Lys			
495	500	505	
gcg caa aaa gcg atc aat gag ctt ccc gcc gga aaa gac aaa tca aat			2069
Ala Gln Lys Ala Ile Asn Glu Leu Pro Ala Gly Lys Asp Lys Ser Asn			
510	515	520	
ctg caa aaa agg ctg aac acc gcg aaa aag caa gca gct gca gcc tat			2117
Leu Gln Lys Arg Leu Asn Thr Ala Lys Lys Gln Ala Ala Ala Tyr			
525	530	535	
aat aaa aaa gtt tct gca gca aag gcc aaa gtc aaa acg gcc gaa caa			2165
Asn Lys Lys Val Ser Ala Ala Lys Ala Lys Val Lys Thr Ala Glu Gln			
540	545	550	555
aag aga acg aaa aaa aca aaa tca gca gcg caa tca gca gta ggc aag			2213
Lys Arg Thr Lys Lys Thr Lys Ser Ala Ala Gln Ser Ala Val Gly Lys			
560	565	570	
ctg aaa gca tcc gcc gaa aaa acg aag ctg caa aaa cgg atc aat gcc			2261
Leu Lys Ala Ser Ala Glu Lys Thr Lys Leu Gln Lys Arg Ile Asn Ala			
575	580	585	
att aag ctg aag tag tacggaaaaa agcccggaat catccgggcc ttttaatttt			2316
Ile Lys Leu Lys			
590			
catatttagc aaatgcgtca ttattgatgc tgttgacta attgacattt cgggctcgtc			2376
atctgcgtaa tcgtattcct tggtcggccg cttactctcc cccgtactct ccaatcactt			2436
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Asn Glu Val Ile Val Val Tyr Lys Asn Thr Ser Gly Lys Glu Thr Val  
35 40 45  
Ile Glu Gln Ala Asp Thr Val Glu His Val Tyr Arg His Ile Pro Ala  
50 55 60  
Ala Ala Val Thr Ala Asp Asp Lys Thr Val Arg Glu Leu Glu His Asp  
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Pro Asp Val Leu Tyr Val Glu Asp Asn Leu Pro Val Ala Ala Ala Asp  
85 90 95  
Ser Thr Ala Leu Lys Ala Phe Ser Ser Ser Thr Ala Gln Asn Ala Ser  
100 105 110  
Ala Phe Ser Gln Trp Asn Ile Lys Leu Ile Gln Ala Ala Leu Ala Trp  
115 120 125  
Asn Lys Gly Leu Thr Gly Lys Gln Val Lys Ile Ala Val Ile Asp Ser  
130 135 140  
Gly Ile Ser Pro His Glu Glu Leu Ser Ile Ala Gly Gly Ala Ser Met  
145 150 155 160  
Val Gly Tyr Thr Ala Ser Tyr Arg Asp Asp Asn Gly His Gly Thr His  
165 170 175  
Val Ala Gly Ile Ile Gly Ala Lys His Asn Gly Arg Gly Ile Asp Gly  
180 185 190  
Ile Ala Pro Gly Ala Gln Leu Tyr Ala Val Lys Ala Leu Asp Arg Asn  
195 200 205  
Gly Ala Gly Asp Leu Lys Gly Ile Leu Gln Gly Ile Asp Trp Ser Ile  
210 215 220  
Gln His Gly Ile Asp Ile Ile Asn Met Ser Leu Val Val Ser Gly Asp  
225 230 235 240

Ser Gln Val Leu His Asp Ala Val Asp Lys Ala Tyr Lys Arg Gly Ile  
245 250 255

Ile Leu Val Gly Ala Ser Gly Asn Ala Gly Asn Gly Lys Ser Val Tyr  
260 265 270

Tyr Pro Ala Ala Tyr Ser Ser Val Ile Ala Val Ser Ala Thr Asn Glu  
275 280 285

Lys Asn Gln Ile Ala Ser Phe Thr Asn Thr Arg Ser Ala Val Ser Tyr  
290 295 300

Ser Ala Pro Ser Thr Ser Ile Ile Asn Thr Ser Gly Asn Arg Gly Tyr  
305 310 315 320

Ala Ile Gly Ser Cys Thr Ala Gln Gly Thr Pro Asp Val Thr Cys Val  
325 330 335

Ile Ala Leu Met Lys Gln Leu His Pro Thr Ala Ser Asn Ala Glu Leu  
340 345 350

Arg Lys Lys Met Gln Phe Tyr Thr Ser Asp Leu Gly Ala Pro Gly Arg  
355 360 365

Asp His Leu Phe Gly Tyr Arg Leu Ile Arg Phe Lys Glu Val Thr Gln  
370 375 380

Pro Leu Glu Lys Ala Gln Lys Ala Val Gly Gln Ala Glu Lys Thr Lys  
385 390 395 400

Lys Lys Ala Asp Ile Gln Thr Ala Gln Lys Ala Ile Glu Pro Leu Pro  
405 410 415

Ala Asp Ala Asp Lys Pro Ala Leu Lys Lys Arg Leu Asn Thr Val Lys  
420 425 430

Glu Gln Leu Lys Lys Thr Ala Glu Ser Lys Val Lys Leu Ala Glu Lys  
435 440 445

Gln Lys Lys Lys Thr Asn Ala Asp Ser Ala Gln Lys Ala Val Asn Glu  
450 455 460

Leu Asp Ser Gly Thr Phe Lys Thr Asn Leu Gln Lys Arg Ile Asn Ala

465 470 475 480

Val Arg Ser Ser Leu Leu Lys Thr Ala Lys Gln Ala Val Ala Lys Ala  
485 490 495

Glu Lys Ala Ala Thr Asp Ser Asn Leu Gly Lys Ala Gln Lys Ala Ile  
500 505 510

Asn Glu Leu Pro Ala Gly Lys Asp Lys Ser Asn Leu Gln Lys Arg Leu  
515 520 525

Asn Thr Ala Lys Lys Gln Ala Ala Ala Ala Tyr Asn Lys Lys Val Ser  
530 535 540

Ala Ala Lys Ala Lys Val Lys Thr Ala Glu Gln Lys Arg Thr Lys Lys  
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Thr Lys Ser Ala Ala Gln Ser Ala Val Gly Lys Leu Lys Ala Ser Ala  
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cgtatcaggg ctccctttgt cgtttttgggt tcataccac caagttcttt tgtatattct 360  
cggtttgttt atttctatg ctgccggctt tgtcttaaca tactcctttg gtttcaagga 420  
cgatatggca gttgaatttg attaaacggt tgtttaaaat ttcccactat gcaattttta 480

acagaaagga gtgaagcaag ctgaaaaagt tt atg atc agt gcg gcc gcg tcc	533
Met Ile Ser Ala Ala Ala Ser	
1 5	
cta ttg ctg ctg aca tgc ttt ttt ccg ctt ccg tcc aca gca cag act	581
Leu Leu Leu Leu Thr Cys Phe Phe Pro Leu Pro Ser Thr Ala Gln Thr	
10 15 20	
gcc atc ggg aac gag aca aaa cag cgg ctg aca tat cct gtt tta acg	629
Ala Ile Gly Asn Glu Thr Lys Gln Arg Leu Thr Tyr Pro Val Leu Thr	
25 30 35	
aaa gcg aaa acg cct gaa gaa gcc ggt ttt tct tcg aaa aag ctt aaa	677
Lys Ala Lys Thr Pro Glu Glu Ala Gly Phe Ser Ser Lys Lys Leu Lys	
40 45 50 55	
gct gtg gac cgt ctg atc gaa cag gat gtc aaa gcg ggc ttt ccc ggc	725
Ala Val Asp Arg Leu Ile Glu Gln Asp Val Lys Ala Gly Phe Pro Gly	
60 65 70	
gct gcc ctt att ttg att aaa gac gga aaa atc atc aaa aaa gaa gtc	773
Ala Ala Leu Ile Leu Ile Lys Asp Gly Lys Ile Ile Lys Lys Glu Val	
75 80 85	
tac ggc tac aag cag aaa tac aac ggc ctc ata gcg ctc aaa cat cca	821
Tyr Gly Tyr Lys Gln Lys Tyr Asn Gly Leu Ile Ala Leu Lys His Pro	
90 95 100	
aaa aaa atg aaa gca aac acg atg ttc gac cta gcc tcc aat aca aaa	869
Lys Lys Met Lys Ala Asn Thr Met Phe Asp Leu Ala Ser Asn Thr Lys	
105 110 115	
atg tat gcc gtc aat ttt gcc ttg cag cat tta gtg agc acc gga aag	917
Met Tyr Ala Val Asn Phe Ala Leu Gln His Leu Val Ser Thr Gly Lys	
120 125 130 135	
ctt gac ttg aac aaa aac att tct caa tat ctc cct gat ttc aaa gat	965
Leu Asp Leu Asn Lys Asn Ile Ser Gln Tyr Leu Pro Asp Phe Lys Asp	
140 145 150	
cac ccg gaa gac gat gta aag gga aaa aac ccg ctc cgc gtg att gat	1013
His Pro Glu Asp Asp Val Lys Gly Lys Asn Arg Leu Arg Val Ile Asp	
155 160 165	
ttg ctt cat cat aac gca ggc ttc cct gca agc tgg aat tat tac gac	1061
Leu Leu His His Asn Ala Gly Phe Pro Ala Ser Trp Asn Tyr Tyr Asp	
170 175 180	
ccg aaa tca gcc gga cac ctc tac tct caa tca ccg agc aaa acg ctt	1109
Pro Lys Ser Ala Gly His Leu Tyr Ser Gln Ser Arg Ser Lys Thr Leu	
185 190 195	
gaa tat ctt gtg aaa acc ccc ttg gca tat gaa ccc ggc aca aag caa	1157
Glu Tyr Leu Val Lys Thr Pro Leu Ala Tyr Glu Pro Gly Thr Lys Gln	
200 205 210 215	



att tac agt gac atc gac tat atg ctc ctc ggg ctg atc att gaa aaa Ile Tyr Ser Asp Ile Asp Tyr Met Leu Leu Gly Leu Ile Ile Glu Lys 220 225 230	1205
atc aca aac gag cgt tta gat acc ttt gtt gaa aac cgg ttt tac cgg Ile Thr Asn Glu Arg Leu Asp Thr Phe Val Glu Asn Arg Phe Tyr Arg 235 240 245	1253
cct ctc gga ttg cgg cat act ttg ttt aat ccg ctc caa aag ggc ttt Pro Leu Gly Leu Arg His Thr Leu Phe Asn Pro Leu Gln Lys Gly Phe 250 255 260	1301
aaa cgg tcg cat ttt gca gct acg gaa cga ttg gga aac acc aga gac Lys Arg Ser His Phe Ala Ala Thr Glu Arg Leu Gly Asn Thr Arg Asp 265 270 275	1349
ggc acc att tcg ttc cca aac atc aga act tac aca ctt cag ggg gaa Gly Thr Ile Ser Phe Pro Asn Ile Arg Thr Tyr Thr Leu Gln Gly Glu 280 285 290 295	1397
gtc cac gat gaa aaa gca ttc tat tca atg gaa ggc gtt tct ggg cat Val His Asp Glu Lys Ala Phe Tyr Ser Met Glu Gly Val Ser Gly His 300 305 310	1445
gcc ggc ctg ttt tcc acc gtt gac gac gca gca gtg ctc ctt caa gtc Ala Gly Leu Phe Ser Thr Val Asp Asp Ala Ala Val Leu Leu Gln Val 315 320 325	1493
atg ctg aac ggc ggc ggt tac gga aga cag cat cta ttc agc agt tct Met Leu Asn Gly Gly Gly Tyr Gly Arg Gln His Leu Phe Ser Ser Ser 330 335 340	1541
gtc att tca caa ttt aca gag ccg tca aaa aca aat ccc aca tat gga Val Ile Ser Gln Phe Thr Glu Pro Ser Lys Thr Asn Pro Thr Tyr Gly 345 350 355	1589
cta gga tgg cgg ctc aac ggc aat acc gat atg gag tgg atg ttc ggc Leu Gly Trp Arg Leu Asn Gly Asn Thr Asp Met Glu Trp Met Phe Gly 360 365 370 375	1637
aag cac gcc agc agc aaa gca tat ggc cat acc ggc tgg acg gga acg Lys His Ala Ser Ser Lys Ala Tyr Gly His Thr Gly Trp Thr Gly Thr 380 385 390	1685
gtt act atc att gat ccc gtg tat caa atc ggc att gtg ttg tta acc Val Thr Ile Ile Asp Pro Val Tyr Gln Ile Gly Ile Val Leu Leu Thr 395 400 405	1733
aat aaa aag cac tct cct gtt atc aac cct aaa gaa aac ccg aat caa Asn Lys Lys His Ser Pro Val Ile Asn Pro Lys Glu Asn Pro Asn Gln 410 415 420	1781
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gct gtt tac gag gcg tta cat cac caa taggaggcga ccctttatat	1876

Ala Val Tyr Glu Ala Leu His His Gln  
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gaaaagattt cttcaatgcg cgttgattgc attgctgtta tcgtctctcg ctttgcagcc 1936  
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cagcatgtcg cttgaagaga aaatcgggca aatgctgatg cctgacttta gaaactggaa 2056  
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Phe Ser Ser Lys Lys Leu Lys Ala Val Asp Arg Leu Ile Glu Gln Asp  
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Val Lys Ala Gly Phe Pro Gly Ala Ala Leu Ile Leu Ile Lys Asp Gly  
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Lys Ile Ile Lys Lys Glu Val Tyr Gly Tyr Lys Gln Lys Tyr Asn Gly  
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Leu Ile Ala Leu Lys His Pro Lys Lys Met Lys Ala Asn Thr Met Phe  
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Asp Leu Ala Ser Asn Thr Lys Met Tyr Ala Val Asn Phe Ala Leu Gln  
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His Leu Val Ser Thr Gly Lys Leu Asp Leu Asn Lys Asn Ile Ser Gln  
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Tyr Leu Pro Asp Phe Lys Asp His Pro Glu Asp Asp Val Lys Gly Lys  
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Asn Arg Leu Arg Val Ile Asp Leu Leu His His Asn Ala Gly Phe Pro  
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Ala Ser Trp Asn Tyr Tyr Asp Pro Lys Ser Ala Gly His Leu Tyr Ser  
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Gln Ser Arg Ser Lys Thr Leu Glu Tyr Leu Val Lys Thr Pro Leu Ala  
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Tyr Glu Pro Gly Thr Lys Gln Ile Tyr Ser Asp Ile Asp Tyr Met Leu  
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Leu Gly Leu Ile Ile Glu Lys Ile Thr Asn Glu Arg Leu Asp Thr Phe  
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Val Glu Asn Arg Phe Tyr Arg Pro Leu Gly Leu Arg His Thr Leu Phe  
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Asn Pro Leu Gln Lys Gly Phe Lys Arg Ser His Phe Ala Ala Thr Glu  
 260 265 270

Arg Leu Gly Asn Thr Arg Asp Gly Thr Ile Ser Phe Pro Asn Ile Arg  
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Thr Tyr Thr Leu Gln Gly Glu Val His Asp Glu Lys Ala Phe Tyr Ser  
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Met Glu Gly Val Ser Gly His Ala Gly Leu Phe Ser Thr Val Asp Asp  
 305 310 315 320

Ala Ala Val Leu Leu Gln Val Met Leu Asn Gly Gly Gly Tyr Gly Arg  
 325 330 335

Gln His Leu Phe Ser Ser Ser Val Ile Ser Gln Phe Thr Glu Pro Ser  
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Lys Thr Asn Pro Thr Tyr Gly Leu Gly Trp Arg Leu Asn Gly Asn Thr  
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Asp Met Glu Trp Met Phe Gly Lys His Ala Ser Ser Lys Ala Tyr Gly  
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His Thr Gly Trp Thr Gly Thr Val Thr Ile Ile Asp Pro Val Tyr Gln  
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Ile Gly Ile Val Leu Leu Thr Asn Lys Lys His Ser Pro Val Ile Asn  
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 gcatgatttg ggacgagtct gaataaattg acttatagag atggatacac caaaagcaac 360  
 ctttagggca ggaggagtgg acgattca atg aaa tgg cac gag atg gga caa 412  
 Met Lys Trp His Glu Met Gly Gln  
 1 5  
 acc gaa ttg tta aat ata aca aaa acg tcc atc gac aaa ggt cta aca 460  
 Thr Glu Leu Leu Asn Ile Thr Lys Thr Ser Ile Asp Lys Gly Leu Thr  
 10 15 20  
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Glu	Lys	Glu	Ala	Gly	Lys	Arg	Leu	Glu	Arg	His	Gly	Thr	Asn	Glu	Leu	
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cag	gaa	ggg	gaa	aaa	aca	tcg	gcg	gtc	gca	ttg	ttt	ttt	tct	caa	ttc	556
Gln	Glu	Gly	Glu	Lys	Thr	Ser	Ala	Val	Ala	Leu	Phe	Phe	Ser	Gln	Phe	
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Lys	Asp	Phe	Met	Val	Leu	Val	Leu	Leu	Ala	Ala	Thr	Leu	Ile	Ser	Gly	
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Phe	Leu	Gly	Glu	Tyr	Ile	Asp	Ala	Ile	Ala	Ile	Ile	Ala	Ile	Ile	Phe	
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Val	Asn	Gly	Ile	Leu	Gly	Phe	Phe	Gln	Glu	Arg	Arg	Ala	Glu	Arg	Ser	
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ctc	gag	gct	ttg	aaa	gaa	ctg	tca	gct	cct	caa	gtg	gct	gtg	ctc	cgg	748
Leu	Glu	Ala	Leu	Lys	Glu	Leu	Ser	Ala	Pro	Gln	Val	Ala	Val	Leu	Arg	
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Glu	Gly	Asn	Trp	Val	Lys	Ile	Pro	Ser	Lys	Glu	Leu	Val	Pro	Gly	Asp	
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Val	Val	Arg	Phe	Ala	Ser	Gly	Asp	Arg	Ile	Gly	Ala	Asp	Leu	Arg	Leu	
			140					145					150			
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Val	Glu	Thr	Lys	Ser	Leu	Glu	Ile	Glu	Glu	Ser	Ala	Leu	Thr	Gly	Glu	
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tcg	ctc	ccc	gtg	tcc	aaa	cag	gca	gat	gct	ttt	cag	gcg	tca	gat	gta	940
Ser	Leu	Pro	Val	Ser	Lys	Gln	Ala	Asp	Ala	Phe	Gln	Ala	Ser	Asp	Val	
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tcg	ctg	ggc	gat	ctg	aag	aat	atg	gct	ttc	atg	gga	acg	ctt	gtc	aca	988
Ser	Leu	Gly	Asp	Leu	Lys	Asn	Met	Ala	Phe	Met	Gly	Thr	Leu	Val	Thr	
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agg	ggg	agc	gga	atc	ggc	gtc	gtc	atc	ggc	acg	ggc	atg	aac	tct	gcg	1036
Arg	Gly	Ser	Gly	Ile	Gly	Val	Val	Ile	Gly	Thr	Gly	Met	Asn	Ser	Ala	
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atg	ggg	aaa	atc	gcc	gat	atg	ctt	gaa	tct	gcc	ggg	aat	acg	gcg	acc	1084
Met	Gly	Lys	Ile	Ala	Asp	Met	Leu	Glu	Ser	Ala	Gly	Asn	Thr	Ala	Thr	
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ccg	ctg	caa	aga	agg	ctt	gaa	gag	ctc	ggc	aaa	att	ttg	att	gtc	gcc	1132
Pro	Leu	Gln	Arg	Arg	Leu	Glu	Glu	Leu	Gly	Lys	Ile	Leu	Ile	Val	Ala	
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gct	ttg	ttc	ctg	aca	ctg	ctt	gtc	gtt	gct	gcc	ggc	gtc	att	cag	ggg	1180
Ala	Leu	Phe	Leu	Thr	Leu	Leu	Val	Val	Ala	Ala	Gly	Val	Ile	Gln	Gly	

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His Asp Leu Tyr Ser Met Phe Leu Ala Gly Val Ser Leu Ala Val Ala			
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gcc ata cct gaa ggg ctg cct gcc att gtc acg gtc gct ctg tct ctc			1276
Ala Ile Pro Glu Gly Leu Pro Ala Ile Val Thr Val Ala Leu Ser Leu			
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ggc gtg cag cgg atg atc agg caa aag tcg atc gtc agg aag ctg ccc			1324
Gly Val Gln Arg Met Ile Arg Gln Lys Ser Ile Val Arg Lys Leu Pro			
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gcg gtt gag acg ctc ggc tgc gcg tcc att att tgc tcc gat aaa acc			1372
Ala Val Glu Thr Leu Gly Cys Ala Ser Ile Ile Cys Ser Asp Lys Thr			
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ggg acg atg acg cag aac aaa atg acg gtc acc cat gtc tgg tca ggc			1420
Gly Thr Met Thr Gln Asn Lys Met Thr Val Thr His Val Trp Ser Gly			
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ggg aag ata tgg aac gtg tca ggg atc ggc tat gag cct gaa ggc tct			1468
Gly Lys Ile Trp Asn Val Ser Gly Ile Gly Tyr Glu Pro Glu Gly Ser			
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Phe Ser Met Asn Gly Arg Asp Val Gln Ala Lys His His Lys Pro Leu			
	365	370	375
cag cag gta cta ttg ttc ggc gca tta tgc aat tca tct tcg att atc			1564
Gln Gln Val Leu Phe Gly Ala Leu Cys Asn Ser Ser Ser Ile Ile			
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gaa aaa gac ggg gag ttt cgt ctt gat ggc gat ccc acc gaa ggg gct			1612
Glu Lys Asp Gly Glu Phe Arg Leu Asp Gly Asp Pro Thr Glu Gly Ala			
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Leu Leu Thr Ala Ala Arg Lys Ala Gly Phe Thr Asp Lys Tyr Val Asp			
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gaa cat ttt aaa atc atc gag gag ttt ccg ttt gat tca acg cgg aaa			1708
Glu His Phe Lys Ile Ile Glu Glu Phe Pro Phe Asp Ser Thr Arg Lys			
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Met Met Ser Val Ile Val Glu Asp Lys Ser Gly Lys Arg Phe Val Ile			
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Thr Lys Gly Ala Pro Asp Val Leu Met Lys Arg Ser Ser His Thr Leu			
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Thr Glu Glu Lys Arg Glu Ile Phe Thr Lys Glu Arg Leu Ala Glu Thr			
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Val Ala Tyr Lys Pro Ile Lys Asp Thr Glu Asn Pro Pro Leu Glu Lys	
505 510 515 520	
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Ala Glu Ser Gly Leu Thr Phe Ile Gly Leu Leu Gly Met Ile Asp Pro	
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Pro Arg Pro Glu Val Lys Thr Ala Ile Lys Glu Cys Arg Glu Ala Gly	
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atc aaa acg gtc atg atc acc ggg gac cat gtg ata acg gcg acg gcg	2092
Ile Lys Thr Val Met Ile Thr Gly Asp His Val Ile Thr Ala Thr Ala	
555 560 565	
att gca aaa gat ctc gga ttg ctg cct ccg cgc gga aag gtc atg gac	2140
Ile Ala Lys Asp Leu Gly Leu Leu Pro Pro Arg Gly Lys Val Met Asp	
570 575 580	
ggc cag atg ctg aac gaa ctc tcg cag gaa gaa ttg gcg gaa att gtt	2188
Gly Gln Met Leu Asn Glu Leu Ser Gln Glu Glu Leu Ala Glu Ile Val	
585 590 595 600	
gac gat gtt tac gta ttt gca agg gtg tcg ccc gaa cat aag ctg aag	2236
Asp Asp Val Tyr Val Phe Ala Arg Val Ser Pro Glu His Lys Leu Lys	
605 610 615	
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Ile Val Thr Ala Tyr Gln Glu Asn Gly His Ile Val Ala Met Thr Gly	
620 625 630	
gac gga gtc aat gat gcc cct gcg att aaa cag gcg gat atc ggc ata	2332
Asp Gly Val Asn Asp Ala Pro Ala Ile Lys Gln Ala Asp Ile Gly Ile	
635 640 645	
tcg atg ggg att acg gga acg gat gtc gcc aag gag gcg tcc tca ctc	2380
Ser Met Gly Ile Thr Gly Thr Asp Val Ala Lys Glu Ala Ser Ser Leu	
650 655 660	
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Ile Leu Val Asp Asp Asn Phe Ala Thr Ile Lys Ser Ala Ile Lys Glu	
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gga cgc aat atc tat gaa aat att aga aag ttc atc aga tac ttg ctc	2476
Gly Arg Asn Ile Tyr Glu Asn Ile Arg Lys Phe Ile Arg Tyr Leu Leu	
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gca tcc aat gtc ggc gaa att ttg gtc atg ctg ttt gca atg ctg ctc	2524
Ala Ser Asn Val Gly Glu Ile Leu Val Met Leu Phe Ala Met Leu Leu	
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gct ctg ccg ctg ccg ctt gtc ccg ata cag att ctg tgg gtc aac ctt	2572
Ala Leu Pro Leu Pro Leu Val Pro Ile Gln Ile Leu Trp Val Asn Leu	
715 720 725	
gta acg gac ggc ctg cct gcc atg gcg ctc ggc atg gat cag cct gag	2620
Val Thr Asp Gly Leu Pro Ala Met Ala Leu Gly Met Asp Gln Pro Glu	
730 735 740	
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Asp Asp Val Met Gln Arg Lys Pro Arg Ser Pro Lys Glu Gly Val Phe	
745 750 755 760	
gca agg ggg ctc ggc tgg aag gtc gta tcg cgc gga ttc tta atc gga	2716
Ala Arg Gly Leu Gly Trp Lys Val Val Ser Arg Gly Phe Leu Ile Gly	
765 770 775	
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Ile Ala Thr Leu Gly Ala Phe Met Phe Ile Tyr Asn Arg Asn Pro Glu	
780 785 790	
gcg ctt gag tat gca cag acg gtt gca ttt gca acg ctc gtc ctt gcg	2812
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Gln Leu Ile His Val Phe Asp Cys Arg Ser Glu Arg Ser Ile Phe Asp	
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Arg Asn Pro Phe Glu Asn Ile Tyr Leu Leu Gly Ala Val Leu Ser Ser	
825 830 835 840	
att ctt ttg atg ctt gtc gtt att tat tat ccg ccg ctg cag ccg att	2956
Ile Leu Leu Met Leu Val Val Ile Tyr Tyr Pro Pro Leu Gln Pro Ile	
845 850 855	
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Phe His Thr Val Pro Ile Leu Met Ala Asp Trp Leu Leu Ile Val Gly	
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Lys Asn	
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                     100                      105                      110  
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 Ser Lys Glu Leu Val Pro Gly Asp Val Val Arg Phe Ala Ser Gly Asp  
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 Ala Phe Met Gly Thr Leu Val Thr Arg Gly Ser Gly Ile Gly Val Val  
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 Glu Ser Ala Gly Asn Thr Ala Thr Pro Leu Gln Arg Arg Leu Glu Glu  
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Val Ala Ala Gly Val Ile Gln Gly His Asp Leu Tyr Ser Met Phe Leu  
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290 295 300

Lys Ser Ile Val Arg Lys Leu Pro Ala Val Glu Thr Leu Gly Cys Ala  
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Ser Ile Ile Cys Ser Asp Lys Thr Gly Thr Met Thr Gln Asn Lys Met  
325 330 335

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355 360 365

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Leu Cys Asn Ser Ser Ser Ile Ile Glu Lys Asp Gly Glu Phe Arg Leu  
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Asp Gly Asp Pro Thr Glu Gly Ala Leu Leu Thr Ala Ala Arg Lys Ala  
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Phe Pro Phe Asp Ser Thr Arg Lys Met Met Ser Val Ile Val Glu Asp  
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Lys Ser Gly Lys Arg Phe Val Ile Thr Lys Gly Ala Pro Asp Val Leu  
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Met Lys Arg Ser Ser His Thr Leu Thr Glu Glu Lys Arg Glu Ile Phe  
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Thr Lys Glu Arg Leu Ala Glu Thr Ser Ala Ala Leu Glu Thr Leu Ala  
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Ser Gln Ala Leu Arg Thr Ile Ala Val Ala Tyr Lys Pro Ile Lys Asp  
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Thr Glu Asn Pro Pro Leu Glu Lys Ala Glu Ser Gly Leu Thr Phe Ile  
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Gly Leu Leu Gly Met Ile Asp Pro Pro Arg Pro Glu Val Lys Thr Ala  
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Asp His Val Ile Thr Ala Thr Ala Ile Ala Lys Asp Leu Gly Leu Leu  
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Gln Glu Glu Leu Ala Glu Ile Val Asp Asp Val Tyr Val Phe Ala Arg  
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Val Ser Pro Glu His Lys Leu Lys Ile Val Thr Ala Tyr Gln Glu Asn  
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Gly His Ile Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Pro Ala  
 625 630 635 640

Ile Lys Gln Ala Asp Ile Gly Ile Ser Met Gly Ile Thr Gly Thr Asp  
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Val Ala Lys Glu Ala Ser Ser Leu Ile Leu Val Asp Asp Asn Phe Ala  
 660 665 670

Thr Ile Lys Ser Ala Ile Lys Glu Gly Arg Asn Ile Tyr Glu Asn Ile  
 675 680 685

Arg Lys Phe Ile Arg Tyr Leu Leu Ala Ser Asn Val Gly Glu Ile Leu  
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Val Met Leu Phe Ala Met Leu Leu Ala Leu Pro Leu Pro Leu Val Pro  
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Arg Ser Pro Lys Glu Gly Val Phe Ala Arg Gly Leu Gly Trp Lys Val  
755 760 765

Val Ser Arg Gly Phe Leu Ile Gly Ile Ala Thr Leu Gly Ala Phe Met  
770 775 780

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785 790 795 800

Ala Phe Ala Thr Leu Val Leu Ala Gln Leu Ile His Val Phe Asp Cys  
805 810 815

Arg Ser Glu Arg Ser Ile Phe Asp Arg Asn Pro Phe Glu Asn Ile Tyr  
820 825 830

Leu Leu Gly Ala Val Leu Ser Ser Ile Leu Leu Met Leu Val Val Ile  
835 840 845

Tyr Tyr Pro Pro Leu Gln Pro Ile Phe His Thr Val Pro Ile Leu Met  
850 855 860

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taaaagaaat ttaccgtggt ttacagggtg acggcacgct gtttctcgct gtgcatctgg      180
aagggcaa at gaaaaaatcg aaaaaaaca aaggcttttc cttataactca gaagagcaaa      240
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actgctgcat ttctgcggtt aaatcatgaa ctttgtatga tcatcccttt caatacggaa      360
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Ser Ala Ser Pro Val Glu Ala Ser Phe Gln Ser Asp Asp Glu Val His
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Gly Ser Phe Lys Ser Lys Ala Gln Ser Ser Gly Val Gln Ala Leu Glu	
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Pro Leu Gly Lys Ser Lys Thr Ala Phe Lys Asp Met Tyr Val Val Glu	
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75

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Tyr Ile Lys Val Glu Asn His His Asp Glu Glu Asn Glu Thr Thr Ser  
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Pro Ser Ile Gln Glu Ala Glu Glu Glu Cys Pro Ala Glu Leu Ser Val  
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Arg Asp Glu Val Leu Ser Lys Thr Glu Lys Gly Lys Glu Leu Ser Ser  
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Thr Asn Asp Asp Gln Lys Ala Ile Ser Arg Leu Tyr Glu Thr Ala Arg  
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Gly Thr Ala Lys Ser Gly Val Thr Val Lys Ile Leu Arg Gly Lys Gln  
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His Gln Ala Glu Thr Ser Leu Arg Thr Val Val Glu Lys Ala Pro Lys  
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att gaa cac gcc gag ctt ctg aca aag gag cgg tat gcg aag cgg ccg	1635
Ile Glu His Ala Glu Leu Leu Thr Lys Glu Arg Tyr Ala Lys Arg Pro	
370 375 380	
gtg atg cag cgg ccc gtc gaa tgg ctg gcg aaa tgc att tca ttc ttt	1683
Val Met Gln Arg Pro Val Glu Trp Leu Ala Lys Ser Ile Ser Phe Phe	
385 390 395	
tta taaaacgtac gtttatcctg catgacatgc gggtaacatt tcaccaaagt	1736
Leu	
gatgattaca tacggagggg atgtacgatg aaccaagcag agtcgattaa actccgcgcc	1796
caatcgatga cgtaaataaa cttgattgag ctgtacaagc tttgccgctc agccagacat	1856
cagctatata tatgctcaag aaaaacgatg tgcaaaatca aagattttaat tgagctggaa	1916
atgttcagaa tggccaatcg cgaaaatgag tgcttgattg tcatcgaagg gaaaatggcg	1976

caggaattag taaaaaaagc acaatcgatt ctttctgacg ctcaagttca ataaggggaag 2036  
gcggaagttc ttcctttgcg agacgcctcc tcaccaaadc aagaaaaaat cccccgttca 2096  
atggacgggg gattcgtttt acattttttc aggcgctgat acgccgatca gcttgagggc 2156  
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<400> 30

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Ala Tyr Glu Pro Val Phe Ser Glu Lys Lys Ser Asp Ile Glu Leu Ile  
35 40 45

His Asn Gly Glu Asp Leu Cys Glu Arg Leu Leu Asp Asp Ile Arg Gln  
50 55 60

Ala Glu Ser Ser Val His Val Met Phe Tyr Ile Val Lys Asn Asp Asp  
65 70 75 80

Ile Ser Leu Glu Phe Leu Lys Val Leu Lys Asp Lys Ala Lys Ser Gly  
85 90 95

Val Cys Val Arg Leu Leu Ile Asp Arg Ile Gly Ala Met Lys Val Lys  
100 105 110

Lys Lys Thr Leu Ser Gly Leu Lys Gln Ser Gly Val His Val Phe Phe  
115 120 125

Ala Asn Lys Pro Gly Phe Pro Tyr Phe Phe Tyr Arg Leu Asn Ala Arg  
130 135 140

Asn His Arg Lys Ile Ala Val Ile Asp Gly Lys Ile Gly Tyr Val Gly  
145 150 155 160

Gly Phe Asn Ile Ala Lys Glu Tyr Leu Gly Lys Lys Ala Glu Phe Gly



165

170

175

Pro Trp Lys Asp Tyr His Leu Arg Met Thr Gly Glu Gly Val Ala Asp  
 180 185 190

Leu Gln His Ile Phe Ile Ser Asp Phe Lys Arg Glu Ala Pro Gln Ala  
 195 200 205

Lys Pro Ala Asn Ser Val Phe Pro Pro Leu Gln Gln Gly Ala Val Thr  
 210 215 220

His Thr Thr His Ala Thr Lys Gly Phe Ser Leu Glu Glu Lys Tyr Ile  
 225 230 235 240

Ser Phe Ile Glu Gln Ala Lys Glu Arg Ile Met Ile Cys Thr Pro Tyr  
 245 250 255

Tyr Ile Pro Ser Pro Ala Leu Gln Gln Ala Val Leu Ser Ala Arg Glu  
 260 265 270

Arg Gly Val Ile Val Ser Val Leu Val Pro Met Lys Pro Asp His Pro  
 275 280 285

Leu Val Lys Glu Ala Ala Tyr Thr His Phe Pro Ala Leu Leu Lys Ala  
 290 295 300

Gly Cys Tyr Ile Tyr Arg Tyr Tyr Arg Gly Phe Tyr His Ala Lys Ala  
 305 310 315 320

Leu Ile Val Asp Asp Arg His Val Met Ile Gly Thr Ser Asn Phe Asp  
 325 330 335

Asn Arg Ser Leu Phe Leu Asn Asp Glu Val Asn Val Val Ile His Asp  
 340 345 350

Lys Asp Trp Thr Lys Gln Phe Phe Asp Val Val Lys Glu Ser Ile Glu  
 355 360 365

His Ala Glu Leu Leu Thr Lys Glu Arg Tyr Ala Lys Arg Pro Val Met  
 370 375 380

Gln Arg Pro Val Glu Trp Leu Ala Lys Ser Ile Ser Phe Phe Leu  
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 aag gaa ttg tgg aca ttg atc gaa cta ttt agt gat tat gtg ctc cat 168  
 Glu Leu Trp Thr Leu Ile Glu Leu Phe Ser Asp Tyr Val Leu His  
 1 5 10 15  
 ttt gaa cgt tat ttt gtt tta agc aga cag agc atg ctt gtc att cag 216  
 Phe Glu Arg Tyr Phe Val Leu Ser Arg Gln Ser Met Leu Val Ile Gln  
 20 25 30  
 tgg tgt gtg aca ggc ctt gtc ctt ttg tat gcc gtg tca ttt cat cca 264  
 Trp Cys Val Thr Gly Leu Val Leu Leu Tyr Ala Val Ser Phe His Pro  
 35 40 45  
 aaa gtg tgc agg cgg cgc ctc ttt ttt tat gca ggc atc gtt ctc agg 312  
 Lys Val Cys Arg Arg Arg Leu Phe Phe Tyr Ala Gly Ile Val Leu Arg  
 50 55 60  
 ctg ata ctg gtt ggc gcc ctt tcg ttt gaa ttg gct cac caa atg aaa 360  
 Leu Ile Leu Val Gly Ala Leu Ser Phe Glu Leu Ala His Gln Met Lys  
 65 70 75  
 gcc gct gag ttt tca aac ctg tac ata gac gaa caa gat gcg ctt ctg 408  
 Ala Ala Glu Phe Ser Asn Leu Tyr Ile Asp Glu Gln Asp Ala Leu Leu  
 80 85 90 95  
 cct ttt atg cag ttt ttg ctg ttc ggc tat att ttg ctt gtc tct ttt 456  
 Pro Phe Met Gln Phe Leu Leu Phe Gly Tyr Ile Leu Leu Val Ser Phe  
 100 105 110  
 cat tat atg atg aca ctc gcg gaa aaa ggg ggc aag ggg ctg ttt ttt 504  
 His Tyr Met Met Thr Leu Ala Glu Lys Gly Gly Lys Gly Leu Phe Phe  
 115 120 125  
 gca ttt gac att gcg gtg atg gcg atg ccg ctt ttc caa tcg ctg ttc 552  
 Ala Phe Asp Ile Ala Val Met Ala Met Pro Leu Phe Gln Ser Leu Phe  
 130 135 140  
 agc ttt gcc gcc tat ttg aag gaa ttt gga gcg gag gag ctt gaa gaa 600  
 Ser Phe Ala Ala Tyr Leu Lys Glu Phe Gly Ala Glu Glu Leu Glu Glu  
 145 150 155

ttg ccg ctc gtt ctg ttg ttg att gtc gga ata ccg gga ctg atg atc Leu Pro Leu Val Leu Leu Leu Ile Val Gly Ile Pro Gly Leu Met Ile 160 165 170 175	648
tgc ttg ttt ttt cag ctt tat tgg aaa aga aac cgt tac gtt ctc ctt Cys Leu Phe Phe Gln Leu Tyr Trp Lys Arg Asn Arg Tyr Val Leu Leu 180 185 190	696
ttg att ttt tat att gtg acg atc ggc ggt ttc ttc atc aaa aag ctt Leu Ile Phe Tyr Ile Val Thr Ile Gly Gly Phe Phe Ile Lys Lys Leu 195 200 205	744
gga tac gaa ttt ttt ccg ctg aac gta ttt ctg aca atg atc ggt ttt Gly Tyr Glu Phe Phe Pro Leu Asn Val Phe Leu Thr Met Ile Gly Phe 210 215 220	792
ctt atg aca tat cac ttg ctg aat gac tcg aga aag cct ttg ttg atg Leu Met Thr Tyr His Leu Leu Asn Asp Ser Arg Lys Pro Leu Leu Met 225 230 235	840
gtg aag cgt gtt tta gcc gcg ggc acc gcc gta ttt ttc acg ctt cac Val Lys Arg Val Leu Ala Ala Gly Thr Ala Val Phe Phe Thr Leu His 240 245 250 255	888
ctc aat cct ttt tac aat ttg gcg gat gcc gct ttt aca atc tca cac Leu Asn Pro Phe Tyr Asn Leu Ala Asp Ala Ala Phe Thr Ile Ser His 260 265 270	936
ccg gag gtt tca gac gtg gtt gat gcc aat ttt cgg cct gtt tcg gtt Pro Glu Val Ser Asp Val Val Asp Ala Asn Phe Arg Pro Val Ser Val 275 280 285	984
aaa gaa gcg aag cag act gtc agc tcg ttt ttt ccg aca gag agc ttt Lys Glu Ala Lys Gln Thr Val Ser Ser Phe Phe Pro Thr Glu Ser Phe 290 295 300	1032
atc tat ttg tca gct acc aac cag gat ttt cat aac gtt tat cat ttc Ile Tyr Leu Ser Ala Thr Asn Gln Asp Phe His Asn Val Tyr His Phe 305 310 315	1080
aaa acg aaa gat tac gat gcg gac gtt gac ggc tgg acg gga atg atc Lys Thr Lys Asp Tyr Asp Ala Asp Val Asp Gly Trp Thr Gly Met Ile 320 325 330 335	1128
acc aat tat cac aat caa aaa aag cct agc ggg aat atc ctg tcc ggt Thr Asn Tyr His Asn Gln Lys Lys Pro Ser Gly Asn Ile Leu Ser Gly 340 345 350	1176
cag gca tat atc aag cgg tcg aag caa ttt cta agg gaa cac ggc cgc Gln Ala Tyr Ile Lys Arg Ser Lys Gln Phe Leu Arg Glu His Gly Arg 355 360 365	1224
gaa ctt gac aaa caa atc aag gca aag gtc agc cgt gat gac ggc gaa Glu Leu Asp Lys Gln Ile Lys Ala Lys Val Ser Arg Asp Asp Gly Glu 370 375 380	1272
gct act gtt gaa ttt tac cgt gaa ggc gag gat cct gaa tta agc aca	1320

Ala Thr Val Glu Phe Tyr Arg Glu Gly Glu Asp Pro Glu Leu Ser Thr	
385 390 395	
atg tgg ttt act tgg cgg aag gag act ctg atg gga ttc cat gag gac	1368
Met Trp Phe Thr Trp Arg Lys Glu Thr Leu Met Gly Phe His Glu Asp	
400 405 410 415	
gcg tct gtt tac agc tta gaa agc gtg aac caa gcc cgc gtt tct ggt	1416
Ala Ser Val Tyr Ser Leu Glu Ser Val Asn Gln Ala Arg Val Ser Gly	
420 425 430	
gag gat atc gag cgg gga gtt gaa gcc gtc tat cgt aag ctg ggc ata	1464
Glu Asp Ile Glu Arg Gly Val Glu Ala Val Tyr Arg Lys Leu Gly Ile	
435 440 445	
ccc gtc tca tct tat cgg ctg aca gat att gat tta tta ttc cca ttc	1512
Pro Val Ser Ser Tyr Arg Leu Thr Asp Ile Asp Leu Leu Phe Pro Phe	
450 455 460	
agc ctc aac tcg gca tcc atc aac ata aag aca agt gac gga atg ggg	1560
Ser Leu Asn Ser Ala Ser Ile Asn Ile Lys Thr Ser Asp Gly Met Gly	
465 470 475	
atg gag ttc cac cct gta aca ggt gca tta acg gct att tcg atc aaa	1608
Met Glu Phe His Pro Val Thr Gly Ala Leu Thr Ala Ile Ser Ile Lys	
480 485 490 495	
tct gaa agc gcc ttg cct tat cgc gga caa gag ctt gaa aaa cgc ttg	1656
Ser Glu Ser Ala Leu Pro Tyr Arg Gly Gln Glu Leu Glu Lys Arg Leu	
500 505 510	
ctt tca tta ttt gat caa gac att tcc aat ctg aaa agg gtg gag tta	1704
Leu Ser Leu Phe Asp Gln Asp Ile Ser Asn Leu Lys Arg Val Glu Leu	
515 520 525	
gaa aag gat ctg ata gaa ttt cag aaa aaa gaa agc gat gct gtg tta	1752
Glu Lys Asp Leu Ile Glu Phe Gln Lys Lys Glu Ser Asp Ala Val Leu	
530 535 540	
aat acg gtc tgg acc atg acg aaa cat gaa gag gga gct tat ctg acg	1800
Asn Thr Val Trp Thr Met Thr Lys His Glu Glu Gly Ala Tyr Leu Thr	
545 550 555	
gtg aga aaa aac ttt caa aaa gca gat gaa aaa ccc ccc tac acg tat	1848
Val Arg Lys Asn Phe Gln Lys Ala Asp Glu Lys Pro Pro Tyr Thr Tyr	
560 565 570 575	
gca gac ggg gaa aaa gct ttt cag aaa gtg tct gaa cgc tat caa aaa	1896
Ala Asp Gly Glu Lys Ala Phe Gln Lys Val Ser Glu Arg Tyr Gln Lys	
580 585 590	
ggg ctg gtc tat cat aaa cgg acg aag ctt gta atc gtt tca gac ggg	1944
Gly Leu Val Tyr His Lys Arg Thr Lys Leu Val Ile Val Ser Asp Gly	
595 600 605	
gat caa aag agc cgt tat gcg tgg ctt gtc atc atc cag ccg ttc ggc	1992
Asp Gln Lys Ser Arg Tyr Ala Trp Leu Val Ile Ile Gln Pro Phe Gly	



Val Cys Arg Arg Arg Leu Phe Phe Tyr Ala Gly Ile Val Leu Arg Leu  
50 55 60  
Ile Leu Val Gly Ala Leu Ser Phe Glu Leu Ala His Gln Met Lys Ala  
65 70 75 80  
Ala Glu Phe Ser Asn Leu Tyr Ile Asp Glu Gln Asp Ala Leu Leu Pro  
85 90 95  
Phe Met Gln Phe Leu Leu Phe Gly Tyr Ile Leu Leu Val Ser Phe His  
100 105 110  
Tyr Met Met Thr Leu Ala Glu Lys Gly Gly Lys Gly Leu Phe Phe Ala  
115 120 125  
Phe Asp Ile Ala Val Met Ala Met Pro Leu Phe Gln Ser Leu Phe Ser  
130 135 140  
Phe Ala Ala Tyr Leu Lys Glu Phe Gly Ala Glu Glu Leu Glu Glu Leu  
145 150 155 160  
Pro Leu Val Leu Leu Leu Ile Val Gly Ile Pro Gly Leu Met Ile Cys  
165 170 175  
Leu Phe Phe Gln Leu Tyr Trp Lys Arg Asn Arg Tyr Val Leu Leu Leu  
180 185 190  
Ile Phe Tyr Ile Val Thr Ile Gly Gly Phe Phe Ile Lys Lys Leu Gly  
195 200 205  
Tyr Glu Phe Phe Pro Leu Asn Val Phe Leu Thr Met Ile Gly Phe Leu  
210 215 220  
Met Thr Tyr His Leu Leu Asn Asp Ser Arg Lys Pro Leu Leu Met Val  
225 230 235 240  
Lys Arg Val Leu Ala Ala Gly Thr Ala Val Phe Phe Thr Leu His Leu  
245 250 255  
Asn Pro Phe Tyr Asn Leu Ala Asp Ala Ala Phe Thr Ile Ser His Pro  
260 265 270

Glu Val Ser Asp Val Val Asp Ala Asn Phe Arg Pro Val Ser Val Lys  
275 280 285

Glu Ala Lys Gln Thr Val Ser Ser Phe Phe Pro Thr Glu Ser Phe Ile  
290 295 300

Tyr Leu Ser Ala Thr Asn Gln Asp Phe His Asn Val Tyr His Phe Lys  
305 310 315 320

Thr Lys Asp Tyr Asp Ala Asp Val Asp Gly Trp Thr Gly Met Ile Thr  
325 330 335

Asn Tyr His Asn Gln Lys Lys Pro Ser Gly Asn Ile Leu Ser Gly Gln  
340 345 350

Ala Tyr Ile Lys Arg Ser Lys Gln Phe Leu Arg Glu His Gly Arg Glu  
355 360 365

Leu Asp Lys Gln Ile Lys Ala Lys Val Ser Arg Asp Asp Gly Glu Ala  
370 375 380

Thr Val Glu Phe Tyr Arg Glu Gly Glu Asp Pro Glu Leu Ser Thr Met  
385 390 395 400

Trp Phe Thr Trp Arg Lys Glu Thr Leu Met Gly Phe His Glu Asp Ala  
405 410 415

Ser Val Tyr Ser Leu Glu Ser Val Asn Gln Ala Arg Val Ser Gly Glu  
420 425 430

Asp Ile Glu Arg Gly Val Glu Ala Val Tyr Arg Lys Leu Gly Ile Pro  
435 440 445

Val Ser Ser Tyr Arg Leu Thr Asp Ile Asp Leu Leu Phe Pro Phe Ser  
450 455 460

Leu Asn Ser Ala Ser Ile Asn Ile Lys Thr Ser Asp Gly Met Gly Met  
465 470 475 480

Glu Phe His Pro Val Thr Gly Ala Leu Thr Ala Ile Ser Ile Lys Ser  
485 490 495

Glu Ser Ala Leu Pro Tyr Arg Gly Gln Glu Leu Glu Lys Arg Leu Leu

500

505

510

Ser Leu Phe Asp Gln Asp Ile Ser Asn Leu Lys Arg Val Glu Leu Glu  
 515 520 525

Lys Asp Leu Ile Glu Phe Gln Lys Lys Glu Ser Asp Ala Val Leu Asn  
 530 535 540

Thr Val Trp Thr Met Thr Lys His Glu Glu Gly Ala Tyr Leu Thr Val  
 545 550 555 560

Arg Lys Asn Phe Gln Lys Ala Asp Glu Lys Pro Pro Tyr Thr Tyr Ala  
 565 570 575

Asp Gly Glu Lys Ala Phe Gln Lys Val Ser Glu Arg Tyr Gln Lys Gly  
 580 585 590

Leu Val Tyr His Lys Arg Thr Lys Leu Val Ile Val Ser Asp Gly Asp  
 595 600 605

Gln Lys Ser Arg Tyr Ala Trp Leu Val Ile Ile Gln Pro Phe Gly Ser  
 610 615 620

Asn Glu His Asp Ala Tyr Leu Val Asp Ala Glu Thr Asp Glu Val Lys  
 625 630 635 640

His Phe Asp Asp Lys  
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 ttatatgacg gctgcatcga ctttgccatt gaggcataatt tgctgggagc cgagtacggg 180  
 aagttcggct atcacggaga acccgttcat cgagcgatga tccgctcaga aaaagaagaa 240



aaacagctac tgcacgagct ttatgaatat gctgtcagct ggtctgaggc ttttaatgtt	300
caagctgctt atgaaccgct ctattatgcc tgcgaatact tcatccaaag ctggtggaag	360
gaaggcttca gccagcggga aagacgcttt aagcttcggc tcagataaaa caaagtttta	420
tgaaaaagtg aggccaagct taatcatatt tcctttcctt gtcccatatc ttgtagtaag	480
gacgagcggg agggaaaggg atg aag aaa aaa ata aaa tgg ctc ggg ttt tta	533
Met Lys Lys Lys Ile Lys Trp Leu Gly Phe Leu	
1 5 10	
ctc ggc ttt gtc gtt tta tta tgt tta ttt caa tat caa ttc aac aat	581
Leu Gly Phe Val Val Leu Leu Cys Leu Phe Gln Tyr Gln Phe Asn Asn	
15 20 25	
gat gat tct tgg cgg tca tgg aat ctt ccg ctg agc ggc aaa atc att	629
Asp Asp Ser Trp Arg Ser Trp Asn Leu Pro Leu Ser Gly Lys Ile Ile	
30 35 40	
tat att gat cct gga cac ggg ggc gcc gat gga ggg gca tca agc ggt	677
Tyr Ile Asp Pro Gly His Gly Gly Ala Asp Gly Gly Ala Ser Ser Gly	
45 50 55	
gaa ctc ctt gaa aaa gac gtg gct ctt gaa gta tcc cta aga atc agg	725
Glu Leu Leu Glu Lys Asp Val Ala Leu Glu Val Ser Leu Arg Ile Arg	
60 65 70 75	
gac tat ctc cag gag cag ggc gcc ttg gtg atg ctg acg cgg gag gac	773
Asp Tyr Leu Gln Glu Gln Gly Ala Leu Val Met Leu Thr Arg Glu Asp	
80 85 90	
gat cat gat ctc gct cct gaa gaa acg agg gga ctc agc aga aga aaa	821
Asp His Asp Leu Ala Pro Glu Glu Thr Arg Gly Leu Ser Arg Arg Lys	
95 100 105	
gct gaa gac ttg cgg aag agg gtc gat atg atc aac aat tct gaa gcc	869
Ala Glu Asp Leu Arg Lys Arg Val Asp Met Ile Asn Asn Ser Glu Ala	
110 115 120	
gat ctt tac ctc agc atc cat ttg aat gcg att cct tcc gcg cga tgg	917
Asp Leu Tyr Leu Ser Ile His Leu Asn Ala Ile Pro Ser Ala Arg Trp	
125 130 135	
agc ggt gcg caa agc ttc tat tac ggg caa tat gaa gag aat gaa cgg	965
Ser Gly Ala Gln Ser Phe Tyr Tyr Gly Gln Tyr Glu Glu Asn Glu Arg	
140 145 150 155	
gcc gcc aag ttt att cag gat gaa tta aga cat aat ctt gaa aac acg	1013
Ala Ala Lys Phe Ile Gln Asp Glu Leu Arg His Asn Leu Glu Asn Thr	
160 165 170	
acg cgg aag gca aag cgg ata cac gga att tat ttg atg caa aat gtt	1061
Thr Arg Lys Ala Lys Arg Ile His Gly Ile Tyr Leu Met Gln Asn Val	
175 180 185	

aaa aag ccc ggg gcc ctt gtc gaa atc ggg ttt ttg tct aac ccg gaa 1109  
 Lys Lys Pro Gly Ala Leu Val Glu Ile Gly Phe Leu Ser Asn Pro Glu  
 190 195 200

gag gca aaa cag ctg gcc aag ccc aaa tat cag gac aaa atc gca gca 1157  
 Glu Ala Lys Gln Leu Ala Lys Pro Lys Tyr Gln Asp Lys Ile Ala Ala  
 205 210 215

tcc gtt tat aaa ggc gta ttg cgc tac ttt aca gaa gac aga gac cct 1205  
 Ser Val Tyr Lys Gly Val Leu Arg Tyr Phe Thr Glu Asp Arg Asp Pro  
 220 225 230 235

cct gaa taagagggtt tctttttgtg tcaaagacac tataaggaaa gatatgctat 1261  
 Pro Glu

acttatttttg taaacgaata caacaaaggg tgagatcaat gttgcgagaa gacgatgtaa 1321

aaaagatagt cggcgatttg gacgagccat ttcttcacaa gccgctcaga gagctggatg 1381

ccgtaaaaga aattaaaata aaacccgaaa aacggcacgt cagcgtaaag gtggcgctcg 1441

caaaaacggg atctgccgaa caaatgcagc ttcagcagga aatcgtcata cggttgaaag 1501

aagccggtgc agagacggtc ggcctgcgtt ttgaggagct gcccgaagaa gtcgtaatga 1561

gttatcaaga gtctgcaaaa gggcaggatc aatctctgct gaatagtga aaacagcctg 1621

tgttttttagc tgtggcaagc ggcaaaggcg gcgtcggcaa gtcgacggtg tcggtcaatt 1681

tggctgtgtc cctggcgcgga atcggaaaga a 1712

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 20 25 30

Ser Trp Asn Leu Pro Leu Ser Gly Lys Ile Ile Tyr Ile Asp Pro Gly  
 35 40 45

His Gly Gly Ala Asp Gly Gly Ala Ser Ser Gly Glu Leu Leu Glu Lys  
 50 55 60

Asp Val Ala Leu Glu Val Ser Leu Arg Ile Arg Asp Tyr Leu Gln Glu

65

70

75

80

Gln Gly Ala Leu Val Met Leu Thr Arg Glu Asp Asp His Asp Leu Ala  
85 90 95

Pro Glu Glu Thr Arg Gly Leu Ser Arg Arg Lys Ala Glu Asp Leu Arg  
100 105 110

Lys Arg Val Asp Met Ile Asn Asn Ser Glu Ala Asp Leu Tyr Leu Ser  
115 120 125

Ile His Leu Asn Ala Ile Pro Ser Ala Arg Trp Ser Gly Ala Gln Ser  
130 135 140

Phe Tyr Tyr Gly Gln Tyr Glu Glu Asn Glu Arg Ala Ala Lys Phe Ile  
145 150 155 160

Gln Asp Glu Leu Arg His Asn Leu Glu Asn Thr Thr Arg Lys Ala Lys  
165 170 175

Arg Ile His Gly Ile Tyr Leu Met Gln Asn Val Lys Lys Pro Gly Ala  
180 185 190

Leu Val Glu Ile Gly Phe Leu Ser Asn Pro Glu Glu Ala Lys Gln Leu  
195 200 205

Ala Lys Pro Lys Tyr Gln Asp Lys Ile Ala Ala Ser Val Tyr Lys Gly  
210 215 220

Val Leu Arg Tyr Phe Thr Glu Asp Arg Asp Pro Pro Glu  
225 230 235

<210> 35  
<211> 1988  
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<222> (501)..(1487)

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aagaatctag ttgagcgggtg gagcagggga ttccttatta tgactgcgat tttgcacatt	180
tctccattttt cctgcaaggt caaaagacat agttcttaag ttttggattt ttggtgtgtt	240
tatttttttgt ttcacaaaact ttaaggtaat tttaagaaag aggcgatctt gccaaccccta	300
aacagggtttt ttcgaacaga atgtcaaata gattagatat ttcataagaa caaggggggaa	360
ttgtctgttt gtgatgaata aaggaggacg ggcggaattt ctgtcaggat gctcagctgg	420
gttcttagaa aaaaatgcgg ctaaataatat atttatagat tgtaaacgct gtcttgtcct	480
cgaccaacag ggggatgaag atg aag aag ctg tta gtt gtt tat gcc gtg atg	533
Met Lys Lys Leu Leu Val Val Tyr Ala Val Met	
1 5 10	
ctc tgt ttg ttt ttt ctg tat gtc tac gac tac tcc cgg ggc gat aaa	581
Leu Cys Leu Phe Phe Leu Tyr Val Tyr Asp Tyr Ser Arg Gly Asp Lys	
15 20 25	
gcc ggt tct gca gaa gaa agc agg agg cct gcg gcc gca ggc agt ctg	629
Ala Gly Ser Ala Glu Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu	
30 35 40	
tcc gaa aaa tac gtg atg gtc acg ttt caa tcg gga atc gaa tat tgg	677
Ser Glu Lys Tyr Val Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp	
45 50 55	
aag agc ggt ctg aaa ggc ttt gag gat gcc gcg cag ctt ttc aac gtc	725
Lys Ser Gly Leu Lys Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val	
60 65 70 75	
tct gtc gag tat cgg ggg gcg gcc cat tat gat gtc cat gag caa acg	773
Ser Val Glu Tyr Arg Gly Ala Ala His Tyr Asp Val His Glu Gln Thr	
80 85 90	
acc gtc ctc gag cag gtg att gca aaa aaa ccg gcg gga atc gct gtt	821
Thr Val Leu Glu Gln Val Ile Ala Lys Lys Pro Ala Gly Ile Ala Val	
95 100 105	
tcg gca ata aac cca aaa gct tta aac cct gtc atc gac aag gcg cac	869
Ser Ala Ile Asn Pro Lys Ala Leu Asn Pro Val Ile Asp Lys Ala His	
110 115 120	
gag cag ggt att ccg atc gtt tta ttt gat tca gac gcc ccg ctc agc	917
Glu Gln Gly Ile Pro Ile Val Leu Phe Asp Ser Asp Ala Pro Leu Ser	
125 130 135	
aaa gct tct aca tat atc ggc aca aat aat atg gaa gcg ggt gct gtg	965
Lys Ala Ser Thr Tyr Ile Gly Thr Asn Asn Met Glu Ala Gly Ala Val	
140 145 150 155	
gcc gca agg cga atg gcc gaa ttt ttg aat gga aag gga gaa acc gcg	1013
Ala Ala Arg Arg Met Ala Glu Phe Leu Asn Gly Lys Gly Glu Thr Ala	
160 165 170	

gtc att acc cag ccg cag cag tac aat cat cag gaa agg acg aag ggc Val Ile Thr Gln Pro Gln Gln Tyr Asn His Gln Glu Arg Thr Lys Gly 175 180 185	1061
ttt gaa caa acg atc aag caa aaa tac ccg aac atg aag gtt gcc gcg Phe Glu Gln Thr Ile Lys Gln Lys Tyr Pro Asn Met Lys Val Ala Ala 190 195 200	1109
gtt ttg gac gga aaa ggg gat gag ctg acg tcg aaa aaa gaa gcg gcg Val Leu Asp Gly Lys Gly Asp Glu Leu Thr Ser Lys Lys Glu Ala Ala 205 210 215	1157
aag att ttg gag gaa aat ccg tcc atc aaa gga att ttc acg act gaa Lys Ile Leu Glu Glu Asn Pro Ser Ile Lys Gly Ile Phe Thr Thr Glu 220 225 230 235	1205
gcc aat gga gcg agc ggc gtg gcc cgt gct gtg aag gag gcg gga ctt Ala Asn Gly Ala Ser Gly Val Ala Arg Ala Val Lys Glu Ala Gly Leu 240 245 250	1253
gaa ggg gaa gta tgt atc atc ggc ttt gat aaa gac aag aaa acg ctg Glu Gly Glu Val Cys Ile Ile Gly Phe Asp Lys Asp Lys Lys Thr Leu 255 260 265	1301
gac ggc atc aaa aac gga tcg att tcc gcg aca atg agc cag gac aca Asp Gly Ile Lys Asn Gly Ser Ile Ser Ala Thr Met Ser Gln Asp Thr 270 275 280	1349
tgg caa atg ggc tat tgg tcg ctg cac atg ctg ttt ttc tca aat cac Trp Gln Met Gly Tyr Trp Ser Leu His Met Leu Phe Phe Ser Asn His 285 290 295	1397
cat ctg aag cat gaa cgc ccg ctt ccg gcc gca atc gac aca ggc att His Leu Lys His Glu Arg Pro Leu Pro Ala Ala Ile Asp Thr Gly Ile 300 305 310 315	1445
acc atc ata acg aaa gaa aat gtg gca gcc tat tat gcg aat Thr Ile Ile Thr Lys Glu Asn Val Ala Ala Tyr Tyr Ala Asn 320 325	1487
gattaaacgt ttgatcaata atgcgccgat ccgtcataag ctgatcagcc ttctcttggt 1547	
aatcagcatg ctgccgacga tcggcctggg cattttatcg ggatgggccc ttgaaaatat 1607	
tattgaaaaa caggtgatcg accaaacact gcagctgatc ggccaagtga acaagacggc 1667	
tgaagtgtat gtcagccaca tgcagaacct gacatattta atatcaatga atgaagaaat 1727	
ggaagcgttt tttagtcata aaaaggagga tggagaggcg gattataagc gaaggacgtt 1787	
tttgcagggc ctgacttctt tatattccga agcagcgggt attctcgttg tcaatgataa 1847	
gggtgagatg atcagcaatg agatgtatga acgcacgccg acagatttga caaaagaacc 1907	
atggtatcag gcggctctcg acaatgaagg gattttcaag atgatcggga agcctgtcaa 1967	
ccggaatatc agaagccatg t 1988	

<210> 36  
 <211> 329  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 36

Met Lys Lys Leu Leu Val Val Tyr Ala Val Met Leu Cys Leu Phe Phe  
 1 5 10 15

Leu Tyr Val Tyr Asp Tyr Ser Arg Gly Asp Lys Ala Gly Ser Ala Glu  
 20 25 30

Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu Ser Glu Lys Tyr Val  
 35 40 45

Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp Lys Ser Gly Leu Lys  
 50 55 60

Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val Ser Val Glu Tyr Arg  
 65 70 75 80

Gly Ala Ala His Tyr Asp Val His Glu Gln Thr Thr Val Leu Glu Gln  
 85 90 95

Val Ile Ala Lys Lys Pro Ala Gly Ile Ala Val Ser Ala Ile Asn Pro  
 100 105 110

Lys Ala Leu Asn Pro Val Ile Asp Lys Ala His Glu Gln Gly Ile Pro  
 115 120 125

Ile Val Leu Phe Asp Ser Asp Ala Pro Leu Ser Lys Ala Ser Thr Tyr  
 130 135 140

Ile Gly Thr Asn Asn Met Glu Ala Gly Ala Val Ala Ala Arg Arg Met  
 145 150 155 160

Ala Glu Phe Leu Asn Gly Lys Gly Glu Thr Ala Val Ile Thr Gln Pro  
 165 170 175

Gln Gln Tyr Asn His Gln Glu Arg Thr Lys Gly Phe Glu Gln Thr Ile  
 180 185 190

Lys Gln Lys Tyr Pro Asn Met Lys Val Ala Ala Val Leu Asp Gly Lys  
 195 200 205

Gly Asp Glu Leu Thr Ser Lys Lys Glu Ala Ala Lys Ile Leu Glu Glu  
 210 215 220

Asn Pro Ser Ile Lys Gly Ile Phe Thr Thr Glu Ala Asn Gly Ala Ser  
 225 230 235 240

Gly Val Ala Arg Ala Val Lys Glu Ala Gly Leu Glu Gly Glu Val Cys  
 245 250 255

Ile Ile Gly Phe Asp Lys Asp Lys Lys Thr Leu Asp Gly Ile Lys Asn  
 260 265 270

Gly Ser Ile Ser Ala Thr Met Ser Gln Asp Thr Trp Gln Met Gly Tyr  
 275 280 285

Trp Ser Leu His Met Leu Phe Phe Ser Asn His His Leu Lys His Glu  
 290 295 300

Arg Pro Leu Pro Ala Ala Ile Asp Thr Gly Ile Thr Ile Ile Thr Lys  
 305 310 315 320

Glu Asn Val Ala Ala Tyr Tyr Ala Asn  
 325

<210> 37  
 <211> 2785  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(2282)

<400> 37  
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 cggaaaccgc aaacaaagcg aaggcaacgg aatttgtgta tcaagtcaac agcttatctc 120  
 acagtgattt aaacaagatg ttcggctctc cagatgcacc ggcagaagcg cagaatctga 180  
 caaaagcggg tatggcggtt ttagagaagg aaaataaata gatcaaacgg ccgactcggc 240  
 ttcctacatg tacttgctga aaggatataa acagctgtta aactagcaga gaaaggccga 300

aaatgttaaa ttcggcctct tctcacactt ggcaccccct tactcataag acatcgatct	360
gaaaattccc aaaatataaa caaaacatta ataaaaatcaa gccatttgat taacaaattt	420
acgatacgat catatagaac ttgatgattg ggaaaagcat tttgagagaa gattaagagc	480
aagggagata tgatgtgaga atg aaa cga tta agg atg agg aag cat tta ctg	533
Met Lys Arg Leu Arg Met Arg Lys His Leu Leu	
1 5 10	
ata gct gtc tgt act ttg gca ctt ctt cta agt tcc ccg att gta agc	581
Ile Ala Val Cys Thr Leu Ala Leu Leu Ser Ser Pro Ile Val Ser	
15 20 25	
gat gcg agc ccg gca act aaa cca aca act gca gat tcg ccg caa tct	629
Asp Ala Ser Pro Ala Thr Lys Pro Thr Thr Ala Asp Ser Pro Gln Ser	
30 35 40	
tcc gga ttt ttc gta gac cat tac aaa aat aat atc tct gcc aat acg	677
Ser Gly Phe Phe Val Asp His Tyr Lys Asn Asn Ile Ser Ala Asn Thr	
45 50 55	
acg gcg gaa tcc aat cct gtc atc ggc ctg ctt tcc gaa ttt aat aaa	725
Thr Ala Glu Ser Asn Pro Val Ile Gly Leu Leu Ser Glu Phe Asn Lys	
60 65 70 75	
ctt tgg act ccc gga aag aca tgg aat acc ggt act aaa ctg aac agc	773
Leu Trp Thr Pro Gly Lys Thr Trp Asn Thr Gly Thr Lys Leu Asn Ser	
80 85 90	
agg gtg ctg gat gcc aac att caa aaa gtc gtg gat att gct gaa cgc	821
Arg Val Leu Asp Ala Asn Ile Gln Lys Val Val Asp Ile Ala Glu Arg	
95 100 105	
cgc acg atg ctt gag gaa aat gct gcc tat ttt gat gat cgg cgg agc	869
Arg Thr Met Leu Glu Glu Asn Ala Ala Tyr Phe Asp Asp Arg Arg Ser	
110 115 120	
cag agc tac agt ata att gac ggc ctc ggc aag ctt gcc ggc gtc tat	917
Gln Ser Tyr Ser Ile Ile Asp Gly Leu Gly Lys Leu Ala Gly Val Tyr	
125 130 135	
cga atg aac gcg gga gcg acg aca acg atc acc agc att ccg gca gat	965
Arg Met Asn Ala Gly Ala Thr Thr Thr Ile Thr Ser Ile Pro Ala Asp	
140 145 150 155	
gcc tcg att aga aaa tac aat gat gaa gga acc aat tcg ggc agc acc	1013
Ala Ser Ile Arg Lys Tyr Asn Asp Glu Gly Thr Asn Ser Gly Ser Thr	
160 165 170	
agc tct gaa ctt gga aat gtc gta agt ttg gtc aat act tta cgc ggc	1061
Ser Ser Glu Leu Gly Asn Val Val Ser Leu Val Asn Thr Leu Arg Gly	
175 180 185	
aac tat tct tca tcg aat ccg gct aaa agc tat ttc aac tat ccc cgc	1109
Asn Tyr Ser Ser Ser Asn Pro Ala Lys Ser Tyr Phe Asn Tyr Pro Arg	
190 195 200	



ccg ttt cgc tgg aaa gac aat tcg atc att gtt cca acg ctt atc ccc Pro Phe Arg Trp Lys Asp Asn Ser Ile Ile Val Pro Thr Leu Ile Pro 205 210 215	1157
gtc atc aat cct gat ccg aac aaa gac gga ggt ttt cca agc gga cac Val Ile Asn Pro Asp Pro Asn Lys Asp Gly Gly Phe Pro Ser Gly His 220 225 230 235	1205
acg aac gcc gca tat ctc agc gct ttt gct atg gcc tat gcg ata ccg Thr Asn Ala Ala Tyr Leu Ser Ala Phe Ala Met Ala Tyr Ala Ile Pro 240 245 250	1253
gag cgt tat cag gag ctg ctg act cgc gct tca gaa ctc ggt cat aac Glu Arg Tyr Gln Glu Leu Leu Thr Arg Ala Ser Glu Leu Gly His Asn 255 260 265	1301
cgg att gtt gcc ggt atg cat tcc ccg ctg gac gtc atg ggg gga cga Arg Ile Val Ala Gly Met His Ser Pro Leu Asp Val Met Gly Gly Arg 270 275 280	1349
gta atg gca aca gct ttg tct gca gca atc ctg tct gac ccc gca aat Val Met Ala Thr Ala Leu Ser Ala Ala Ile Leu Ser Asp Pro Ala Asn 285 290 295	1397
gaa aga ttg aag aaa acg gct ttt gat gaa gcc cgc cgt aaa tta tta Glu Arg Leu Lys Lys Thr Ala Phe Asp Glu Ala Arg Arg Lys Leu Leu 300 305 310 315	1445
acg caa acc ggt aca gct gaa gac aga tac agc gat tat gag aag aat Thr Gln Thr Gly Thr Ala Glu Asp Arg Tyr Ser Asp Tyr Glu Lys Asn 320 325 330	1493
aaa aaa caa tat acg gaa cga ttg aca tat gga ttt cga caa atg aac Lys Lys Gln Tyr Thr Glu Arg Leu Thr Tyr Gly Phe Arg Gln Met Asn 335 340 345	1541
aaa acc gcc aaa cca atg gca gtt cca aag gga gcc gaa gtc ctg ctg Lys Thr Ala Lys Pro Met Ala Val Pro Lys Gly Ala Glu Val Leu Leu 350 355 360	1589
gaa aca cgt ttt cct tac ctt gac aaa aag cag cgc cgt tcg gtt tta Glu Thr Arg Phe Pro Tyr Leu Asp Lys Lys Gln Arg Arg Ser Val Leu 365 370 375	1637
gcc act acc ggt ctt ccg gcc ggc tac cct gtt ctt gat gat cga gaa Ala Thr Thr Gly Leu Pro Ala Gly Tyr Pro Val Leu Asp Asp Arg Glu 380 385 390 395	1685
gga tgg gga agg ctt aat ctc ttt tcc gcg gca gat ggg tat ggg gct Gly Trp Gly Arg Leu Asn Leu Phe Ser Ala Ala Asp Gly Tyr Gly Ala 400 405 410	1733
ttt acc aaa aat gtt acc gtg acc atg gat tcc gca aaa ggc ggc ttc Phe Thr Lys Asn Val Thr Val Thr Met Asp Ser Ala Lys Gly Gly Phe 415 420 425	1781

cat aca gcc gat cgc tgg cgc aac gac atc tcc ggc acc gga aag ctg	1829
His Thr Ala Asp Arg Trp Arg Asn Asp Ile Ser Gly Thr Gly Lys Leu	
430 435 440	
acc aaa aaa ggg aca ggc gct ttg aag ctg gaa ggg gat aat aca tat	1877
Thr Lys Lys Gly Thr Gly Ala Leu Lys Leu Glu Gly Asp Asn Thr Tyr	
445 450 455	
tcc ggc ggt aca cgg att gat caa gga aca ctt gag ggc ggt tcg gag	1925
Ser Gly Gly Thr Arg Ile Asp Gln Gly Thr Leu Glu Gly Gly Ser Glu	
460 465 470 475	
aca gct ttc ggg aga ggt gat gtt gca cta aac gga ggc atc ctt aag	1973
Thr Ala Phe Gly Arg Gly Asp Val Ala Leu Asn Gly Gly Ile Leu Lys	
480 485 490	
gaa gat gcg ccg gga aaa ctg atc atc gaa gga gac tac aaa caa tct	2021
Glu Asp Ala Pro Gly Lys Leu Ile Ile Glu Gly Asp Tyr Lys Gln Ser	
495 500 505	
gct aaa gga ata ctt gaa ctt cag ctc agc ggc aaa aaa gat cag ttg	2069
Ala Lys Gly Ile Leu Glu Leu Gln Leu Ser Gly Lys Lys Asp Gln Leu	
510 515 520	
aaa att aag gga aaa gca aga ttg aaa ggg aca ttg cgt ctc aat ttt	2117
Lys Ile Lys Gly Lys Ala Arg Leu Lys Gly Thr Leu Arg Leu Asn Phe	
525 530 535	
acg gac aat tac gta ccg gct gac gga tcg gcg atc ata acc ttc cgc	2165
Thr Asp Asn Tyr Val Pro Ala Asp Gly Ser Ala Ile Ile Thr Phe Arg	
540 545 550 555	
aag cgt cat gga tca ttt tct tcc gtc gag acc agt gga ttg cca agc	2213
Lys Arg His Gly Ser Phe Ser Ser Val Glu Thr Ser Gly Leu Pro Ser	
560 565 570	
aag tat aaa gtg aag atc atc tat aaa tcc aac agt att cag ttg aaa	2261
Lys Tyr Lys Val Lys Ile Ile Tyr Lys Ser Asn Ser Ile Gln Leu Lys	
575 580 585	
gtt gag caa aag ggg aga agc tgatctgcaa gaggattcac tcaaaagctg	2312
Val Glu Gln Lys Gly Arg Ser	
590	
caagctggcg catactgccg ccagcttgct tttagttttg atgaaatcac agccagaatg	2372
gctgtacatc ttgaatgggg aatcttaaaa aatagtcggc accattcccc cgtccatacg	2432
gatcggggac cctttaaatg cggatgcata gggactgcat acaaatgcag ccagtctgcc	2492
gatttcaata ggcttgataa atcgctgtat ttcggattga ggcaggtttg tcgtcataaa	2552
tttcttctct ttttctgaaa aagtcatccc ttcatcgggg tacattccct caatgatttg	2612
cttcacattc tcagagagcg tcggccccgg catgatcgta ttgactgtca cttctgttcc	2672
gattgttaat tttgataagc tttttgacaa tgataaatagc attgattttg tcatacaata	2732

ctgaggcatc tggcctgaag gcatcatcgc ttcttcactt gcgataaaga tga

2785

<210> 38  
<211> 594  
<212> PRT  
<213> Bacillus licheniformis

<400> 38

Met Lys Arg Leu Arg Met Arg Lys His Leu Leu Ile Ala Val Cys Thr  
1 5 10 15

Leu Ala Leu Leu Leu Ser Ser Pro Ile Val Ser Asp Ala Ser Pro Ala  
20 25 30

Thr Lys Pro Thr Thr Ala Asp Ser Pro Gln Ser Ser Gly Phe Phe Val  
35 40 45

Asp His Tyr Lys Asn Asn Ile Ser Ala Asn Thr Thr Ala Glu Ser Asn  
50 55 60

Pro Val Ile Gly Leu Leu Ser Glu Phe Asn Lys Leu Trp Thr Pro Gly  
65 70 75 80

Lys Thr Trp Asn Thr Gly Thr Lys Leu Asn Ser Arg Val Leu Asp Ala  
85 90 95

Asn Ile Gln Lys Val Val Asp Ile Ala Glu Arg Arg Thr Met Leu Glu  
100 105 110

Glu Asn Ala Ala Tyr Phe Asp Asp Arg Arg Ser Gln Ser Tyr Ser Ile  
115 120 125

Ile Asp Gly Leu Gly Lys Leu Ala Gly Val Tyr Arg Met Asn Ala Gly  
130 135 140

Ala Thr Thr Thr Ile Thr Ser Ile Pro Ala Asp Ala Ser Ile Arg Lys  
145 150 155 160

Tyr Asn Asp Glu Gly Thr Asn Ser Gly Ser Thr Ser Ser Glu Leu Gly  
165 170 175

Asn Val Val Ser Leu Val Asn Thr Leu Arg Gly Asn Tyr Ser Ser Ser  
180 185 190

Asn Pro Ala Lys Ser Tyr Phe Asn Tyr Pro Arg Pro Phe Arg Trp Lys  
 195 200 205

Asp Asn Ser Ile Ile Val Pro Thr Leu Ile Pro Val Ile Asn Pro Asp  
 210 215 220

Pro Asn Lys Asp Gly Gly Phe Pro Ser Gly His Thr Asn Ala Ala Tyr  
 225 230 235 240

Leu Ser Ala Phe Ala Met Ala Tyr Ala Ile Pro Glu Arg Tyr Gln Glu  
 245 250 255

Leu Leu Thr Arg Ala Ser Glu Leu Gly His Asn Arg Ile Val Ala Gly  
 260 265 270

Met His Ser Pro Leu Asp Val Met Gly Gly Arg Val Met Ala Thr Ala  
 275 280 285

Leu Ser Ala Ala Ile Leu Ser Asp Pro Ala Asn Glu Arg Leu Lys Lys  
 290 295 300

Thr Ala Phe Asp Glu Ala Arg Arg Lys Leu Leu Thr Gln Thr Gly Thr  
 305 310 315 320

Ala Glu Asp Arg Tyr Ser Asp Tyr Glu Lys Asn Lys Lys Gln Tyr Thr  
 325 330 335

Glu Arg Leu Thr Tyr Gly Phe Arg Gln Met Asn Lys Thr Ala Lys Pro  
 340 345 350

Met Ala Val Pro Lys Gly Ala Glu Val Leu Leu Glu Thr Arg Phe Pro  
 355 360 365

Tyr Leu Asp Lys Lys Gln Arg Arg Ser Val Leu Ala Thr Thr Gly Leu  
 370 375 380

Pro Ala Gly Tyr Pro Val Leu Asp Asp Arg Glu Gly Trp Gly Arg Leu  
 385 390 395 400

Asn Leu Phe Ser Ala Ala Asp Gly Tyr Gly Ala Phe Thr Lys Asn Val  
 405 410 415

Thr Val Thr Met Asp Ser Ala Lys Gly Gly Phe His Thr Ala Asp Arg  
420 425 430

Trp Arg Asn Asp Ile Ser Gly Thr Gly Lys Leu Thr Lys Lys Gly Thr  
435 440 445

Gly Ala Leu Lys Leu Glu Gly Asp Asn Thr Tyr Ser Gly Gly Thr Arg  
450 455 460

Ile Asp Gln Gly Thr Leu Glu Gly Gly Ser Glu Thr Ala Phe Gly Arg  
465 470 475 480

Gly Asp Val Ala Leu Asn Gly Gly Ile Leu Lys Glu Asp Ala Pro Gly  
485 490 495

Lys Leu Ile Ile Glu Gly Asp Tyr Lys Gln Ser Ala Lys Gly Ile Leu  
500 505 510

Glu Leu Gln Leu Ser Gly Lys Lys Asp Gln Leu Lys Ile Lys Gly Lys  
515 520 525

Ala Arg Leu Lys Gly Thr Leu Arg Leu Asn Phe Thr Asp Asn Tyr Val  
530 535 540

Pro Ala Asp Gly Ser Ala Ile Ile Thr Phe Arg Lys Arg His Gly Ser  
545 550 555 560

Phe Ser Ser Val Glu Thr Ser Gly Leu Pro Ser Lys Tyr Lys Val Lys  
565 570 575

Ile Ile Tyr Lys Ser Asn Ser Ile Gln Leu Lys Val Glu Gln Lys Gly  
580 585 590

Arg Ser

<210> 39  
<211> 2009  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS

<222> (501) .. (1526)

<400> 39

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ccctgagcag cgcaaaaact gccggtcagc ggccgaaaac agcagagggtg aagttttctt	120
actttgttaa agaaaaatca aatggctatg ttctatcaaa cggaaaactt tcttaaaaaa	180
cagcgattat ttccgtgacg acgactcaat taagatcgat gctgggcggc atgaatatga	240
agagcacgta tgcttctgta tccagcaata cgaacgcttt tactctcagc ggtaaaggat	300
tcggacacgg catcggcatg agtcagtacg gatcaaatgc cagagctgct gccgggcacg	360
attacaagaa gattttaagt ttctactatc caaatacgac tctatcaagc tattaataga	420
gtttgaacag gaagcagcag tgccctcctt gttcatgttc atgggaaaac ataacattta	480
catttttggg gggtattttt ttg aag gtc ttt ctt aaa gct gta cct atg ttg	533
Leu Lys Val Phe Leu Lys Ala Val Pro Met Leu	
1 5 10	
tcg tta cgg ttc ttt ttg ttt gtg cct aat gta ttt gcg gcc aac tct	581
Ser Leu Arg Phe Phe Leu Phe Val Pro Asn Val Phe Ala Ala Asn Ser	
15 20 25	
gtc aca aga ttg gac ggt gca aac cga tat gag gtt gcg gtg aac gtt	629
Val Thr Arg Leu Asp Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val	
30 35 40	
tcc aag cag ggg tgg aca agt gca agc act gtg att gtt gca aat gga	677
Ser Lys Gln Gly Trp Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly	
45 50 55	
aag gca tat gca gac gtc ctt tca gcg act cca ttt gcc tat cga aac	725
Lys Ala Tyr Ala Asp Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn	
60 65 70 75	
aac gcg cct gtt cta tta acg gaa gcg tct aaa ctg cca acg gcc act	773
Asn Ala Pro Val Leu Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr	
80 85 90	
aaa aac cga atc agt caa tta aaa cct agc aaa gtg atc gta atc ggc	821
Lys Asn Arg Ile Ser Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly	
95 100 105	
gga acc gtc agc gtt caa aac ggt gtc gta agc gag atc aaa aag ctt	869
Gly Thr Val Ser Val Gln Asn Gly Val Val Ser Glu Ile Lys Lys Leu	
110 115 120	
ggt gtg tca tct gtc gaa cgc atc ggc gga gcg aat cgc tac gag gtt	917
Gly Val Ser Ser Val Glu Arg Ile Gly Gly Ala Asn Arg Tyr Glu Val	
125 130 135	
gcg gcg aat att gcg aat aag ctg ccg agc aat tcg aaa gct gtc atc	965
Ala Ala Asn Ile Ala Asn Lys Leu Pro Ser Asn Ser Lys Ala Val Ile	

140	145	150	155	
gca aac ggg acg gcc tat gct gac agc ctt gcg atc ggc gca tat gcc				1013
Ala Asn Gly Thr Ala Tyr Ala Asp Ser Leu Ala Ile Gly Ala Tyr Ala				
	160	165	170	
gcg aga aac ggc atc ccg att ctt tta aca tcg tcg aat tcc ata ccg				1061
Ala Arg Asn Gly Ile Pro Ile Leu Leu Thr Ser Ser Asn Ser Ile Pro				
	175	180	185	
aca gcg aca aaa aat gcg atg aag agc aaa gga aca aca tcg acc att				1109
Thr Ala Thr Lys Asn Ala Met Lys Ser Lys Gly Thr Thr Ser Thr Ile				
	190	195	200	
gtc gta ggc ggt gaa gtc agc atc tcc agc agc gtt tac aaa cag ctt				1157
Val Val Gly Gly Glu Val Ser Ile Ser Ser Ser Val Tyr Lys Gln Leu				
	205	210	215	
gct tct ccg acg cgg atc ggc ggc agc aac cgc tat gaa gtc gcg gcc				1205
Ala Ser Pro Thr Arg Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala				
	220	225	230	235
aat gtc gtc aag aaa tat tat tct tct gcc aag aat gca atc atc agc				1253
Asn Val Val Lys Lys Tyr Tyr Ser Ser Ala Lys Asn Ala Ile Ile Ser				
	240	245	250	
aac ggc tat gcg tat gcc gac gga tta aca gga tct gtt ctg gcg gct				1301
Asn Gly Tyr Ala Tyr Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala				
	255	260	265	
aag caa aac cgt ccg atg atg ttc acg aat gca tca tct ttg ccg aca				1349
Lys Gln Asn Arg Pro Met Met Phe Thr Asn Ala Ser Ser Leu Pro Thr				
	270	275	280	
ccg aca aga gaa gtg atc ggt tcc aaa aac atg acg acg ttt act gtg				1397
Pro Thr Arg Glu Val Ile Gly Ser Lys Asn Met Thr Thr Phe Thr Val				
	285	290	295	
ctt ggc gga acg gtt tct ctt caa tcc aat gtc gtg tca cag ctg aag				1445
Leu Gly Gly Thr Val Ser Leu Gln Ser Asn Val Val Ser Gln Leu Lys				
	300	305	310	315
aat ccg atc gtc ggc aaa aaa atc ttc att gat gca ggg cac gga ggt				1493
Asn Pro Ile Val Gly Lys Lys Ile Phe Ile Asp Ala Gly His Gly Gly				
	320	325	330	
aca gac agc ggt gcc cgt cgg caa cgg ttt ata tgagaaaagc gtgaacctg				1546
Thr Asp Ser Gly Ala Arg Arg Gln Arg Phe Ile				
	335	340		
atgttgcaaa attaattaat acgaaactat caaacggcgg tgctctgccca attatggcga				1606
gaacgaacga cacttacctg acgctcgcac agcgcgtgtc aaaagcgcag tcaaatacatg				1666
cggattttgtt tgtcagcatc catgcaaact cggcaacgcc agctgcttcc ggaacagaaa				1726
cctactatta tacaacatat gaatctgccca acagcaaacg gctggcaacc gagattcaaa				1786

accgtctcta tgttgcatg aatacaaaaa accgcggtgt aaagatcggc aacttccatg 1846  
 tcatcagga atcaaaaatg ccaagctgcc ttgttgaact tgcgtttatc agcaatgtaa 1906  
 gcgatgcgac aaaactcaaa agctcgactt acaaagaaaa aggcgctaaa gcgatttacg 1966  
 acggaatcgt tgcttactat taaaatataa acagaaaact cgt 2009

<210> 40  
 <211> 342  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 40

Leu Lys Val Phe Leu Lys Ala Val Pro Met Leu Ser Leu Arg Phe Phe  
 1 5 10 15

Leu Phe Val Pro Asn Val Phe Ala Ala Asn Ser Val Thr Arg Leu Asp  
 20 25 30

Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val Ser Lys Gln Gly Trp  
 35 40 45

Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly Lys Ala Tyr Ala Asp  
 50 55 60

Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn Asn Ala Pro Val Leu  
 65 70 75 80

Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr Lys Asn Arg Ile Ser  
 85 90 95

Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly Gly Thr Val Ser Val  
 100 105 110

Gln Asn Gly Val Val Ser Glu Ile Lys Lys Leu Gly Val Ser Ser Val  
 115 120 125

Glu Arg Ile Gly Gly Ala Asn Arg Tyr Glu Val Ala Ala Asn Ile Ala  
 130 135 140

Asn Lys Leu Pro Ser Asn Ser Lys Ala Val Ile Ala Asn Gly Thr Ala  
 145 150 155 160



Tyr Ala Asp Ser Leu Ala Ile Gly Ala Tyr Ala Ala Arg Asn Gly Ile  
165 170 175

Pro Ile Leu Leu Thr Ser Ser Asn Ser Ile Pro Thr Ala Thr Lys Asn  
180 185 190

Ala Met Lys Ser Lys Gly Thr Thr Ser Thr Ile Val Val Gly Gly Glu  
195 200 205

Val Ser Ile Ser Ser Ser Val Tyr Lys Gln Leu Ala Ser Pro Thr Arg  
210 215 220

Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala Asn Val Val Lys Lys  
225 230 235 240

Tyr Tyr Ser Ser Ala Lys Asn Ala Ile Ile Ser Asn Gly Tyr Ala Tyr  
245 250 255

Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala Lys Gln Asn Arg Pro  
260 265 270

Met Met Phe Thr Asn Ala Ser Ser Leu Pro Thr Pro Thr Arg Glu Val  
275 280 285

Ile Gly Ser Lys Asn Met Thr Thr Phe Thr Val Leu Gly Gly Thr Val  
290 295 300

Ser Leu Gln Ser Asn Val Val Ser Gln Leu Lys Asn Pro Ile Val Gly  
305 310 315 320

Lys Lys Ile Phe Ile Asp Ala Gly His Gly Gly Thr Asp Ser Gly Ala  
325 330 335

Arg Arg Gln Arg Phe Ile  
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<210> 41  
<211> 2044  
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<220>  
<221> CDS  
<222> (469) .. (1566)

<400> 41  
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ttaaaaaccg gtttttcaga agttcataaa ggaaaaaacc agattgagac ttccggccga 180  
tacttttcag agattaaaaa taaagtgacg gatatggctg gccgtgtatc ggacatttcg 240  
gaggcattat cgcatttcag acgttcaagc gaggagatta acggctcggc cgagcatatc 300  
gcggcgattt ccgaagaaag cgcggccggc tctgaagaaa tttcagcgtc cgtacatgag 360  
caaagcggct cgattgaaaa gatggacgaa agcgcgaaggc ttctgggaga gatggttgaa 420  
cggatgaatg tgatgatcaa acggtttaag ctctgatgcc gatacaga atg ggg ggt 477  
Met Gly Gly  
1  
ttt aat gtt gtc gat ata tgt gaa aag agg gct gtt ggc act tgc gct 525  
Phe Asn Val Val Asp Ile Cys Glu Lys Arg Ala Val Gly Thr Cys Ala  
5 10 15  
gtt cag tct cct cac agc tgt tgc cgg gtg ctc att caa ttc tgc tta 573  
Val Gln Ser Pro His Ser Cys Cys Arg Val Leu Ile Gln Phe Cys Leu  
20 25 30 35  
aaa aag cgc caa ccg tta aga aaa agt aaa gct gat tgc cga ctc cga 621  
Lys Lys Arg Gln Pro Leu Arg Lys Ser Lys Ala Asp Cys Arg Leu Arg  
40 45 50  
caa att gta cgt cgg ttt tgc cat cga tac gct gaa gga aga acg ctg 669  
Gln Ile Val Arg Arg Phe Cys His Arg Tyr Ala Glu Gly Arg Thr Leu  
55 60 65  
gta caa aga tca aga agc gtt cga gaa aga agt tca aaa cct cgg ggg 717  
Val Gln Arg Ser Arg Ser Val Arg Glu Arg Ser Ser Lys Pro Arg Gly  
70 75 80  
gga agt caa gac gct tgc cgc tca cgg aaa tca aga agt tca gat tca 765  
Gly Ser Gln Asp Ala Cys Arg Ser Arg Lys Ser Arg Ser Ser Asp Ser  
85 90 95  
gca ggc cga gct ctt gat cag cga agg cgt cga cgt gct tgt tgt tgt 813  
Ala Gly Arg Ala Leu Asp Gln Arg Arg Arg Arg Arg Ala Cys Cys Cys  
100 105 110 115  
acc ggc aga tgc gga tgc cgc ggc gga gat cgt gaa aaa ggc gca cag 861  
Thr Gly Arg Cys Gly Cys Arg Gly Gly Asp Arg Glu Lys Gly Ala Gln  
120 125 130  
cgc cgg tgt aaa agt gat ttc gta tta ccg gct gat tcg aaa cgc gga 909  
Arg Arg Cys Lys Ser Asp Phe Val Leu Pro Ala Asp Ser Lys Arg Gly  
135 140 145  
tgt tta tta tta cgt ttc att tta tca cga aaa ggt cgg gga act gca 957

Cys	Leu	Leu	Leu	Arg	Phe	Ile	Leu	Ser	Arg	Lys	Gly	Arg	Gly	Thr	Ala		
	150						155					160					
ggc	gga	agc	gat	tgt	aaa	aaa	agc	gaa	gaa	agg	aaa	ctt	cgt	ata	tat	1005	
Gly	Gly	Ser	Asp	Cys	Lys	Lys	Ser	Glu	Glu	Arg	Lys	Leu	Arg	Ile	Tyr		
	165					170					175						
cgg	cgg	atc	gtc	tct	tta	caa	caa	tgc	ggt	ctt	att	ccg	gaa	cgg	cgc	1053	
Arg	Arg	Ile	Val	Ser	Leu	Gln	Gln	Cys	Gly	Leu	Ile	Pro	Glu	Arg	Arg		
	180					185				190					195		
cat	gaa	agt	gct	cga	acc	gtt	gaa	gcg	gca	ggg	tca	agt	caa	gct	cgt	1101	
His	Glu	Ser	Ala	Arg	Thr	Val	Glu	Ala	Ala	Gly	Ser	Ser	Gln	Ala	Arg		
				200					205					210			
gct	tta	cga	ata	tac	gaa	aga	ctg	gct	acc	aga	aga	agc	gaa	aaa	gaa	1149	
Ala	Leu	Arg	Ile	Tyr	Glu	Arg	Leu	Ala	Thr	Arg	Arg	Ser	Glu	Lys	Glu		
			215					220					225				
cat	gaa	aaa	agc	att	gaa	caa	gac	gag	aga	tat	cga	cgc	cgt	gat	cgc	1197	
His	Glu	Lys	Ser	Ile	Glu	Gln	Asp	Glu	Arg	Tyr	Arg	Arg	Arg	Asp	Arg		
		230					235					240					
cgc	caa	tta	cgg	tac	ggc	tgg	cgg	ggt	gat	cga	ggc	gct	tca	gga	ggc	1245	
Arg	Gln	Leu	Arg	Tyr	Gly	Trp	Arg	Gly	Asp	Arg	Gly	Ala	Ser	Gly	Gly		
	245					250					255						
ggg	cct	ggc	cgg	gaa	aat	tcc	ggt	gtc	cgg	aca	gga	cgc	gga	aat	tca	1293	
Gly	Pro	Gly	Arg	Glu	Asn	Ser	Gly	Val	Arg	Thr	Gly	Arg	Gly	Asn	Ser		
	260				265					270					275		
agg	cgt	ccg	acg	aat	tgt	gaa	cgg	tac	gca	gac	gat	gac	cgt	tta	caa	1341	
Arg	Arg	Pro	Thr	Asn	Cys	Glu	Arg	Tyr	Ala	Asp	Asp	Asp	Arg	Leu	Gln		
				280					285					290			
acc	gat	tcc	cgc	gct	tgc	caa	aaa	aag	cgc	tta	aat	ggc	tgt	tca	agc	1389	
Thr	Asp	Ser	Arg	Ala	Cys	Gln	Lys	Lys	Arg	Leu	Asn	Gly	Cys	Ser	Ser		
			295					300					305				
ggc	gaa	agg	cga	agc	gat	tca	aac	cga	tac	aac	cgt	cga	aaa	cgg	caa	1437	
Gly	Glu	Arg	Arg	Ser	Asp	Ser	Asn	Arg	Tyr	Asn	Arg	Arg	Lys	Arg	Gln		
		310					315					320					
agc	caa	agt	acc	ggc	gat	ttt	act	tta	gcc	gta	tgc	cgt	tac	gaa	agg	1485	
Ser	Gln	Ser	Thr	Gly	Asp	Phe	Thr	Leu	Ala	Val	Cys	Arg	Tyr	Glu	Arg		
	325					330					335						
caa	tat	caa	tta	gac	tgt	gat	caa	aga	cgg	cca	tct	gtc	caa	aaa	aga	1533	
Gln	Tyr	Gln	Leu	Asp	Cys	Asp	Gln	Arg	Arg	Pro	Ser	Val	Gln	Lys	Arg		
	340				345					350					355		
tat	tca	tca	ata	aaa	cga	agt	cag	cca	tcc	gct	acaggatggc	tgactttgtt				1586	
Tyr	Ser	Ser	Ile	Lys	Arg	Ser	Gln	Pro	Ser	Ala							
				360					365								
aaattttccac	tttcacatcg	gcgctttttct	taagctttttc	gacctgctgt	ccgagttttt												1646

cctgtctttt ttgctgtttg agcatatctt ggatttgctg tttgacatcg tcaaacgcag 1706  
gtgtgttttt ctgtccgctg tctttttgct gtgcggcaaa ttgatcataa tagtctttga 1766  
tttctttgtc tgtaacctga tctgtcggca gttctttgtc aatatatttc tctgttttga 1826  
tgctgtcggc aatgtcgctt ttcagcgtgt tcatgtttaa gcctgctttt ttgaccgctt 1886  
cctcaaaatc ttgctcgttt ttatactgct ttttgctttc gtccagctgt ttttcaattt 1946  
ctttctcaga tgctttgtag ctttttttgt ccgcttcctg cgtaattaat gcctgtccga 2006  
tcaggtgtgc gatcgctgc tttttgattt gctgcgcc 2044

<210> 42  
<211> 366  
<212> PRT  
<213> Bacillus licheniformis

<400> 42

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20 25 30

Phe Cys Leu Lys Lys Arg Gln Pro Leu Arg Lys Ser Lys Ala Asp Cys  
35 40 45

Arg Leu Arg Gln Ile Val Arg Arg Phe Cys His Arg Tyr Ala Glu Gly  
50 55 60

Arg Thr Leu Val Gln Arg Ser Arg Ser Val Arg Glu Arg Ser Ser Lys  
65 70 75 80

Pro Arg Gly Gly Ser Gln Asp Ala Cys Arg Ser Arg Lys Ser Arg Ser  
85 90 95

Ser Asp Ser Ala Gly Arg Ala Leu Asp Gln Arg Arg Arg Arg Arg Ala  
100 105 110

Cys Cys Cys Thr Gly Arg Cys Gly Cys Arg Gly Gly Asp Arg Glu Lys  
115 120 125

Gly Ala Gln Arg Arg Cys Lys Ser Asp Phe Val Leu Pro Ala Asp Ser  
130 135 140

Lys Arg Gly Cys Leu Leu Leu Arg Phe Ile Leu Ser Arg Lys Gly Arg  
 145 150 155 160

Gly Thr Ala Gly Gly Ser Asp Cys Lys Lys Ser Glu Glu Arg Lys Leu  
 165 170 175

Arg Ile Tyr Arg Arg Ile Val Ser Leu Gln Gln Cys Gly Leu Ile Pro  
 180 185 190

Glu Arg Arg His Glu Ser Ala Arg Thr Val Glu Ala Ala Gly Ser Ser  
 195 200 205

Gln Ala Arg Ala Leu Arg Ile Tyr Glu Arg Leu Ala Thr Arg Arg Ser  
 210 215 220

Glu Lys Glu His Glu Lys Ser Ile Glu Gln Asp Glu Arg Tyr Arg Arg  
 225 230 235 240

Arg Asp Arg Arg Gln Leu Arg Tyr Gly Trp Arg Gly Asp Arg Gly Ala  
 245 250 255

Ser Gly Gly Gly Pro Gly Arg Glu Asn Ser Gly Val Arg Thr Gly Arg  
 260 265 270

Gly Asn Ser Arg Arg Pro Thr Asn Cys Glu Arg Tyr Ala Asp Asp Asp  
 275 280 285

Arg Leu Gln Thr Asp Ser Arg Ala Cys Gln Lys Lys Arg Leu Asn Gly  
 290 295 300

Cys Ser Ser Gly Glu Arg Arg Ser Asp Ser Asn Arg Tyr Asn Arg Arg  
 305 310 315 320

Lys Arg Gln Ser Gln Ser Thr Gly Asp Phe Thr Leu Ala Val Cys Arg  
 325 330 335

Tyr Glu Arg Gln Tyr Gln Leu Asp Cys Asp Gln Arg Arg Pro Ser Val  
 340 345 350

Gln Lys Arg Tyr Ser Ser Ile Lys Arg Ser Gln Pro Ser Ala  
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<210> 43  
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 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (480)..(1208)

<400> 43  
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 cccgcaggcg acattgctga tcctcgggtgt ggcaagggag ttgtccgccca atgtcagtgc 180  
 atcgattccg gctgatttta gctcctctgc ggcgtagcaaa aatttctcaa agtttaattg 240  
 ttttggagga tcgagctcga cgataatgga ccgtttctgc ttagccagat agtcaagagc 300  
 aggctatgtc ctttcgtttt ggacggcaag cgccgctttc tttgggattt tcactagttt 360  
 ttcggtgact ggaggaagtt ctttgacggc cctcggcatc gttctaccct gagtgtcttt 420  
 tatgcccgtc tttaggcggc cccgtcaacg aataatgcat aaaaaaggaa gattcatat 479  
 gaa aat cgt aaa cgt tct gct cgc tat ttt att gac cgc aat cat gtt 527  
 Glu Asn Arg Lys Arg Ser Ala Arg Tyr Phe Ile Asp Arg Asn His Val  
 1 5 10 15  
 aag cgg ttg ttt gta ccc tta aga aag aaa ggc gaa aaa cag cgc acc 575  
 Lys Arg Leu Phe Val Pro Leu Arg Lys Lys Gly Glu Lys Gln Arg Thr  
 20 25 30  
 gca tca gca cca gct caa aga agt gca ggc ggc cgt tta tta att cag 623  
 Ala Ser Ala Pro Ala Gln Arg Ser Ala Gly Gly Arg Leu Leu Ile Gln  
 35 40 45  
 gga ggc gac ggg agg gct tct gcc gat tca gac aag gga tat ggg cgt 671  
 Gly Gly Asp Gly Arg Ala Ser Ala Asp Ser Asp Lys Gly Tyr Gly Arg  
 50 55 60  
 gcc aat cta tca aaa ata ccc tat cga ttt tca cag gct gtc ccc ccg 719  
 Ala Asn Leu Ser Lys Ile Pro Tyr Arg Phe Ser Gln Ala Val Pro Pro  
 65 70 75 80  
 gta tat ggc tta gcc gcc ggg cac atc cta tta aaa cgg cgg aga gta 767  
 Val Tyr Gly Leu Ala Ala Gly His Ile Leu Leu Lys Arg Arg Arg Val  
 85 90 95  
 ctt gta cgt tct tgt cga tgt gga aaa aaa gcc gac ggt caa gct cat 815  
 Leu Val Arg Ser Cys Arg Cys Gly Lys Lys Ala Asp Gly Gln Ala His  
 100 105 110  
 tta tgt aaa aat gtc gga aat gat cag gga gtt aaa gct tcg ggt cga 863  
 Leu Cys Lys Asn Val Gly Asn Asp Gln Gly Val Lys Ala Ser Gly Arg

115	120	125	
aat gta tca aga tca gca caa gta tcc gcc gta tca aaa agt cgt atc			911
Asn Val Ser Arg Ser Ala Gln Val Ser Ala Val Ser Lys Ser Arg Ile			
130	135	140	
caa gaa ctt att cat gct tta cca tta aaa gct cgg act gaa aga ggc			959
Gln Glu Leu Ile His Ala Leu Pro Leu Lys Ala Arg Thr Glu Arg Gly			
145	150	155	160
gcc ttc tgt cac gag tcc gct ttc ggg cac ctc gct gcc gct tct cgt			1007
Ala Phe Cys His Glu Ser Ala Phe Gly His Leu Ala Ala Ala Ser Arg			
	165	170	175
cga tta aaa agg cga cat tca agt gga tta ccg gat gga ttt ggc caa			1055
Arg Leu Lys Arg Arg His Ser Ser Gly Leu Pro Asp Gly Phe Gly Gln			
	180	185	190
gct gat gaa gaa gtc gaa aaa aac ggt aaa gcc ggg cga gga agt cca			1103
Ala Asp Glu Glu Val Glu Lys Asn Gly Lys Ala Gly Arg Gly Ser Pro			
	195	200	205
aga ttt gat gtg gga aga gac gcc ttt cgt tcc ggc gtt ttc ggt aaa			1151
Arg Phe Asp Val Gly Arg Asp Ala Phe Arg Ser Gly Val Phe Gly Lys			
	210	215	220
gta cac agt gaa tta caa aca gga acc tgt ttt tct cga ata gaa tat			1199
Val His Ser Glu Leu Gln Thr Gly Thr Cys Phe Ser Arg Ile Glu Tyr			
	225	230	235
cgg tca aaa tgcaagtatc agtcatgaac ctttctcctc ggcatacaat			1248
Arg Ser Lys			
gaggagaaaag gttttttcat gtatgccgaa aaaattttccc taagctgtca tattgaaata			1308
ggacaacgtc atacactata gtgtcctgtt tttgattgat gaagaagtaa aaaattgaaa			1368
aggattggaa gtccgggagg ggatcacttg gaaaaggctg atattttcaa ggatatcgct			1428
gaacgaacag gaggcgatat atacttaggt gtcgtaggag ctgtacgtac aggaaaatct			1488
acgtttatca aaaaatttat ggagctagtgt gtgctcccga atatcaacaa tgaagcagac			1548
cgggcgcgcg cacaagatga gctcccccaa agtgccgctg gcaaaaaccat tatgacaacc			1608
tgaaccgaag tttgttccga atcaggcaat gtcagttcat gtcagtgacg gactcgatgt			1668
gaatataagg cttgtcgact gc			1690
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<212>	PRT		
<213>	Bacillus licheniformis		
<400>	44		

Glu Asn Arg Lys Arg Ser Ala Arg Tyr Phe Ile Asp Arg Asn His Val  
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Lys Arg Leu Phe Val Pro Leu Arg Lys Lys Gly Glu Lys Gln Arg Thr  
 20 25 30

Ala Ser Ala Pro Ala Gln Arg Ser Ala Gly Gly Arg Leu Leu Ile Gln  
 35 40 45

Gly Gly Asp Gly Arg Ala Ser Ala Asp Ser Asp Lys Gly Tyr Gly Arg  
 50 55 60

Ala Asn Leu Ser Lys Ile Pro Tyr Arg Phe Ser Gln Ala Val Pro Pro  
 65 70 75 80

Val Tyr Gly Leu Ala Ala Gly His Ile Leu Leu Lys Arg Arg Arg Val  
 85 90 95

Leu Val Arg Ser Cys Arg Cys Gly Lys Lys Ala Asp Gly Gln Ala His  
 100 105 110

Leu Cys Lys Asn Val Gly Asn Asp Gln Gly Val Lys Ala Ser Gly Arg  
 115 120 125

Asn Val Ser Arg Ser Ala Gln Val Ser Ala Val Ser Lys Ser Arg Ile  
 130 135 140

Gln Glu Leu Ile His Ala Leu Pro Leu Lys Ala Arg Thr Glu Arg Gly  
 145 150 155 160

Ala Phe Cys His Glu Ser Ala Phe Gly His Leu Ala Ala Ala Ser Arg  
 165 170 175

Arg Leu Lys Arg Arg His Ser Ser Gly Leu Pro Asp Gly Phe Gly Gln  
 180 185 190

Ala Asp Glu Glu Val Glu Lys Asn Gly Lys Ala Gly Arg Gly Ser Pro  
 195 200 205

Arg Phe Asp Val Gly Arg Asp Ala Phe Arg Ser Gly Val Phe Gly Lys  
 210 215 220



Val His Ser Glu Leu Gln Thr Gly Thr Cys Phe Ser Arg Ile Glu Tyr  
 225 230 235 240

Arg Ser Lys

<210> 45  
 <211> 1759  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (476) .. (1267)

<400> 45  
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 tgttttgcct cagcatccgg ggccttttgt gcgatttttt ggtagcagac gaccgcactg 180  
 tgctctccgt ttaccgcttt ttctagatct ttgatcagcc tgttgttttg cctggcgggga 240  
 taggcgggat gatacggctg aacataccac atgtttttca cctcaatatc ttatatatttg 300  
 ccgtcctgtc attatatgta agtcgaagct tgcattgtcc tactggaagg gcgcatctcg 360  
 gacatgtggc aaaatggtgt ggggagagcg caatctatct taaaaaatg aagtttgacg 420  
 taaaatgggtt gttagtgccg aatggtgaca tacatatcaa aatggagtga gacta ttg 478  
 Leu  
 1  
 aaa aag gca ata ttg acg gtc ata gct gta ttg acg tcg gtt gtt ttg 526  
 Lys Lys Ala Ile Leu Thr Val Ile Ala Val Leu Thr Ser Val Val Leu  
 5 10 15  
 ttc gcc ggc tgc caa gcg gaa aaa ggg gga tca gcc aag ggg cag tct 574  
 Phe Ala Gly Cys Gln Ala Glu Lys Gly Gly Ser Ala Lys Gly Gln Ser  
 20 25 30  
 gaa aaa gtt caa att acg gtt tcc gcg gct gcg agt ctc aag gat gtt 622  
 Glu Lys Val Gln Ile Thr Val Ser Ala Ala Ala Ser Leu Lys Asp Val  
 35 40 45  
 tta aca gaa ctt tcc tcc gtc tat gag aaa gac cat ccg aat gtc tct 670  
 Leu Thr Glu Leu Ser Ser Val Tyr Glu Lys Asp His Pro Asn Val Ser  
 50 55 60 65  
 ata aag ttt aat ttt ggt tca tcg ggt gca ttg cag cag cag atc gaa 718  
 Ile Lys Phe Asn Phe Gly Ser Ser Gly Ala Leu Gln Gln Gln Ile Glu  
 70 75 80

cag ggc gct ccg gct gat ttg ttt ttt tct gcc gct gaa gac aaa ttt	766
Gln Gly Ala Pro Ala Asp Leu Phe Phe Ser Ala Ala Glu Asp Lys Phe	
85 90 95	
aat aga gta gtt gat caa ggg tta att gac aaa aaa gac tct gtc aag	814
Asn Arg Val Val Asp Gln Gly Leu Ile Asp Lys Lys Asp Ser Val Lys	
100 105 110	
ctg gtc gaa aac agt ctg gtg ctg atc gtg ccg aaa gga aaa agt cag	862
Leu Val Glu Asn Ser Leu Val Leu Ile Val Pro Lys Gly Lys Ser Gln	
115 120 125	
cat gtc aac agc ttc aag gat ttg gcg gat gac aaa gtc gaa aaa att	910
His Val Asn Ser Phe Lys Asp Leu Ala Asp Asp Lys Val Glu Lys Ile	
130 135 140 145	
gcg atc ggc aaa cct gaa tca gtg cca gcc gga aaa tac gca aaa gaa	958
Ala Ile Gly Lys Pro Glu Ser Val Pro Ala Gly Lys Tyr Ala Lys Glu	
150 155 160	
acg ttg acg aac ctt gac gta tgg tct aaa gtg caa tct aaa gtc gtc	1006
Thr Leu Thr Asn Leu Asp Val Trp Ser Lys Val Gln Ser Lys Val Val	
165 170 175	
tac agc aaa gat gta agg cag gtc ctt tct tat atc gaa aca ggc aac	1054
Tyr Ser Lys Asp Val Arg Gln Val Leu Ser Tyr Ile Glu Thr Gly Asn	
180 185 190	
gcg gat gcc gga atc gtt tac cgg acg gac gcc ctt tca tca gat cag	1102
Ala Asp Ala Gly Ile Val Tyr Arg Thr Asp Ala Leu Ser Ser Asp Gln	
195 200 205	
gtc gag acc gta gag acg gcg aaa agc gat ctg cat aca ccg att gtc	1150
Val Glu Thr Val Glu Thr Ala Lys Ser Asp Leu His Thr Pro Ile Val	
210 215 220 225	
tat ccg ctc gga att gtg aaa aat aca aag cac agg gaa cag tct gag	1198
Tyr Pro Leu Gly Ile Val Lys Asn Thr Lys His Arg Glu Gln Ser Glu	
230 235 240	
gaa ttt tat caa ttc ctg caa agc gac caa gcc gtc aag gcg atg gaa	1246
Glu Phe Tyr Gln Phe Leu Gln Ser Asp Gln Ala Val Lys Ala Met Glu	
245 250 255	
aag tac gga ttt aag aag ggc tgaccgccgt tatgcttgag gagttcttat	1297
Lys Tyr Gly Phe Lys Lys Gly	
260	
cccccaattga aatttccatc caagtatcag ccgcagcggg catcatcgcc gttttgcttg	1357
gaactgctgc agcgaggctc ctggcgaaca gaaactttaa aggcaagtcc attatcgaga	1417
cggtgatgat gctgccgctc gttctgccgc cgaccgttgt cggattttttt ttaattgtga	1477
tcttcggaag gcagagcgtg atcggacgct tgattgaaaa cgtgtttcaa gcgccggtta	1537
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agtctgcaaa atccggattt ctggctgtcg accgcgacat cgaggatgca gcgaggggttg 1657  
 acggagcaaaa cgaatggagg gtgttcctct ttgtcaccgt tccccttgca tccaatggaa 1717  
 tcatgacggg gattgtgctc agctttgcga gggcgcttgg cg 1759

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 <211> 264  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 46

Leu Lys Lys Ala Ile Leu Thr Val Ile Ala Val Leu Thr Ser Val Val  
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Leu Phe Ala Gly Cys Gln Ala Glu Lys Gly Gly Ser Ala Lys Gly Gln  
 20 25 30

Ser Glu Lys Val Gln Ile Thr Val Ser Ala Ala Ala Ser Leu Lys Asp  
 35 40 45

Val Leu Thr Glu Leu Ser Ser Val Tyr Glu Lys Asp His Pro Asn Val  
 50 55 60

Ser Ile Lys Phe Asn Phe Gly Ser Ser Gly Ala Leu Gln Gln Gln Ile  
 65 70 75 80

Glu Gln Gly Ala Pro Ala Asp Leu Phe Phe Ser Ala Ala Glu Asp Lys  
 85 90 95

Phe Asn Arg Val Val Asp Gln Gly Leu Ile Asp Lys Lys Asp Ser Val  
 100 105 110

Lys Leu Val Glu Asn Ser Leu Val Leu Ile Val Pro Lys Gly Lys Ser  
 115 120 125

Gln His Val Asn Ser Phe Lys Asp Leu Ala Asp Asp Lys Val Glu Lys  
 130 135 140

Ile Ala Ile Gly Lys Pro Glu Ser Val Pro Ala Gly Lys Tyr Ala Lys  
 145 150 155 160

Glu Thr Leu Thr Asn Leu Asp Val Trp Ser Lys Val Gln Ser Lys Val  
 165 170 175

Val Tyr Ser Lys Asp Val Arg Gln Val Leu Ser Tyr Ile Glu Thr Gly  
 180 185 190

Asn Ala Asp Ala Gly Ile Val Tyr Arg Thr Asp Ala Leu Ser Ser Asp  
 195 200 205

Gln Val Glu Thr Val Glu Thr Ala Lys Ser Asp Leu His Thr Pro Ile  
 210 215 220

Val Tyr Pro Leu Gly Ile Val Lys Asn Thr Lys His Arg Glu Gln Ser  
 225 230 235 240

Glu Glu Phe Tyr Gln Phe Leu Gln Ser Asp Gln Ala Val Lys Ala Met  
 245 250 255

Glu Lys Tyr Gly Phe Lys Lys Gly  
 260

<210> 47  
 <211> 2449  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1946)

<400> 47  
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 tataccgatg tatattgatt tcagcgattg acgattcccg cttatacaga ctatagattc 180  
 atataaaaaa ggtgtctttc cgcttaaaat cgggtgtcatt tgcataaaaa tgtataggaa 240  
 aagaggaaact tagaccagtt gagtcccaga gatgagtata ttagaatgat ggtaattcaa 300  
 tatcgtcggg attgttactg tctaagcagg caagacctaa aatgtgtgaa gggcgaaatc 360  
 tatctttttgc ctatatgaac ttgcacattt taggtctttt ttctgttctt caggacaatg 420  
 ccgcagttag gagggatgat tgggaacggt catgttgtca gaagcaatct attacatatt 480  
 gaaaaaggga ggaaatattg atg aac atc aaa aac att gct aaa aaa gcg tca 533  
 Met Asn Ile Lys Asn Ile Ala Lys Lys Ala Ser  
 1 5 10

gcc tta acc gtt gct gcg gca ctg ctg gcc gga ggt gcg ccg caa acc	581
Ala Leu Thr Val Ala Ala Ala Leu Leu Ala Gly Gly Ala Pro Gln Thr	
15 20 25	
ttt gca aaa gaa acg cag gat tac aag aaa agc tac gga ttt tct cat	629
Phe Ala Lys Glu Thr Gln Asp Tyr Lys Lys Ser Tyr Gly Phe Ser His	
30 35 40	
atc aca aga cat gac atg ctg aaa att ccc gag cag caa aag agc gaa	677
Ile Thr Arg His Asp Met Leu Lys Ile Pro Glu Gln Gln Lys Ser Glu	
45 50 55	
caa ttt aaa gtt cct caa ttc gat ccg aaa aca atc aaa aac atc cct	725
Gln Phe Lys Val Pro Gln Phe Asp Pro Lys Thr Ile Lys Asn Ile Pro	
60 65 70 75	
tct gca aaa ggg tat aac aaa aat gga gag ctg atc gat tta gac gta	773
Ser Ala Lys Gly Tyr Asn Lys Asn Gly Glu Leu Ile Asp Leu Asp Val	
80 85 90	
tgg gac agc tgg ccg ctg caa aat gcc gac ggg acg gtt gct aca tac	821
Trp Asp Ser Trp Pro Leu Gln Asn Ala Asp Gly Thr Val Ala Thr Tyr	
95 100 105	
cac ggc tac aat ctt gtt ttc gcg ctg gcg ggc gat ccg aaa gac gtc	869
His Gly Tyr Asn Leu Val Phe Ala Leu Ala Gly Asp Pro Lys Asp Val	
110 115 120	
gat gac aca tcc atc tat ttg ttc tat caa aag aaa ggc gaa act tct	917
Asp Asp Thr Ser Ile Tyr Leu Phe Tyr Gln Lys Lys Gly Glu Thr Ser	
125 130 135	
atc gac agc tgg aaa aac gcc ggc aga gtg ttt aaa gac agc gac aaa	965
Ile Asp Ser Trp Lys Asn Ala Gly Arg Val Phe Lys Asp Ser Asp Lys	
140 145 150 155	
ttt gtt cca gac gat ccg tac ctc aaa cat caa aca cag gaa tgg tca	1013
Phe Val Pro Asp Asp Pro Tyr Leu Lys His Gln Thr Gln Glu Trp Ser	
160 165 170	
ggt tct gcc acg ctg aca aaa gac gga aaa gtc cga ctg ttt tac aca	1061
Gly Ser Ala Thr Leu Thr Lys Asp Gly Lys Val Arg Leu Phe Tyr Thr	
175 180 185	
gct ttt tcc ggc acg caa tac ggc aag cag acg ctg aca aca gct cag	1109
Ala Phe Ser Gly Thr Gln Tyr Gly Lys Gln Thr Leu Thr Thr Ala Gln	
190 195 200	
gtc aat ttc tct cag ccg gat tcg gac acg ctc aaa att gac ggt gta	1157
Val Asn Phe Ser Gln Pro Asp Ser Asp Thr Leu Lys Ile Asp Gly Val	
205 210 215	
gaa gat cat aaa tcg gtc ttt gac ggc gcc gac ggc acg gta tac caa	1205
Glu Asp His Lys Ser Val Phe Asp Gly Ala Asp Gly Thr Val Tyr Gln	
220 225 230 235	
aac gtt cag caa ttc att gac gaa gga aac tac agc tcc ggc gac aac	1253

Asn Val Gln Gln Phe Ile Asp Glu Gly Asn Tyr Ser Ser Gly Asp Asn	
240 245 250	
cat acg atg aga gac ccg cat tat gtg gaa gac cgc ggc cat aaa tat	1301
His Thr Met Arg Asp Pro His Tyr Val Glu Asp Arg Gly His Lys Tyr	
255 260 265	
ctc gta ttt gaa gcc aat acg gga aca aaa acc ggc tac caa gga gaa	1349
Leu Val Phe Glu Ala Asn Thr Gly Thr Lys Thr Gly Tyr Gln Gly Glu	
270 275 280	
gac tcc cta ttc aac aga gcc tac tac ggg ggc agc aag aag ttc ttt	1397
Asp Ser Leu Phe Asn Arg Ala Tyr Tyr Gly Gly Ser Lys Lys Phe Phe	
285 290 295	
aaa gaa gaa agc agc aag ctg ctg caa ggt gcg aac aaa aag aac gct	1445
Lys Glu Glu Ser Ser Lys Leu Leu Gln Gly Ala Asn Lys Lys Asn Ala	
300 305 310 315	
tcg ctg gct aac ggc gct ctc gga atc atc gaa tta aat aac gat tat	1493
Ser Leu Ala Asn Gly Ala Leu Gly Ile Ile Glu Leu Asn Asn Asp Tyr	
320 325 330	
aca ctg aaa aaa gtc atg aag cct ttg atc gcc tcc aat acg gtg aca	1541
Thr Leu Lys Lys Val Met Lys Pro Leu Ile Ala Ser Asn Thr Val Thr	
335 340 345	
gat gaa atc gaa cgg gcc aac ctc ttc aaa atg aat gga aaa tgg tat	1589
Asp Glu Ile Glu Arg Ala Asn Leu Phe Lys Met Asn Gly Lys Trp Tyr	
350 355 360	
ctg ttc aca gat tca aga gga tca aaa atg aca att gac ggc atc ggt	1637
Leu Phe Thr Asp Ser Arg Gly Ser Lys Met Thr Ile Asp Gly Ile Gly	
365 370 375	
tca aaa gac att tat atg ctc ggc tat gta tca ggt tca tta acc gga	1685
Ser Lys Asp Ile Tyr Met Leu Gly Tyr Val Ser Gly Ser Leu Thr Gly	
380 385 390 395	
cca ttc aag cct tta aac aaa tcc gga ctt gtt ttg cat atg gac cag	1733
Pro Phe Lys Pro Leu Asn Lys Ser Gly Leu Val Leu His Met Asp Gln	
400 405 410	
gat tac aat gac atc acg ttt act tat tca cac ttt gcc gta ccg cag	1781
Asp Tyr Asn Asp Ile Thr Phe Thr Tyr Ser His Phe Ala Val Pro Gln	
415 420 425	
aaa aaa ggc gac gaa gtc gtc att aca agc tac atc aca aac aga ggg	1829
Lys Lys Gly Asp Glu Val Val Ile Thr Ser Tyr Ile Thr Asn Arg Gly	
430 435 440	
att tcg aac gag cat cac gcc acg ttt gca cca agc ttt ttg ctg aag	1877
Ile Ser Asn Glu His His Ala Thr Phe Ala Pro Ser Phe Leu Leu Lys	
445 450 455	
atc aaa gga tca aaa aca tcc gtt gtc aaa aac agc atc ctt gaa cag	1925
Ile Lys Gly Ser Lys Thr Ser Val Val Lys Asn Ser Ile Leu Glu Gln	

460		465		470		475	
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<212> PRT
<213> Bacillus licheniformis
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 115 120 125

Tyr Leu Phe Tyr Gln Lys Lys Gly Glu Thr Ser Ile Asp Ser Trp Lys  
 130 135 140

Asn Ala Gly Arg Val Phe Lys Asp Ser Asp Lys Phe Val Pro Asp Asp  
 145 150 155 160

Pro Tyr Leu Lys His Gln Thr Gln Glu Trp Ser Gly Ser Ala Thr Leu  
 165 170 175

Thr Lys Asp Gly Lys Val Arg Leu Phe Tyr Thr Ala Phe Ser Gly Thr  
 180 185 190

Gln Tyr Gly Lys Gln Thr Leu Thr Thr Ala Gln Val Asn Phe Ser Gln  
 195 200 205

Pro Asp Ser Asp Thr Leu Lys Ile Asp Gly Val Glu Asp His Lys Ser  
 210 215 220

Val Phe Asp Gly Ala Asp Gly Thr Val Tyr Gln Asn Val Gln Gln Phe  
 225 230 235 240

Ile Asp Glu Gly Asn Tyr Ser Ser Gly Asp Asn His Thr Met Arg Asp  
 245 250 255

Pro His Tyr Val Glu Asp Arg Gly His Lys Tyr Leu Val Phe Glu Ala  
 260 265 270

Asn Thr Gly Thr Lys Thr Gly Tyr Gln Gly Glu Asp Ser Leu Phe Asn  
 275 280 285

Arg Ala Tyr Tyr Gly Gly Ser Lys Lys Phe Phe Lys Glu Glu Ser Ser  
 290 295 300

Lys Leu Leu Gln Gly Ala Asn Lys Lys Asn Ala Ser Leu Ala Asn Gly  
 305 310 315 320

Ala Leu Gly Ile Ile Glu Leu Asn Asn Asp Tyr Thr Leu Lys Lys Val  
 325 330 335



Met Lys Pro Leu Ile Ala Ser Asn Thr Val Thr Asp Glu Ile Glu Arg  
 340 345 350

Ala Asn Leu Phe Lys Met Asn Gly Lys Trp Tyr Leu Phe Thr Asp Ser  
 355 360 365

Arg Gly Ser Lys Met Thr Ile Asp Gly Ile Gly Ser Lys Asp Ile Tyr  
 370 375 380

Met Leu Gly Tyr Val Ser Gly Ser Leu Thr Gly Pro Phe Lys Pro Leu  
 385 390 395 400

Asn Lys Ser Gly Leu Val Leu His Met Asp Gln Asp Tyr Asn Asp Ile  
 405 410 415

Thr Phe Thr Tyr Ser His Phe Ala Val Pro Gln Lys Lys Gly Asp Glu  
 420 425 430

Val Val Ile Thr Ser Tyr Ile Thr Asn Arg Gly Ile Ser Asn Glu His  
 435 440 445

His Ala Thr Phe Ala Pro Ser Phe Leu Leu Lys Ile Lys Gly Ser Lys  
 450 455 460

Thr Ser Val Val Lys Asn Ser Ile Leu Glu Gln Gly Gln Leu Thr Val  
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Asn Lys

<210> 49  
 <211> 1669  
 <212> DNA  
 <213> Bacillus licheniformis

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 gcgcaaaagc tgcaaaaact gctcagaaaa gttgtcacat ctgaaaaggg gacggggccgg 180

cgcttcagcg atcttccgta cgatgtagcg ggaaaatcgg gcacagcgca gacaggcagg 240  
 acgacagatg acaaaaaaac gctctatcat aaatggtttg ccggttattt tccggcggac 300  
 aagccgaaat atgcgctcgt cgtcgtccat atggatacgc cggatagcaa ggctgcgaca 360  
 aatgccgtat tttatgatat tgtaaataaa gtatatgaaa ttgaaaagaa ccagacatag 420  
 aagaatgcct caggtgatga taaaatagga agcgaggcaa gagggaaaaa ggagtgcatt 480  
 gaacttg agc gaa aca agg gaa tct cgt ttt gaa aat cgt gat aag cgc 529  
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     1                    5                    10  
 agg aaa gcg aat ctt gtg ctt aac att tta ata ggc atc gta ttg gta 577  
 Arg Lys Ala Asn Leu Val Leu Asn Ile Leu Ile Gly Ile Val Leu Val  
 15                    20                    25                    30  
 tta atc gtt gtc gtt gcc agc agt ctg atg atg aac agt ccg aag gag 625  
 Leu Ile Val Val Val Ala Ser Ser Leu Met Met Asn Ser Pro Lys Glu  
                     35                    40                    45  
 cag gcg cag caa gat gtc tcg aaa aac gat tct gaa cag acg aca gaa 673  
 Gln Ala Gln Gln Asp Val Ser Lys Asn Asp Ser Glu Gln Thr Thr Glu  
                     50                    55                    60  
 gcg cct gct tcc gac aat aag aaa caa aca tct gat gaa gat gta aaa 721  
 Ala Pro Ala Ser Asp Asn Lys Lys Gln Thr Ser Asp Glu Asp Val Lys  
                     65                    70                    75  
 gat gag gac aaa gga aaa agc gat tct gcc gat aaa gaa gac agc gat 769  
 Asp Glu Asp Lys Gly Lys Ser Asp Ser Ala Asp Lys Glu Asp Ser Asp  
     80                    85                    90  
 tcc gac tca gac aag gat aaa gaa tct gct tca gac gag gac aag tca 817  
 Ser Asp Ser Asp Lys Asp Lys Glu Ser Ala Ser Asp Glu Asp Lys Ser  
 95                    100                    105                    110  
 aca tca gat gat ccg ttt gaa gga gcc gaa gtg aca gaa ggc ggt tca 865  
 Thr Ser Asp Asp Pro Phe Glu Gly Ala Glu Val Thr Glu Gly Gly Ser  
                     115                    120                    125  
 agc gcc aat gtt gaa aaa acg atc atc aat cct gac tgg gag cct gtc 913  
 Ser Ala Asn Val Glu Lys Thr Ile Ile Asn Pro Asp Trp Glu Pro Val  
                     130                    135                    140  
 ggc aca caa cag agc gga cag cat acc gca aca tat gat tcc tct tca 961  
 Gly Thr Gln Gln Ser Gly Gln His Thr Ala Thr Tyr Asp Ser Ser Ser  
                     145                    150                    155  
 caa gac tgg aag gaa atg ctt gaa gcc att tca tat gcg aca ggg gtt 1009  
 Gln Asp Trp Lys Glu Met Leu Glu Ala Ile Ser Tyr Ala Thr Gly Val  
     160                    165                    170  
 tct aag gat aac atg acg gtg atc tgg ctc gga aac aac ggc agc ccg 1057  
 Ser Lys Asp Asn Met Thr Val Ile Trp Leu Gly Asn Asn Gly Ser Pro  
 175                    180                    185                    190

caa gat gcg aaa gga acc att cgg gcg aag gac act ggc gtc aaa tac	1105
Gln Asp Ala Lys Gly Thr Ile Arg Ala Lys Asp Thr Gly Val Lys Tyr	
195 200 205	

cag gta gcc att act tgg gtt gac gga aaa ggc tgg aag ccg aca aaa	1153
Gln Val Ala Ile Thr Trp Val Asp Gly Lys Gly Trp Lys Pro Thr Lys	
210 215 220	

gtt gaa caa ttg aaa taaagaaaaa agcggccggt tgctaaaacc gggcgctttt	1208
Val Glu Gln Leu Lys	
225	

tttatgattc ggcttttaaaa tgaacgactg cgctgtagtg gatccgtccg tcaataaccg	1268
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ccgtatggtg ggaaaccgaa tggaccctca gcaaaatcgc ctggttggtt tcaatctgct	1328
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gactgatctt tttttcaagc tcctctaagc tcagtgcctc aaaaaactca attttatctt	1388
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tgatcagatc gaggccgaag ttcataaacc aatcctccat tcgtttcaag tcatttttta	1448
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ttaaagcaga gaagcggccg ggtgacaagg gaaatataac caagcctttt ttgtacccaa	1508
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aacgaatgac ttgtggtagg ataagaacta atcaatcgaa taaatcatac tataactata	1568
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ggaattgtaa aaatagatgg agagtgcga caaaatggga agagagttca ttcctttatt	1628
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tgagaactgg gcaaattctt atgatgatac agtagttggc c	1669
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<210> 50

<211> 227

<212> PRT

<213> Bacillus licheniformis

<400> 50

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Ala Asn Leu Val Leu Asn Ile Leu Ile Gly Ile Val Leu Val Leu Ile
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Val Val Val Ala Ser Ser Leu Met Met Asn Ser Pro Lys Glu Gln Ala
35 40 45

Gln Gln Asp Val Ser Lys Asn Asp Ser Glu Gln Thr Thr Glu Ala Pro
50 55 60

Ala Ser Asp Asn Lys Lys Gln Thr Ser Asp Glu Asp Val Lys Asp Glu
65 70 75 80

Asp Lys Gly Lys Ser Asp Ser Ala Asp Lys Glu Asp Ser Asp Ser Asp  
85 90 95

Ser Asp Lys Asp Lys Glu Ser Ala Ser Asp Glu Asp Lys Ser Thr Ser  
100 105 110

Asp Asp Pro Phe Glu Gly Ala Glu Val Thr Glu Gly Gly Ser Ser Ala  
115 120 125

Asn Val Glu Lys Thr Ile Ile Asn Pro Asp Trp Glu Pro Val Gly Thr  
130 135 140

Gln Gln Ser Gly Gln His Thr Ala Thr Tyr Asp Ser Ser Ser Gln Asp  
145 150 155 160

Trp Lys Glu Met Leu Glu Ala Ile Ser Tyr Ala Thr Gly Val Ser Lys  
165 170 175

Asp Asn Met Thr Val Ile Trp Leu Gly Asn Asn Gly Ser Pro Gln Asp  
180 185 190

Ala Lys Gly Thr Ile Arg Ala Lys Asp Thr Gly Val Lys Tyr Gln Val  
195 200 205

Ala Ile Thr Trp Val Asp Gly Lys Gly Trp Lys Pro Thr Lys Val Glu  
210 215 220

Gln Leu Lys  
225

<210> 51  
<211> 1700  
<212> DNA  
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<222> (437)..(1213)

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cagctcgtca ttcagagaga gacgtatgag gatatcgtca agctggatct gccgctgaaa 180

tcgaaagtca aacaataaaa aaatggagat tccctaagag gggggtctcc aattttaatt	240
caagcacgaa aaacacttcc cggtgatcgg gaggtgtttt ttgttaaaaa gatcatgaca	300
tgcatagaac agcgaccggg ctaattgtat ataatatcgt gaattttaaca aaaaatttac	360
aaaggagatg ataaaggcga tgaccagggg gaaaaggatg agaattgctg atttggttga	420
tttagaggcg gagtag atg aaa ccg gcc aaa gta tcc cta ctc cac cga ttg	472
Met Lys Pro Ala Lys Val Ser Leu Leu His Arg Leu	
1 5 10	
ctc cag tgc ctg aag caa tgt gtc gat tgt tac aca gta gat cgt gtg	520
Leu Gln Cys Leu Lys Gln Cys Val Asp Cys Tyr Thr Val Asp Arg Val	
15 20 25	
aca gca ata aac att ttt gtg aat att tta ttg att tcg gct gtg atc	568
Thr Ala Ile Asn Ile Phe Val Asn Ile Leu Leu Ile Ser Ala Val Ile	
30 35 40	
tca ttc cca tat tct gct gcg gcc cat ggc gca aca cag tcc ggc gat	616
Ser Phe Pro Tyr Ser Ala Ala Ala His Gly Ala Thr Gln Ser Gly Asp	
45 50 55 60	
caa tat tca gct ttt gaa gaa ttg gag cgg aat gaa gat cca gct tct	664
Gln Tyr Ser Ala Phe Glu Glu Leu Glu Arg Asn Glu Asp Pro Ala Ser	
65 70 75	
tac cga att acg gag aag aac gca aga gtg ccg atg ctc atc atg gcc	712
Tyr Arg Ile Thr Glu Lys Asn Ala Arg Val Pro Met Leu Ile Met Ala	
80 85 90	
atc cat gga ggc ggc atc gaa ccc gga acg agc gaa atc gcc aat gaa	760
Ile His Gly Gly Gly Ile Glu Pro Gly Thr Ser Glu Ile Ala Asn Glu	
95 100 105	
gtg tcc aaa aac tat tcc ctg tac ttg ttt gaa ggg ctg aaa tca tca	808
Val Ser Lys Asn Tyr Ser Leu Tyr Leu Phe Glu Gly Leu Lys Ser Ser	
110 115 120	
ggc aat acg gac ctt cac att aca agc acg cgt ttt gac gag cca gcg	856
Gly Asn Thr Asp Leu His Ile Thr Ser Thr Arg Phe Asp Glu Pro Ala	
125 130 135 140	
gcg ctc gca att act gca agc cac cag tat gtc atg tcg ctc cac ggc	904
Ala Leu Ala Ile Thr Ala Ser His Gln Tyr Val Met Ser Leu His Gly	
145 150 155	
tat tac agt gaa gac cgc gat att aaa gta ggc ggc aca gac cgc gct	952
Tyr Tyr Ser Glu Asp Arg Asp Ile Lys Val Gly Gly Thr Asp Arg Ala	
160 165 170	
aaa atc aga ata ttg gtt gat gag ctg aac cgc tcg ggg ttt gcc gct	1000
Lys Ile Arg Ile Leu Val Asp Glu Leu Asn Arg Ser Gly Phe Ala Ala	
175 180 185	
gaa atg ctg ggg aca gat gac aag tat gcc gga acc cat ccg aat aac	1048

Glu Met Leu Gly Thr Asp Asp Lys Tyr Ala Gly Thr His Pro Asn Asn	
190 195 200	
atc gcc aac aag tcg ctt tcc ggg ctg agc att cag ctt gaa atg agc	1096
Ile Ala Asn Lys Ser Leu Ser Gly Leu Ser Ile Gln Leu Glu Met Ser	
205 210 215 220	
acg ggt ttc cgc aaa tct tta ttc gac cgg ttt aca cta aaa gac agg	1144
Thr Gly Phe Arg Lys Ser Leu Phe Asp Arg Phe Thr Leu Lys Asp Arg	
225 230 235	
gcg gcg acg caa aac gaa acg ttt tac cga ttt aca aag ctg ctg aca	1192
Ala Ala Thr Gln Asn Glu Thr Phe Tyr Arg Phe Thr Lys Leu Leu Thr	
240 245 250	
gat ttt att cat gaa aac tat gaagaagacg gaggggattt cccctctgca	1243
Asp Phe Ile His Glu Asn Tyr	
255	
aaaataaaac acccccttca agtgtgaact gacccgttaa aatgagactt agaaaaaaca	1303
cctatgctgc ctgtcccttg tattccagtg gggacaggta gtttaatttt gcctgaattc	1363
gtacatgatt atatcgatac atgtattgat ttacaatttg tactacttta gaattggata	1423
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 <212> PRT  
 <213> Bacillus licheniformis

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Ile Phe Val Asn Ile Leu Leu Ile Ser Ala Val Ile Ser Phe Pro Tyr
35 40 45

Ser Ala Ala Ala His Gly Ala Thr Gln Ser Gly Asp Gln Tyr Ser Ala
50 55 60

Phe Glu Glu Leu Glu Arg Asn Glu Asp Pro Ala Ser Tyr Arg Ile Thr  
 65 70 75 80

Glu Lys Asn Ala Arg Val Pro Met Leu Ile Met Ala Ile His Gly Gly  
 85 90 95

Gly Ile Glu Pro Gly Thr Ser Glu Ile Ala Asn Glu Val Ser Lys Asn  
 100 105 110

Tyr Ser Leu Tyr Leu Phe Glu Gly Leu Lys Ser Ser Gly Asn Thr Asp  
 115 120 125

Leu His Ile Thr Ser Thr Arg Phe Asp Glu Pro Ala Ala Leu Ala Ile  
 130 135 140

Thr Ala Ser His Gln Tyr Val Met Ser Leu His Gly Tyr Tyr Ser Glu  
 145 150 155 160

Asp Arg Asp Ile Lys Val Gly Gly Thr Asp Arg Ala Lys Ile Arg Ile  
 165 170 175

Leu Val Asp Glu Leu Asn Arg Ser Gly Phe Ala Ala Glu Met Leu Gly  
 180 185 190

Thr Asp Asp Lys Tyr Ala Gly Thr His Pro Asn Asn Ile Ala Asn Lys  
 195 200 205

Ser Leu Ser Gly Leu Ser Ile Gln Leu Glu Met Ser Thr Gly Phe Arg  
 210 215 220

Lys Ser Leu Phe Asp Arg Phe Thr Leu Lys Asp Arg Ala Ala Thr Gln  
 225 230 235 240

Asn Glu Thr Phe Tyr Arg Phe Thr Lys Leu Leu Thr Asp Phe Ile His  
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Glu Asn Tyr

<210> 53  
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 <212> DNA

<213> Bacillus licheniformis

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<222> (472)..(1026)

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aaagatcatg ccaacccccga taaaccagaa aagaacagac agaatctcca atacctcgaa      240
ggaaagaaac agctccttat atcttcccca ctctatggca aaaccgacaa tacttgtagt      300
caaagctccg acacccaata cggaaaaagaa aaatcggacg agattacggc ttttcattgt      360
agacttccca acccctaaat aaaccgctgt aacagcgata ttttgttatg tataaatttt      420
taaaagacat tcatattaaa ggtaagacga gttttcgaaa ggagcttaag c atg ttc      477
                                     Met Phe
                                     1

aag acc gca atg cta tcg ata agc tgt ttt ctg ttt cta tct gta aca      525
Lys Thr Ala Met Leu Ser Ile Ser Cys Phe Leu Phe Leu Ser Val Thr
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gct tgt gct ccc acg gac caa gca gct gag atg gac tat gat caa acc      573
Ala Cys Ala Pro Thr Asp Gln Ala Ala Glu Met Asp Tyr Asp Gln Thr
      20                      25                      30

aaa aaa atg gtt gtc gat ata tta aag aca gat gac gga aaa aaa gcg      621
Lys Lys Met Val Val Asp Ile Leu Lys Thr Asp Asp Gly Lys Lys Ala
      35                      40                      45                      50

att caa gaa ata tta aat gat gac aaa tta aat gaa aca ctt gta atg      669
Ile Gln Glu Ile Leu Asn Asp Asp Lys Leu Asn Glu Thr Leu Val Met
      55                      60                      65

gat gaa aaa act gtc aaa gaa acc gtt gaa aaa aca atg acc tcc aaa      717
Asp Glu Lys Thr Val Lys Glu Thr Val Glu Lys Thr Met Thr Ser Lys
      70                      75                      80

aaa gga gct gaa ttt tgg aaa aaa gtc ttt gaa gat cca aaa ttc gct      765
Lys Gly Ala Glu Phe Trp Lys Lys Val Phe Glu Asp Pro Lys Phe Ala
      85                      90                      95

gaa ggc ttt gcc aaa aca ctt caa aat gaa cat gaa aaa gtg ctg aaa      813
Glu Gly Phe Ala Lys Thr Leu Gln Asn Glu His Glu Lys Val Leu Lys
      100                      105                      110

aaa ctg atg aaa gat cct gag tac caa aaa atg ctg atg cag gtc atg      861
Lys Leu Met Lys Asp Pro Glu Tyr Gln Lys Met Leu Met Gln Val Met
      115                      120                      125                      130
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cag gat cct gaa atg gcc aaa aaa tac ggt gaa ctt gtc aga agc cag 909  
 Gln Asp Pro Glu Met Ala Lys Lys Tyr Gly Glu Leu Val Arg Ser Gln  
 135 140 145

gaa ttc cga agc cac ctg cag gaa gtc ata tct gac act ctg aca agc 957  
 Glu Phe Arg Ser His Leu Gln Glu Val Ile Ser Asp Thr Leu Thr Ser  
 150 155 160

cct ctt tac aga aag cag ttt gaa gag gaa ctg aaa aaa gct gct gct 1005  
 Pro Leu Tyr Arg Lys Gln Phe Glu Glu Glu Leu Lys Lys Ala Ala Ala  
 165 170 175

gaa agc atg aaa gaa gaa atg aaaggcggcg aagaaaaaca aagctgagcc 1056  
 Glu Ser Met Lys Glu Glu Met  
 180 185

gcttttcatt ccctaaaagc ttctttctgcg gaggaagctt tttttgctct ttaagctttt 1116

gcgccaatgc tttcgtcgat ttttttggcg atatccaaat aaatggcgcc ggtcgggtgg 1176

ctttcatcat aaacggacgg cgcaaattcg ctgtcatccc aatccggctg cttcagcgga 1236

attttgccca gaattggaac gcctagtacc tctgcgagct tttcgccctcc gcctttgccg 1296

aatacatatt ctttctcgcc tgttttgacg ctttcgtaat aagccatatt ttcaacgac 1356

cccacgattt catgatcggt cttcaaggcc atcgcgcccg ctcttgacgc gacaaacgcg 1416

gcagtagggg gcggcgtcga cacgatcacc tctttgcagc ttggaagcat tgagtgaaca 1476

tcaagcgcta catcgccctgt tcccggcggc aggtctaaga taa 1519

<210> 54  
 <211> 185  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 54

Met Phe Lys Thr Ala Met Leu Ser Ile Ser Cys Phe Leu Phe Leu Ser  
 1 5 10 15

Val Thr Ala Cys Ala Pro Thr Asp Gln Ala Ala Glu Met Asp Tyr Asp  
 20 25 30

Gln Thr Lys Lys Met Val Val Asp Ile Leu Lys Thr Asp Asp Gly Lys  
 35 40 45

Lys Ala Ile Gln Glu Ile Leu Asn Asp Asp Lys Leu Asn Glu Thr Leu  
 50 55 60

Val Met Asp Glu Lys Thr Val Lys Glu Thr Val Glu Lys Thr Met Thr  
65 70 75 80

Ser Lys Lys Gly Ala Glu Phe Trp Lys Lys Val Phe Glu Asp Pro Lys  
85 90 95

Phe Ala Glu Gly Phe Ala Lys Thr Leu Gln Asn Glu His Glu Lys Val  
100 105 110

Leu Lys Lys Leu Met Lys Asp Pro Glu Tyr Gln Lys Met Leu Met Gln  
115 120 125

Val Met Gln Asp Pro Glu Met Ala Lys Lys Tyr Gly Glu Leu Val Arg  
130 135 140

Ser Gln Glu Phe Arg Ser His Leu Gln Glu Val Ile Ser Asp Thr Leu  
145 150 155 160

Thr Ser Pro Leu Tyr Arg Lys Gln Phe Glu Glu Glu Leu Lys Lys Ala  
165 170 175

Ala Ala Glu Ser Met Lys Glu Glu Met  
180 185

<210> 55  
<211> 2404  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(1901)

<400> 55  
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ttgattttcc ggaaacggaa gaagccgata atggctgcac ttcagcaatg gttctatgaa 180  
atcgtgcgag aaattaatca ggatgcgttc gaactcttga acttccgtgc ttgacgttcg 240  
gtggagggtcg tggggattga tgatgatcat cgtgcctttt tccgcggtat agacgctttg 300  
gttaataaaa tacgtgcgtt ctccgctcag cagataatac agttcatagc cttcatgaac 360  
atgcggcgcg ttcattctcg taaatccttt tctctgcata tattgaatcg aaaaagaatg 420

ctcggctatg aaatathtag gatggagcat gtcgggcatt cctccttgag agcgttttct	480
taacaaacgg gagggatcgt atg aaa aag tta tgt tgc ctg atc ttg gtc ttg	533
Met Lys Lys Leu Cys Cys Leu Ile Leu Val Leu	
1 5 10	
gtt ttt tcc gcg ggc tgt act cag caa aag gca tca acg gaa gag gac	581
Val Phe Ser Ala Gly Cys Thr Gln Gln Lys Ala Ser Thr Glu Glu Asp	
15 20 25	
ggg gcg ctt gaa atc aat tgg ctc gta ccg ctc cac aca ccg cag cct	629
Gly Ala Leu Glu Ile Asn Trp Leu Val Pro Leu His Thr Pro Gln Pro	
30 35 40	
ccg aaa gag aag gcg ctt gac atc att gaa gac aaa acg aat aca aag	677
Pro Lys Glu Lys Ala Leu Asp Ile Ile Glu Asp Lys Thr Asn Thr Lys	
45 50 55	
ctg aag ctc atc tgg gtt ccg gat tca aca aaa gaa gag cgg atc aat	725
Leu Lys Leu Ile Trp Val Pro Asp Ser Thr Lys Glu Glu Arg Ile Asn	
60 65 70 75	
aca acc ctt gca agc gga aac atg cct aaa gta atg aca ttg cct gat	773
Thr Thr Leu Ala Ser Gly Asn Met Pro Lys Val Met Thr Leu Pro Asp	
80 85 90	
ctt gaa gat tca gcg gtt gtc agc gcg ctg cgc tcg gga atg ttc tgg	821
Leu Glu Asp Ser Ala Val Val Ser Ala Leu Arg Ser Gly Met Phe Trp	
95 100 105	
gaa atc gga ccg tat ttc aaa gac tat ccg aat tta aga aaa ctt gat	869
Glu Ile Gly Pro Tyr Phe Lys Asp Tyr Pro Asn Leu Arg Lys Leu Asp	
110 115 120	
aaa act ata ttg aaa aat att tcg gtt gat ggc aaa gtt tac ggg att	917
Lys Thr Ile Leu Lys Asn Ile Ser Val Asp Gly Lys Val Tyr Gly Ile	
125 130 135	
tat aga gaa agg ccg atg gcc agg cag gga gtc gtg att cgg aaa gac	965
Tyr Arg Glu Arg Pro Met Ala Arg Gln Gly Val Val Ile Arg Lys Asp	
140 145 150 155	
tgg ctc gac aat ctc gga ttg gaa atg ccg gaa acc gtt gat gac ctt	1013
Trp Leu Asp Asn Leu Gly Leu Glu Met Pro Glu Thr Val Asp Asp Leu	
160 165 170	
tat aaa ata gcg aaa gca ttt aca gaa cag gac ccc gat caa aac gga	1061
Tyr Lys Ile Ala Lys Ala Phe Thr Glu Gln Asp Pro Asp Gln Asn Gly	
175 180 185	
aaa gac gac acg ttc ggt ctc gcc gac cgc aat gat ctc acc ttc gga	1109
Lys Asp Asp Thr Phe Gly Leu Ala Asp Arg Asn Asp Leu Thr Phe Gly	
190 195 200	
gcg ttt aaa acc ctg gct tcg tac ttt ggc gcg ccg aac gaa tgg gga	1157
Ala Phe Lys Thr Leu Ala Ser Tyr Phe Gly Ala Pro Asn Glu Trp Gly	
205 210 215	

acg gac gaa gac gga aat ctc ttc ccc tat ttt aag cat gag gcc tat	1205
Thr Asp Glu Asp Gly Asn Leu Phe Pro Tyr Phe Lys His Glu Ala Tyr	
220 225 230 235	
aaa gac gca atg gca tac atg aaa aag ctt tat gaa gaa ggc ctg atg	1253
Lys Asp Ala Met Ala Tyr Met Lys Lys Leu Tyr Glu Glu Gly Leu Met	
240 245 250	
aac agg gac ttt gcg gtg aca agc aaa acg cag cag cag gat tta gtg	1301
Asn Arg Asp Phe Ala Val Thr Ser Lys Thr Gln Gln Gln Asp Leu Val	
255 260 265	
att cag ggg aaa gcg gga atc tat atc ggc gcg atg agc gat gcc atg	1349
Ile Gln Gly Lys Ala Gly Ile Tyr Ile Gly Ala Met Ser Asp Ala Met	
270 275 280	
aac ttg cgt gat cag gga ctc gct ttg aac ccc ggc ttt cag ctt gat	1397
Asn Leu Arg Asp Gln Gly Leu Ala Leu Asn Pro Gly Phe Gln Leu Asp	
285 290 295	
atc gca aac cgg atc aag ggc ccc gac ggc aag gag cgc aca tgg gcg	1445
Ile Ala Asn Arg Ile Lys Gly Pro Asp Gly Lys Glu Arg Thr Trp Ala	
300 305 310 315	
ctc ggc ggg cat ggc ggg atg ttc gcc att tcg aaa tca agc gtc aag	1493
Leu Gly Gly His Gly Gly Met Phe Ala Ile Ser Lys Ser Ser Val Lys	
320 325 330	
act gaa aaa gag gtc aga aaa atc ctc gca ttt ttt gac aga atc gct	1541
Thr Glu Lys Glu Val Arg Lys Ile Leu Ala Phe Phe Asp Arg Ile Ala	
335 340 345	
gaa gaa gac ctc aac aat ttg atg ttg tat gga ata gaa ggc gta cac	1589
Glu Glu Asp Leu Asn Asn Leu Met Leu Tyr Gly Ile Glu Gly Val His	
350 355 360	
tat gaa aag aaa ggg ggg agc ggc tat ttt cga aag cag gaa aac tac	1637
Tyr Glu Lys Lys Gly Gly Ser Gly Tyr Phe Arg Lys Gln Glu Asn Tyr	
365 370 375	
cat ctg tgg gaa gcg gaa att cag ccg tta aac cag ctg att ggc gtc	1685
His Leu Trp Glu Ala Glu Ile Gln Pro Leu Asn Gln Leu Ile Gly Val	
380 385 390 395	
aat aaa caa gct tta aaa agc gct gaa gat ccg ctc cgc gcc aaa aat	1733
Asn Lys Gln Ala Leu Lys Ser Ala Glu Asp Pro Leu Arg Ala Lys Asn	
400 405 410	
gaa aag ctt gag gag gac aac cgg gca atc gca gtc cag aat ccg gcc	1781
Glu Lys Leu Glu Glu Asp Asn Arg Ala Ile Ala Val Gln Asn Pro Ala	
415 420 425	
gaa ccg ctg tat tct gcc gca cag atg gac agg gga aca gaa ttg aag	1829
Glu Pro Leu Tyr Ser Ala Ala Gln Met Asp Arg Gly Thr Glu Leu Lys	
430 435 440	

aaa atc att gat gac gcc aca ttt caa ttt att ctc ggg gaa atc aat 1877  
 Lys Ile Ile Asp Asp Ala Thr Phe Gln Phe Ile Leu Gly Glu Ile Asn  
 445 450 455

gaa aaa gct ttg acc agg cag tcc tgaaatggga gaagcatggc ggcggaaaga 1931  
 Glu Lys Ala Leu Thr Arg Gln Ser  
 460 465

tcatgaaaga actgaatgaa gatctgaaaa aagcaaacta aacagaaaac cctttccatt 1991

tttttgaaaa ggaaagggtt tttcatcgta ttcgctccaa gttcattttc tttaaattct 2051

gcaaaataaa caatataatt ccatcatagg acgaaaagga ggaagcgata tgcagactgc 2111

cgttatatat gcacacccaa atccaaacag tttcaacgga gccattttta atcaagtcatt 2171

aaaggcgctt gaggacggta agcattttta tgacgtcatt gatttgtata gagaccggtt 2231

tgatcccgtt ctattatttg atgaaaagaa aaggcgctca gatatgaatc gcgatccgga 2291

aactgccgaa tatcgaagaa ttgtcaaaaa cgccgaccat ctgattttca tttatccgct 2351

ttggtggggc ggaatgccag cgatcatgaa aggctttatt gaccgcgttt ttg 2404

<210> 56

<211> 467

<212> PRT

<213> Bacillus licheniformis

<400> 56

Met Lys Lys Leu Cys Cys Leu Ile Leu Val Leu Val Phe Ser Ala Gly  
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Cys Thr Gln Gln Lys Ala Ser Thr Glu Glu Asp Gly Ala Leu Glu Ile  
 20 25 30

Asn Trp Leu Val Pro Leu His Thr Pro Gln Pro Pro Lys Glu Lys Ala  
 35 40 45

Leu Asp Ile Ile Glu Asp Lys Thr Asn Thr Lys Leu Lys Leu Ile Trp  
 50 55 60

Val Pro Asp Ser Thr Lys Glu Glu Arg Ile Asn Thr Thr Leu Ala Ser  
 65 70 75 80

Gly Asn Met Pro Lys Val Met Thr Leu Pro Asp Leu Glu Asp Ser Ala  
 85 90 95

Val Val Ser Ala Leu Arg Ser Gly Met Phe Trp Glu Ile Gly Pro Tyr

100

105

110

Phe Lys Asp Tyr Pro Asn Leu Arg Lys Leu Asp Lys Thr Ile Leu Lys  
 115 120 125

Asn Ile Ser Val Asp Gly Lys Val Tyr Gly Ile Tyr Arg Glu Arg Pro  
 130 135 140

Met Ala Arg Gln Gly Val Val Ile Arg Lys Asp Trp Leu Asp Asn Leu  
 145 150 155 160

Gly Leu Glu Met Pro Glu Thr Val Asp Asp Leu Tyr Lys Ile Ala Lys  
 165 170 175

Ala Phe Thr Glu Gln Asp Pro Asp Gln Asn Gly Lys Asp Asp Thr Phe  
 180 185 190

Gly Leu Ala Asp Arg Asn Asp Leu Thr Phe Gly Ala Phe Lys Thr Leu  
 195 200 205

Ala Ser Tyr Phe Gly Ala Pro Asn Glu Trp Gly Thr Asp Glu Asp Gly  
 210 215 220

Asn Leu Phe Pro Tyr Phe Lys His Glu Ala Tyr Lys Asp Ala Met Ala  
 225 230 235 240

Tyr Met Lys Lys Leu Tyr Glu Glu Gly Leu Met Asn Arg Asp Phe Ala  
 245 250 255

Val Thr Ser Lys Thr Gln Gln Gln Asp Leu Val Ile Gln Gly Lys Ala  
 260 265 270

Gly Ile Tyr Ile Gly Ala Met Ser Asp Ala Met Asn Leu Arg Asp Gln  
 275 280 285

Gly Leu Ala Leu Asn Pro Gly Phe Gln Leu Asp Ile Ala Asn Arg Ile  
 290 295 300

Lys Gly Pro Asp Gly Lys Glu Arg Thr Trp Ala Leu Gly Gly His Gly  
 305 310 315 320

Gly Met Phe Ala Ile Ser Lys Ser Ser Val Lys Thr Glu Lys Glu Val  
 325 330 335

Arg Lys Ile Leu Ala Phe Phe Asp Arg Ile Ala Glu Glu Asp Leu Asn  
 340 345 350

Asn Leu Met Leu Tyr Gly Ile Glu Gly Val His Tyr Glu Lys Lys Gly  
 355 360 365

Gly Ser Gly Tyr Phe Arg Lys Gln Glu Asn Tyr His Leu Trp Glu Ala  
 370 375 380

Glu Ile Gln Pro Leu Asn Gln Leu Ile Gly Val Asn Lys Gln Ala Leu  
 385 390 395 400

Lys Ser Ala Glu Asp Pro Leu Arg Ala Lys Asn Glu Lys Leu Glu Glu  
 405 410 415

Asp Asn Arg Ala Ile Ala Val Gln Asn Pro Ala Glu Pro Leu Tyr Ser  
 420 425 430

Ala Ala Gln Met Asp Arg Gly Thr Glu Leu Lys Lys Ile Ile Asp Asp  
 435 440 445

Ala Thr Phe Gln Phe Ile Leu Gly Glu Ile Asn Glu Lys Ala Leu Thr  
 450 455 460

Arg Gln Ser  
 465

<210> 57  
 <211> 1589  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501) .. (1388)

<400> 57  
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 ccggcattcg tttatttact tccggccatc ttctttttca atatcggggg tgtgccgggt 120  
 gttgtcgcgtt ccgttatctt tgcgatgcct ccgacaatcc ggatgacgat cttagggatc 180  
 cagcaggtgc ctgaagatct gattgaagct acagaagcat ttggttcaac gacaagccag 240

cggtctttaa aagtgcagct gccgctcgcg acgaaaacca ttctggccgg tatcaatcaa	300
agcatcatgc ttgctttgtc aatggtcgtt attgcatcaa tggtaggcgc gcccggaactc	360
ggagaagaag tttaccgggc tgtgacccag ctgcaaaccgg gtaccgggtgt agaaaccgga	420
cttgcgattg ttattattgc gatcgactt gaccgggtta. cacaaaatat aaaattgaaa	480
aagagcaggg ggaatgcata atg tgg aaa aag ata gcg gga atc ggc act gca	533
Met Trp Lys Lys Ile Ala Gly Ile Gly Thr Ala	
1 5 10	
gcg gta ctc aca ttg ggt ctg gct gcc tgc gga agc agc aat aat aat	581
Ala Val Leu Thr Leu Gly Leu Ala Ala Cys Gly Ser Ser Asn Asn Asn	
15 20 25	
gaa aat gcg tca gta ggc gat caa gtc aat tat aaa att acc ggc att	629
Glu Asn Ala Ser Val Gly Asp Gln Val Asn Tyr Lys Ile Thr Gly Ile	
30 35 40	
gat cct gga gcg ggc att atg aat gcg acg gac cag gcg ctc aag gac	677
Asp Pro Gly Ala Gly Ile Met Asn Ala Thr Asp Gln Ala Leu Lys Asp	
45 50 55	
tac gat ctc agc aag tgg act gta acg tca gga tca agc tca gca atg	725
Tyr Asp Leu Ser Lys Trp Thr Val Thr Ser Gly Ser Ser Ser Ala Met	
60 65 70 75	
aca gcc gca ttg aaa aaa gct tat gac aaa aaa gat ccg atc atc att	773
Thr Ala Ala Leu Lys Lys Ala Tyr Asp Lys Lys Asp Pro Ile Ile Ile	
80 85 90	
acg ggc tgg acg ccg cat tgg atg ttt gca aaa tac gat ctg aaa tat	821
Thr Gly Trp Thr Pro His Trp Met Phe Ala Lys Tyr Asp Leu Lys Tyr	
95 100 105	
tta aaa gat cct aaa ggt tcc tac ggc gat gcc gaa gaa atc cat act	869
Leu Lys Asp Pro Lys Gly Ser Tyr Gly Asp Ala Glu Glu Ile His Thr	
110 115 120	
gtt acg cgc aaa gga ttc aag gac gac cat ccg ggc gca aac aag ctg	917
Val Thr Arg Lys Gly Phe Lys Asp Asp His Pro Gly Ala Asn Lys Leu	
125 130 135	
ctc agc caa ttc agc tgg aca gag gat gat atg gga gaa gtc atg ctt	965
Leu Ser Gln Phe Ser Trp Thr Glu Asp Asp Met Gly Glu Val Met Leu	
140 145 150 155	
gcc gtt cag gaa ggc aaa aaa ccg gaa gaa gct gca gca gac ttc gtg	1013
Ala Val Gln Glu Gly Lys Lys Pro Glu Glu Ala Ala Ala Asp Phe Val	
160 165 170	
aaa aaa cat caa gat cta gtt aag aaa tgg aca aag ggc gtc gat aag	1061
Lys Lys His Gln Asp Leu Val Lys Lys Trp Thr Lys Gly Val Asp Lys	
175 180 185	
cgg acg gtg aaa aaa tta agc tcg gct atg tgg cat ggg aca gcg aaa	1109



Arg	Thr	Val	Lys	Lys	Leu	Ser	Ser	Ala	Met	Trp	His	Gly	Thr	Ala	Lys		
		190					195					200					
atg	cga	gca	cga	atg	tca	tcg	caa	agt	tct	tta	aga	cta	ggg	ata	cag		1157
Met	Arg	Ala	Arg	Met	Ser	Ser	Gln	Ser	Ser	Leu	Arg	Leu	Gly	Ile	Gln		
	205					210					215						
cgt	acg	ctc	agc	cca	agt	aga	agc	agg	ccc	gat	gtg	agc	tgg	cat	gca		1205
Arg	Thr	Leu	Ser	Pro	Ser	Arg	Ser	Arg	Pro	Asp	Val	Ser	Trp	His	Ala		
220					225				230						235		
aaa	tgg	aag	cgt	cga	tgc	ttc	act	tgc	tgc	atg	gct	gcc	gca	acg	caa		1253
Lys	Trp	Lys	Arg	Arg	Cys	Phe	Thr	Cys	Cys	Met	Ala	Ala	Ala	Thr	Gln		
				240					245					250			
tca	aac	ata	tgc	tta	aaa	ata	caa	agg	caa	ata	cga	aga	tat	cgg	tac		1301
Ser	Asn	Ile	Cys	Leu	Lys	Ile	Gln	Arg	Gln	Ile	Arg	Arg	Tyr	Arg	Tyr		
			255					260					265				
tcg	cat	gac	agg	cgt	aaa	aat	tgg	cct	tgt	cgt	tcc	gac	ata	tat	gaa		1349
Ser	His	Asp	Arg	Arg	Lys	Asn	Trp	Pro	Cys	Arg	Ser	Asp	Ile	Tyr	Glu		
	270						275					280					
aga	tgt	caa	ttc	aat	cga	aga	ctt	gaa	aaa	ata	acg	aac	aaagccggcg				1398
Arg	Cys	Gln	Phe	Asn	Arg	Arg	Leu	Glu	Lys	Ile	Thr	Asn					
	285					290					295						
aacccatctc	gcgggcttat	ttttgccgga	aagggataac	cgctcatcac	ccgaatcctc												1458
ccggatgcaa	aaaaaacatc	ctaaaacggt	aaaccgcttt	aggatgctgg	actcaactga												1518
agccttccat	agcagagaca	gcttcgggta	ttaatttttc	gttttaattt	ttccgccccca												1578
ttttttgaac	c																1589

<210> 58  
 <211> 296  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 58

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Gly	Leu	Ala	Ala	Cys	Gly	Ser	Ser	Asn	Asn	Asn	Glu	Asn	Ala	Ser	Val		
			20					25					30				
Gly	Asp	Gln	Val	Asn	Tyr	Lys	Ile	Thr	Gly	Ile	Asp	Pro	Gly	Ala	Gly		
		35					40					45					
Ile	Met	Asn	Ala	Thr	Asp	Gln	Ala	Leu	Lys	Asp	Tyr	Asp	Leu	Ser	Lys		
	50					55					60						

Trp Thr Val Thr Ser Gly Ser Ser Ser Ala Met Thr Ala Ala Leu Lys  
65 70 75 80

Lys Ala Tyr Asp Lys Lys Asp Pro Ile Ile Ile Thr Gly Trp Thr Pro  
85 90 95

His Trp Met Phe Ala Lys Tyr Asp Leu Lys Tyr Leu Lys Asp Pro Lys  
100 105 110

Gly Ser Tyr Gly Asp Ala Glu Glu Ile His Thr Val Thr Arg Lys Gly  
115 120 125

Phe Lys Asp Asp His Pro Gly Ala Asn Lys Leu Leu Ser Gln Phe Ser  
130 135 140

Trp Thr Glu Asp Asp Met Gly Glu Val Met Leu Ala Val Gln Glu Gly  
145 150 155 160

Lys Lys Pro Glu Glu Ala Ala Ala Asp Phe Val Lys Lys His Gln Asp  
165 170 175

Leu Val Lys Lys Trp Thr Lys Gly Val Asp Lys Arg Thr Val Lys Lys  
180 185 190

Leu Ser Ser Ala Met Trp His Gly Thr Ala Lys Met Arg Ala Arg Met  
195 200 205

Ser Ser Gln Ser Ser Leu Arg Leu Gly Ile Gln Arg Thr Leu Ser Pro  
210 215 220

Ser Arg Ser Arg Pro Asp Val Ser Trp His Ala Lys Trp Lys Arg Arg  
225 230 235 240

Cys Phe Thr Cys Cys Met Ala Ala Ala Thr Gln Ser Asn Ile Cys Leu  
245 250 255

Lys Ile Gln Arg Gln Ile Arg Arg Tyr Arg Tyr Ser His Asp Arg Arg  
260 265 270

Lys Asn Trp Pro Cys Arg Ser Asp Ile Tyr Glu Arg Cys Gln Phe Asn  
275 280 285

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Gln Val Asn Phe Ser Tyr Ile Asn Phe Val Asn Glu Gln His Gly Arg	
95 100 105	
ggc tct gaa ttg agc gcc ctc gct tcc gag cag gta tgg aag gaa gat	869
Gly Ser Glu Leu Ser Ala Leu Ala Ser Glu Gln Val Trp Lys Glu Asp	
110 115 120	
ccg gat tca ttc tgg aag ttc cat gag gcg ttg tac aag gcg cag cct	917
Pro Asp Ser Phe Trp Lys Phe His Glu Ala Leu Tyr Lys Ala Gln Pro	
125 130 135	
gac aat gac acg atg gaa aac gag tgg gcg acg ccg gca aaa ttg gcg	965
Asp Asn Asp Thr Met Glu Asn Glu Trp Ala Thr Pro Ala Lys Leu Ala	
140 145 150 155	
gac atc acg gaa gcc aat acg aaa atc aaa cgc gat aag ctt gtc agc	1013
Asp Ile Thr Glu Ala Asn Thr Lys Ile Lys Arg Asp Lys Leu Val Ser	
160 165 170	
agc tta aat gac aaa acg ttc gct gag caa tta aaa acg gac aat tcg	1061
Ser Leu Asn Asp Lys Thr Phe Ala Glu Gln Leu Lys Thr Asp Asn Ser	
175 180 185	
ctc atc aac aaa tac ggt gta gac tcg acg ccg acg atc ttt gtc aac	1109
Leu Ile Asn Lys Tyr Gly Val Asp Ser Thr Pro Thr Ile Phe Val Asn	
190 195 200	
ggc gta aaa atc gac aaa ccg ttt gat tat gac aaa atc aaa gaa acg	1157
Gly Val Lys Ile Asp Lys Pro Phe Asp Tyr Asp Lys Ile Lys Glu Thr	
205 210 215	
atc gag aaa gag ctg aaa ggc cag tctgatgaaa aataaactgc tttttctgta	1211
Ile Glu Lys Glu Leu Lys Gly Gln	
220 225	
cgggcgcttg atcgtctcat taacggcgac gctaggcagc ttgtacttca gcgaaatccg	1271
caaatttatt ccttgcgaaac tgtgctggta tcagcggatt atgatgtatc cgctcgtgct	1331
gattctcgga attgcgacat ttcagggcga tgcccgctg aaaaaatacg tgctgccgat	1391
ggcggatgac ggcgcaggca tttccctgat gcactacatg gaacaaaaaa ttcccggatt	1451
caacggcatt aaaccgtgtg tcacaggagt gccttgctca gggcagtata tcaattgggt	1511
cggtttcatc acgattccgt ttctcgccct tattgcattt attttgatta tcatttttat	1571
gtgctttctc aaggggaaaag acgagtaaaa agagcattgt ctgacaatgc tcttttttta	1631
tttcttatac atgttcaata gaaaggatgt tataatatat ggaaattatc a	1682

<210> 60  
 <211> 227  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 60

Val Lys Lys Lys Gln Gln Ser Pro Met Lys Phe Ala Val Ile Met Thr  
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Val Val Val Val Phe Leu Ile Gly Ala Leu Val Val Ile Asn Asn Gln  
20 25 30

Thr Gln Asn Ala Ser Gln Thr Phe Asp Asp Lys Pro Ser Thr Glu Gly  
35 40 45

Gln Pro Leu Leu Gly Asn Lys Asp Ala Ala Val Thr Ile Thr Glu Phe  
50 55 60

Gly Asp Tyr Lys Cys Pro Ser Cys Lys Gln Trp Thr Glu Thr Val Phe  
65 70 75 80

Pro Asp Leu Lys Lys Asp Tyr Ile Asp Lys Asp Gln Val Asn Phe Ser  
85 90 95

Tyr Ile Asn Phe Val Asn Glu Gln His Gly Arg Gly Ser Glu Leu Ser  
100 105 110

Ala Leu Ala Ser Glu Gln Val Trp Lys Glu Asp Pro Asp Ser Phe Trp  
115 120 125

Lys Phe His Glu Ala Leu Tyr Lys Ala Gln Pro Asp Asn Asp Thr Met  
130 135 140

Glu Asn Glu Trp Ala Thr Pro Ala Lys Leu Ala Asp Ile Thr Glu Ala  
145 150 155 160

Asn Thr Lys Ile Lys Arg Asp Lys Leu Val Ser Ser Leu Asn Asp Lys  
165 170 175

Thr Phe Ala Glu Gln Leu Lys Thr Asp Asn Ser Leu Ile Asn Lys Tyr  
180 185 190

Gly Val Asp Ser Thr Pro Thr Ile Phe Val Asn Gly Val Lys Ile Asp  
195 200 205

Lys Pro Phe Asp Tyr Asp Lys Ile Lys Glu Thr Ile Glu Lys Glu Leu  
210 215 220

Lys Gly Gln  
225

<210> 61  
<211> 2308  
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gcaggaagat agtgaacggg gcgtaccagg atcaactcac acccaccccc agatcccggc      240
agtccgttaa cccatgacca gtatgtatat accccggcac aagaccattc attttcaccc      300
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tcgttcataa caatcgacag ggcatttgtc ataacatttc acaatggtgt cccaaacaat      420
agcagcacia tatgttgttt tctgtatttt tatagcatat attagttttt gtgaaaaaat      480
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gcc ctg ttg ctg ctc ggg aca tct gcg cca atc gaa gcg gca gac tac      581
Ala Leu Leu Leu Leu Gly Thr Ser Ala Pro Ile Glu Ala Ala Asp Tyr
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gga cgc gac gtc ctc ggc tca aaa gac ggc tgg ggc gct tat gga aaa      629
Gly Arg Asp Val Leu Gly Ser Lys Asp Gly Trp Gly Ala Tyr Gly Lys
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gga acg acc gga ggc gct gac gct tct tct gat cag gta tat acg gtc      677
Gly Thr Thr Gly Gly Ala Asp Ala Ser Ser Asp Gln Val Tyr Thr Val
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aaa aac cgc aag cag ctt gtt gag gca tta ggg gga gac aat aaa aag      725
Lys Asn Arg Lys Gln Leu Val Glu Ala Leu Gly Gly Asp Asn Lys Lys
60             65             70             75

aac agc gaa aat gat acg ccg aag atc atc tat gtg aag gga aca atc      773
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Lys	Asp	Pro	Glu	Tyr	Ser	Ile	Glu	Ala	Tyr	Leu	Lys	Ala	Tyr	Asp	Pro	
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Gly	Gly	Leu	Tyr	Val	Lys	Asn	Ala	Glu	Asn	Val	Ile	Ile	Arg	Asn	Ile	
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Glu	Phe	Glu	Asn	Ala	Tyr	Asp	Phe	Phe	Pro	Gly	Trp	Asp	Pro	Thr	Asp	
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ggg	agc	agc	ggc	aac	tgg	aat	tca	gaa	tat	gac	aac	ctg	ctg	atc	gaa	1157
Gly	Ser	Ser	Gly	Asn	Trp	Asn	Ser	Glu	Tyr	Asp	Asn	Leu	Leu	Ile	Glu	
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cag	cct	gat	gag	ctg	act	gaa	acg	cat	ttc	ggg	cgc	gaa	ttc	cag	cat	1253
Gln	Pro	Asp	Glu	Leu	Thr	Glu	Thr	His	Phe	Gly	Arg	Glu	Phe	Gln	His	
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cac	gac	gga	ctg	ctt	gat	atc	aaa	aag	cag	tcg	gat	ttc	att	acg	gtg	1301
His	Asp	Gly	Leu	Leu	Asp	Ile	Lys	Lys	Gln	Ser	Asp	Phe	Ile	Thr	Val	
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Ser	Tyr	Ser	Ile	Phe	Ser	Gly	His	Ser	Lys	Asn	Thr	Ile	Ile	Gly	Ser	
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Ser	Asp	Ser	Tyr	Lys	Ala	Asp	Asn	Gly	His	Leu	Arg	Val	Thr	Phe	His	
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Asp Asn Tyr Phe Asp Leu Pro Glu Gly Thr Lys Pro Gln Lys Leu Met			
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aag gtc ttt aaa ggt gac gct tta tat gaa aaa gat acg atc gta aac			1637
Lys Val Phe Lys Gly Asp Ala Leu Tyr Glu Lys Asp Thr Ile Val Asn			
365	370	375	
aac caa aaa agc gtc gca aaa att gat gtt gtc agc aca tac aac aaa			1685
Asn Gln Lys Ser Val Ala Lys Ile Asp Val Val Ser Thr Tyr Asn Lys			
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Ala Asn Asn Ala Ser Ile Lys Lys Ser Ala Gly Trp Lys Pro Thr Leu			
400	405	410	
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Phe Glu Lys Ile Asp Asp Ala Glu Asp Val Pro Ala Ile Val Glu Ala			
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His Ala Gly Ala Gly Lys Leu Lys			
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Gly Ser Lys Asp Gly Trp Gly Ala Tyr Gly Lys Gly Thr Thr Gly Gly  
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Ala Asp Ala Ser Ser Asp Gln Val Tyr Thr Val Lys Asn Arg Lys Gln  
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Leu Val Glu Ala Leu Gly Gly Asp Asn Lys Lys Asn Ser Glu Asn Asp  
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Thr Pro Lys Ile Ile Tyr Val Lys Gly Thr Ile Asn Leu Ser Val Asp  
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Asp Asp Asn Asn Pro Leu Gly Tyr Glu Asp Tyr Lys Asp Pro Glu Tyr  
100 105 110

Ser Ile Glu Ala Tyr Leu Lys Ala Tyr Asp Pro Lys Lys Trp Gly Lys  
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Lys Glu Pro Thr Gly Lys Leu Glu Glu Ala Arg Leu Arg Ser Lys Asp  
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Asn Gln Lys Glu Arg Val Leu Ile Arg Val Gly Ser Asn Thr Thr Ile  
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Ile Gly Leu Gly Asp Asp Ala Lys Ile Val Gly Gly Gly Leu Tyr Val  
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Lys Asn Ala Glu Asn Val Ile Ile Arg Asn Ile Glu Phe Glu Asn Ala  
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Tyr Asp Phe Phe Pro Gly Trp Asp Pro Thr Asp Gly Ser Ser Gly Asn  
195 200 205

Trp Asn Ser Glu Tyr Asp Asn Leu Leu Ile Glu Met Ser Lys Asn Ile  
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Trp Ile Asp His Cys Ser Phe Asn Asp Gly Asp Gln Pro Asp Glu Leu  
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Thr Glu Thr His Phe Gly Arg Glu Phe Gln His His Asp Gly Leu Leu  
245 250 255

Asp Ile Lys Lys Gln Ser Asp Phe Ile Thr Val Ser Tyr Ser Ile Phe  
260 265 270

Ser Gly His Ser Lys Asn Thr Ile Ile Gly Ser Ser Asp Ser Tyr Lys  
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Ala Asp Asn Gly His Leu Arg Val Thr Phe His His Asn Leu Tyr Glu  
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Asn Ile Lys Glu Arg Ala Pro Arg Val Arg Tyr Gly Lys Val His Ile  
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Tyr Asn Asn Tyr Phe Lys Ser Thr Lys Asp Ser Tyr Asn Tyr Ser Trp  
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Gly Val Gly Tyr Ser Ser Lys Ile Tyr Ala Glu Asp Asn Tyr Phe Asp  
340 345 350

Leu Pro Glu Gly Thr Lys Pro Gln Lys Leu Met Lys Val Phe Lys Gly  
355 360 365

Asp Ala Leu Tyr Glu Lys Asp Thr Ile Val Asn Asn Gln Lys Ser Val  
370 375 380

Ala Lys Ile Asp Val Val Ser Thr Tyr Asn Lys Ala Asn Asn Ala Ser  
385 390 395 400

Ile Lys Lys Ser Ala Gly Trp Lys Pro Thr Leu Phe Glu Lys Ile Asp  
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Lys Leu Lys  
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acacgaggaa gacgcggaat aaggaggaac atagtgcgc aggggtgaacg gtagggaggg 180

tggcaaatag tagtatgata tttgaaagac ggggtcccgtc cgaaatcggg gaaaaacaaa 240

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ctggaccgcg ataaagacaa aattgcctgt gagcgtgat atatccaaaa aaagatctct 360

gccaaaggat ctttttttgt ttatcaggaa atttatgaaa attaaagact gctgaaacat 420

aatcttaaca gtgcgaacct atactttggc aagagaagag caaa agg gga gtg gat 476  
Arg Gly Val Asp  
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gat gtg tca gct tta ttc aaa aaa ttg atg tta tct tca ttg atc ggg 524  
Asp Val Ser Ala Leu Phe Lys Lys Leu Met Leu Ser Ser Leu Ile Gly  
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Val Ser Ile Gly Ser Ala Leu Phe Ala Pro Asn Ala Gly Ala Gln Glu  
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Pro Ala Val Lys Pro Lys Lys Val Asp Val Ile Ala His Arg Gly Ala  
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tcg gga tat gcg ccg gaa aac acg atg gct gct ttt gat aaa gcg ctt 668  
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cag atg aaa gca gat tat atc gag ctg gat gtt caa atg tcc aaa gac 716  
Gln Met Lys Ala Asp Tyr Ile Glu Leu Asp Val Gln Met Ser Lys Asp  
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ggg gag ctt gtc atc att cac gat acg acc gta aac cgt acg aca gat 764  
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att gac tca gtg ctg ccg gtt gcc gta aag gat ttg acg ctt gcc gag 812  
Ile Asp Ser Val Leu Pro Val Ala Val Lys Asp Leu Thr Leu Ala Glu  
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ctg cgc aag ctt gat gcc ggc agc ttc ttc ggt ccg cag ttc gca gga 860  
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gag cgc att ccg aca ttt gaa gaa gtg ctt gac cgg tat aaa ggg aag 908

Glu Arg Ile Pro Thr Phe Glu Glu Val Leu Asp Arg Tyr Lys Gly Lys	
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Val Gly Met Leu Ile Glu Leu Lys Glu Pro Ala Arg Tyr Pro Gly Ile	
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gaa gga aaa gtg tca gca gca ttg aaa gag cgg aga atg gat aag cct	1004
Glu Gly Lys Val Ser Ala Ala Leu Lys Glu Arg Arg Met Asp Lys Pro	
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Lys Asn Gly Lys Ile Ile Val Gln Ser Phe Asp Phe Asn Ser Val Tyr	
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Lys Ile His Gln Leu Leu Pro Ser Met Pro Thr Gly Val Leu Thr Ser	
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Lys Ala Ala Asp Leu Thr Asp Ala Lys Leu Lys Glu Phe Ser Gly Tyr	
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Ala Lys Tyr Val Asn Ala Asn Leu Lys Asn Val Ala Ala Asp Pro Thr	
230 235 240	
ctt gtg ccg aga att cat gcg ctc ggc atg aag ata cgc cct tgg acc	1244
Leu Val Pro Arg Ile His Ala Leu Gly Met Lys Ile Arg Pro Trp Thr	
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gtc cgc tcc cgc gat gaa gtg cct ccg cta tca agg ccc gcg tgg aac	1292
Val Arg Ser Arg Asp Glu Val Pro Pro Leu Ser Arg Pro Ala Trp Asn	
265 270 275	
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Gly Ile Val Thr Lys Leu Ser Arg Leu Leu Phe Gln Lys Ser Thr Gly	
280 285 290	
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Ala Pro Ile Lys Asn Pro	
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1856

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35 40 45

His Arg Gly Ala Ser Gly Tyr Ala Pro Glu Asn Thr Met Ala Ala Phe  
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Asp Lys Ala Leu Gln Met Lys Ala Asp Tyr Ile Glu Leu Asp Val Gln  
65 70 75 80

Met Ser Lys Asp Gly Glu Leu Val Ile Ile His Asp Thr Thr Val Asn  
85 90 95

Arg Thr Thr Asp Ile Asp Ser Val Leu Pro Val Ala Val Lys Asp Leu  
100 105 110

Thr Leu Ala Glu Leu Arg Lys Leu Asp Ala Gly Ser Phe Phe Gly Pro  
115 120 125

Gln Phe Ala Gly Glu Arg Ile Pro Thr Phe Glu Glu Val Leu Asp Arg  
130 135 140

Tyr Lys Gly Lys Val Gly Met Leu Ile Glu Leu Lys Glu Pro Ala Arg  
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Tyr Pro Gly Ile Glu Gly Lys Val Ser Ala Ala Leu Lys Glu Arg Arg  
165 170 175

Met Asp Lys Pro Lys Asn Gly Lys Ile Ile Val Gln Ser Phe Asp Phe  
180 185 190

Asn Ser Val Tyr Lys Ile His Gln Leu Leu Pro Ser Met Pro Thr Gly  
 195 200 205

Val Leu Thr Ser Lys Ala Ala Asp Leu Thr Asp Ala Lys Leu Lys Glu  
 210 215 220

Phe Ser Gly Tyr Ala Lys Tyr Val Asn Ala Asn Leu Lys Asn Val Ala  
 225 230 235 240

Ala Asp Pro Thr Leu Val Pro Arg Ile His Ala Leu Gly Met Lys Ile  
 245 250 255

Arg Pro Trp Thr Val Arg Ser Arg Asp Glu Val Pro Pro Leu Ser Arg  
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 aaaatgtggg tcagcggggt ggccgtctcc atatttgcac tctggaaaat cattgctgct 480  
 gtaatgggag gcggggcggtg atg aga agt tta ttg aga agc gcg atg atc tta 533

Met Arg Ser Leu Leu Arg Ser Ala Met Ile Leu  
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Cys Met Ile Phe Leu Val Phe Ile Pro Ile Ala Ser Gly Ala Ala Ala	
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tct gaa cag aag cgg ttt gtt tat gat gaa gcc ggg ctt ctg acc aaa	629
Ser Glu Gln Lys Arg Phe Val Tyr Asp Glu Ala Gly Leu Leu Thr Lys	
30 35 40	
cag gaa atc gag aag ctg gaa acg ctg gca gcc aaa ttg ggc gcc gaa	677
Gln Glu Ile Glu Lys Leu Glu Thr Leu Ala Ala Lys Leu Gly Ala Glu	
45 50 55	
cgg gag acc gac ttt atc att gtg acg acc aat gat aca aac ggc cgc	725
Arg Glu Thr Asp Phe Ile Ile Val Thr Thr Asn Asp Thr Asn Gly Arg	
60 65 70 75	
gat gta aag aaa tat gcg gag gac ttc tat gac gaa aaa gcg ccc ggc	773
Asp Val Lys Lys Tyr Ala Glu Asp Phe Tyr Asp Glu Lys Ala Pro Gly	
80 85 90	
tac cag aag aag cac gga aat gca gcc gta tta acg gta gat atg gag	821
Tyr Gln Lys Lys His Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu	
95 100 105	
cat aga gaa gtc tat ctt gcc ggc ttt aaa aag gct gaa gaa tat ttg	869
His Arg Glu Val Tyr Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu	
110 115 120	
aat gac gcc agg ctg gac aaa att aga gaa aaa atc acg ccg gat ata	917
Asn Asp Ala Arg Leu Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile	
125 130 135	
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Ser Asp Lys His Tyr Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala	
140 145 150 155	
cat gat gat atg gag aag aaa ccg tgg gcg gac agc atc ttt ttt aag	1013
His Asp Asp Met Glu Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys	
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Thr Trp Phe Gln Leu Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val	
175 180 185	
gcc att atg aaa tac aat tca ggc ggc aaa gtg aca gta agt gca agc	1109
Ala Ile Met Lys Tyr Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser	
190 195 200	
act tat atg aac ggt gat acg tcc gga gtg atc aga aat aat gac gaa	1157
Thr Tyr Met Asn Gly Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu	
205 210 215	
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cgg gga agc ttt tagaaagggga aaggaagagc ttaaattggtg ttttttagaa				1305
Arg Gly Ser Phe				
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tcttttttaaa caacggaaaa attgaaggca ttttccagga tgagggcgac tatgatattg				1485
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agaatgcat caatatcccg gctgcaggac ttccgggcgg catgccgac agggcgaaacg				1665
gaagatttaa ctttaagggtg aatgattatg tcgcattaat cgataaaatt gccggtgtga				1725
aaqatcaqta tqttgtggaa gatatcaaaa tacggatcac atc				1768

Met Arg Ser Leu Leu Arg Ser Ala Met Ile Leu Cys Met Ile Phe Leu  
1 5 10 15



Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu His Arg Glu Val Tyr  
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Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu Asn Asp Ala Arg Leu  
 115 120 125

Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile Ser Asp Lys His Tyr  
 130 135 140

Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala His Asp Asp Met Glu  
 145 150 155 160

Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys Thr Trp Phe Gln Leu  
 165 170 175

Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val Ala Ile Met Lys Tyr  
 180 185 190

Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser Thr Tyr Met Asn Gly  
 195 200 205

Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu Tyr Ile Arg Thr Thr  
 210 215 220

Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys Ser Ser Gly Gly Gly  
 225 230 235 240

Thr Thr Ser Gly Gly His Ser His Ser Gly Ser Arg Gly Ser Phe  
 245 250 255

<210> 67  
 <211> 2206  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1703)

<400> 67  
 tctcccgag ttcttcccaa taggatacct cttcgtactc caaatgctcg atcggcgcac 60  
 cggtataaat catgccgtcg aattttcggg ccctgattga agaaaaagtt gtataaaact 120  
 gttccaaatg ctgccttggt gtatgttttg gcgtgtgtgt agacggtatt aaaaaagtga 180

aatatacctg taaaggagaa ttccccgagca tcttgagcag ctgtgtctcg gtcttgattt	240
tctgcggcat cagattaaga atcacaatat ttaaagggtct gatgtcctga tgaaaagccc	300
gtttttcatc catgacaaaa atattttcac tttcaagaat ctgctttgct ggcaaattga	360
taggtatggt gataggcaac acgccacctc cggttttctc cgctgatttt tcttcatatc	420
ggagcgacag tctgtcggtta agctggcagc tgacatcgta tgaattaaaa ggaatcttga	480
acaactgccg gccgaagggtg atg ttt tat gac ttg gaa ttt gcc gat ata cta	533
Met Phe Tyr Asp Leu Glu Phe Ala Asp Ile Leu	
1 5 10	
acg ccg ctc cgc gaa cag ctt cag ttc tgc ctg atg att gaa gcg ggt	581
Thr Pro Leu Arg Glu Gln Leu Gln Phe Cys Leu Met Ile Glu Ala Gly	
15 20 25	
gcg gga atg aac acg act gaa cag ttt gag agc tta ttt aaa aac agg	629
Ala Gly Met Asn Thr Thr Glu Gln Phe Glu Ser Leu Phe Lys Asn Arg	
30 35 40	
ccg ctg aag gtg gaa gct gag cag gtg aca gag cat gat ttg gct tta	677
Pro Leu Lys Val Glu Ala Glu Gln Val Thr Glu His Asp Leu Ala Leu	
45 50 55	
atg ctg ttc acc tcg ggc acg acg gga aac ccg aaa ggc tgc atg gtc	725
Met Leu Phe Thr Ser Gly Thr Thr Gly Asn Pro Lys Gly Cys Met Val	
60 65 70 75	
aac cac ggc agt ctg gcc gca tac ttg aca gag gtg aac gtg aaa tcg	773
Asn His Gly Ser Leu Ala Ala Tyr Leu Thr Glu Val Asn Val Lys Ser	
80 85 90	
aag cag ctg aaa ggc acg cgc ttt tta gcg agc cac ccg ctc tat cat	821
Lys Gln Leu Lys Gly Thr Arg Phe Leu Ala Ser His Pro Leu Tyr His	
95 100 105	
atg agc tcg ctc aac cat gtt ttt cag gcg gct ttt gaa gga att gcc	869
Met Ser Ser Leu Asn His Val Phe Gln Ala Ala Phe Glu Gly Ile Ala	
110 115 120	
ctt tat ttc tta tgg gat ccc gaa ccg ttt gaa atc ctg cag gag atc	917
Leu Tyr Phe Leu Trp Asp Pro Glu Pro Phe Glu Ile Leu Gln Glu Ile	
125 130 135	
gag aag aaa cgc att cat atg atg atg gcg ttt cct tcc gtc tac acc	965
Glu Lys Lys Arg Ile His Met Met Met Ala Phe Pro Ser Val Tyr Thr	
140 145 150 155	
tac atg ctg gag gaa atg aaa aga cat cca ttc gac ctg tca tct gtg	1013
Tyr Met Leu Glu Glu Met Lys Arg His Pro Phe Asp Leu Ser Ser Val	
160 165 170	
aaa atg ctt gtt tcc ggc ggc acc aag gtg ccg gcg cgg ctg att aag	1061
Lys Met Leu Val Ser Gly Gly Thr Lys Val Pro Ala Arg Leu Ile Lys	

175	180	185	
gag tac aat gac cat gga atc atg atg gtg cag ggg tac ggc agc aca			1109
Glu Tyr Asn Asp His Gly Ile Met Met Val Gln Gly Tyr Gly Ser Thr			
190	195	200	
gaa gca tgg acg gtc agc gta tgg cgg cct gac atg ggc tgg gat aaa			1157
Glu Ala Trp Thr Val Ser Val Trp Arg Pro Asp Met Gly Trp Asp Lys			
205	210	215	
gtc act tca gcc ggc aag ccg att ccg caa gtc agc ata aaa atc gaa			1205
Val Thr Ser Ala Gly Lys Pro Ile Pro Gln Val Ser Ile Lys Ile Glu			
220	225	230	235
gac cct gat aca cat gaa gag ctg ccg acg gga gaa gtc gga gaa gtc			1253
Asp Pro Asp Thr His Glu Glu Leu Pro Thr Gly Glu Val Gly Glu Val			
240	245	250	
gtc gtc aaa agc ccg tat gtt ttt gaa ggg tat tac caa aat cct tcc			1301
Val Val Lys Ser Pro Tyr Val Phe Glu Gly Tyr Tyr Gln Asn Pro Ser			
255	260	265	
gcc acg caa aag gtg ctg aaa gac ggc tgg ttc tat atg ggg gac tcc			1349
Ala Thr Gln Lys Val Leu Lys Asp Gly Trp Phe Tyr Met Gly Asp Ser			
270	275	280	
ggc aaa ctc gat gaa gac gga ttt tta tat att acc ggc cgg tat aaa			1397
Gly Lys Leu Asp Glu Asp Gly Phe Leu Tyr Ile Thr Gly Arg Tyr Lys			
285	290	295	
gac gtc att gtc tac gga ggc gac aac att tat ccg gac caa gtg gaa			1445
Asp Val Ile Val Tyr Gly Gly Asp Asn Ile Tyr Pro Asp Gln Val Glu			
300	305	310	315
gaa atc atc gat caa gtg ccc gga gta gtt gaa tct gcc gtc atc ggc			1493
Glu Ile Ile Asp Gln Val Pro Gly Val Val Glu Ser Ala Val Ile Gly			
320	325	330	
gtc ccg gat gaa atg tac ggc gag gtt ccg agg gcg tat gtg gtg aaa			1541
Val Pro Asp Glu Met Tyr Gly Glu Val Pro Arg Ala Tyr Val Val Lys			
335	340	345	
aat gaa agc gcc ggc ctc aag aag gag gac att atc gcg tat tgc aaa			1589
Asn Glu Ser Ala Gly Leu Lys Lys Glu Asp Ile Ile Ala Tyr Cys Lys			
350	355	360	
gag cgc ctg tcc gac tat aaa att cct gaa atc gtc ttt atc gac agc			1637
Glu Arg Leu Ser Asp Tyr Lys Ile Pro Glu Ile Val Phe Ile Asp Ser			
365	370	375	
ctt ccg aaa aac agg ctc ggc aaa atc gtc aaa aaa gat ctg cgt gaa			1685
Leu Pro Lys Asn Arg Leu Gly Lys Ile Val Lys Lys Asp Leu Arg Glu			
380	385	390	395
ctg gca gtc aaa ggg cag tgagcgcaat gattgaccga aagcttatcc			1733
Leu Ala Val Lys Gly Gln			
400			

agcattggat aagctttttg tgctgattcc ttgcatcagc tgccgttttt tgtaacgttt 1793  
 tccagtgcta aaccactac aacattagga ggtgttgaca attgaaatcg aaatggagtg 1853  
 caatgggtggt tattgccggt cttttattgc tggccggatg cgggtgcactg aaggaggctg 1913  
 atccccgcg cggcagatca gcgcaaaaaa cggaagcctc gttttctgaa gctgaacagc 1973  
 gatttgcgct cgccttgttt caagacatga taaaagaaga agggagccgg aaaaacatct 2033  
 tcctctcgcc ttacagtatt cagcaggcac ttttgatgac ggcaaacggt gccgcgggag 2093  
 acagcagaaa ggacctgatc agcactttac atctcagcca ggcggatatg gcatcgatca 2153  
 acgggatatc aaaatctggt aatcgttctc ttgaaacgct gcctcacggt gaa 2206

<210> 68  
 <211> 401  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 68

Met Phe Tyr Asp Leu Glu Phe Ala Asp Ile Leu Thr Pro Leu Arg Glu  
 1 5 10 15

Gln Leu Gln Phe Cys Leu Met Ile Glu Ala Gly Ala Gly Met Asn Thr  
 20 25 30

Thr Glu Gln Phe Glu Ser Leu Phe Lys Asn Arg Pro Leu Lys Val Glu  
 35 40 45

Ala Glu Gln Val Thr Glu His Asp Leu Ala Leu Met Leu Phe Thr Ser  
 50 55 60

Gly Thr Thr Gly Asn Pro Lys Gly Cys Met Val Asn His Gly Ser Leu  
 65 70 75 80

Ala Ala Tyr Leu Thr Glu Val Asn Val Lys Ser Lys Gln Leu Lys Gly  
 85 90 95

Thr Arg Phe Leu Ala Ser His Pro Leu Tyr His Met Ser Ser Leu Asn  
 100 105 110

His Val Phe Gln Ala Ala Phe Glu Gly Ile Ala Leu Tyr Phe Leu Trp  
 115 120 125

Asp Pro Glu Pro Phe Glu Ile Leu Gln Glu Ile Glu Lys Lys Arg Ile  
 130 135 140

His Met Met Met Ala Phe Pro Ser Val Tyr Thr Tyr Met Leu Glu Glu  
 145 150 155 160

Met Lys Arg His Pro Phe Asp Leu Ser Ser Val Lys Met Leu Val Ser  
 165 170 175

Gly Gly Thr Lys Val Pro Ala Arg Leu Ile Lys Glu Tyr Asn Asp His  
 180 185 190

Gly Ile Met Met Val Gln Gly Tyr Gly Ser Thr Glu Ala Trp Thr Val  
 195 200 205

Ser Val Trp Arg Pro Asp Met Gly Trp Asp Lys Val Thr Ser Ala Gly  
 210 215 220

Lys Pro Ile Pro Gln Val Ser Ile Lys Ile Glu Asp Pro Asp Thr His  
 225 230 235 240

Glu Glu Leu Pro Thr Gly Glu Val Gly Glu Val Val Val Lys Ser Pro  
 245 250 255

Tyr Val Phe Glu Gly Tyr Tyr Gln Asn Pro Ser Ala Thr Gln Lys Val  
 260 265 270

Leu Lys Asp Gly Trp Phe Tyr Met Gly Asp Ser Gly Lys Leu Asp Glu  
 275 280 285

Asp Gly Phe Leu Tyr Ile Thr Gly Arg Tyr Lys Asp Val Ile Val Tyr  
 290 295 300

Gly Gly Asp Asn Ile Tyr Pro Asp Gln Val Glu Glu Ile Ile Asp Gln  
 305 310 315 320

Val Pro Gly Val Val Glu Ser Ala Val Ile Gly Val Pro Asp Glu Met  
 325 330 335

Tyr Gly Glu Val Pro Arg Ala Tyr Val Val Lys Asn Glu Ser Ala Gly  
 340 345 350

Leu Lys Lys Glu Asp Ile Ile Ala Tyr Cys Lys Glu Arg Leu Ser Asp

355

360

365

Tyr Lys Ile Pro Glu Ile Val Phe Ile Asp Ser Leu Pro Lys Asn Arg  
 370 375 380

Leu Gly Lys Ile Val Lys Lys Asp Leu Arg Glu Leu Ala Val Lys Gly  
 385 390 395 400

Gln

<210> 69  
 <211> 1547  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1046)

<400> 69  
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 tctggcgcggt tttcattcat agacaatttt tgatattcat aaattaattg atccagctcc 120  
 tggctccgcc tgatcgtttc atccccctgta tatccataga tttcagcggc ttcaaccatc 180  
 atttgccgct tcttgctgat ggaaacgagc aatgcttctt tttcaatata cctttgcacc 240  
 cgctcccggg aggtcccaaa aaaatttttt tgcaaaaaaa aatttttccc cataaggctc 300  
 tagtgttatg agaaaaaaat ccgggaacgg aatcaaggac cataaaaaatt ttttctggcc 360  
 aacccaaaac cccggtgcgt ttaagtcgtc ataaataaga aaccagcgga ggaaaaat 420  
 ttctcgcaac cctcttgtaa tctatctgac gttattgtaa catttgtaat ataagagata 480  
 tatttaagga gagaggacca ttg aaa aag tta atc gtt tgt tta tta gct gtt 533  
 Leu Lys Lys Leu Ile Val Cys Leu Leu Ala Val  
 1 5 10  
 tta ctg atc ttg cct gcc gga gcg tcc ctc gca gcg aaa aat caa aca 581  
 Leu Leu Ile Leu Pro Ala Gly Ala Ser Leu Ala Ala Lys Asn Gln Thr  
 15 20 25  
 tca ggg aat tta aca aat aag caa gtc atg caa tta acc ttg cag gca 629  
 Ser Gly Asn Leu Thr Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala  
 30 35 40  
 cgg gag cac ttt tgg aat acg atg agc ggc cac aat cca aaa gcg aaa 677  
 Arg Glu His Phe Trp Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys  
 45 50 55

aac tca act tgc cca tcc aaa aca ttt gaa tac cgc ggt ctt cca tat	725
Asn Ser Thr Cys Pro Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr	
60 65 70 75	
acg tat atg tgc agt gaa ttc agc aca aaa gca aaa tta aca gac tac	773
Thr Tyr Met Cys Ser Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr	
80 85 90	
ttg acg ccg gtt ttc aca aaa gac gcc att aaa aaa ggc ttg gaa aaa	821
Leu Thr Pro Val Phe Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys	
95 100 105	
tac aac atc att tct tat aaa gga aaa atg gcc gtg cct gtc ggc gat	869
Tyr Asn Ile Ile Ser Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp	
110 115 120	
ggg gac aac ctc tta gga tgg gac aag gca aaa atc aaa ctg atc tct	917
Gly Asp Asn Leu Leu Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser	
125 130 135	
caa aaa aac aat acc cgc act tat gaa ttt tcc gta ccg gca ttg gat	965
Gln Lys Asn Asn Thr Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp	
140 145 150 155	
gga tcg gtg act gcg aaa aga aag atc acg ttt gtg aaa gaa aac aac	1013
Gly Ser Val Thr Ala Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn	
160 165 170	
aaa tgg aaa atc aat cag ctc gat gct gcc atc taaacgaaaa agctaattgc	1066
Lys Trp Lys Ile Asn Gln Leu Asp Ala Ala Ile	
175 180	
taaaaacgga cattagcttt tttccgtcaa acggtcagtt caacgatggt gccgtcagga	1126
tccagaatga ctctttcata ataccgtct cccgtgacgc gcggctttcc ggcaacctgg	1186
tatccttcct tttcaaagcg gctcgtcatc tcgtcaacct cttgccgcga ccctaaggaa	1246
aacgccatat gtgcatagcc ggaagcggtc tcctctcctt ttgcaaggtc ggggctctc	1306
atcagctcaa gccgtgttcc cgattcaaac tggatgaaat atgattcgaa atgctttttc	1366
ggattgacat atttttcatt cgtctttccg tgaaaaaac gggatatagaa atctttcatt	1426
tcctctaaat tgttcgtcca tatggcgatg tgttcgattt tcataaatct ccctccatt	1486
tcatattacc atatagatcc tctgcctttt ttacacttt tttaaattga taagtattca	1546
t	1547

<210> 70  
 <211> 182  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 70

Leu Lys Lys Leu Ile Val Cys Leu Leu Ala Val Leu Leu Ile Leu Pro  
1 5 10 15

Ala Gly Ala Ser Leu Ala Ala Lys Asn Gln Thr Ser Gly Asn Leu Thr  
20 25 30

Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala Arg Glu His Phe Trp  
35 40 45

Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys Asn Ser Thr Cys Pro  
50 55 60

Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr Thr Tyr Met Cys Ser  
65 70 75 80

Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr Leu Thr Pro Val Phe  
85 90 95

Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys Tyr Asn Ile Ile Ser  
100 105 110

Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp Gly Asp Asn Leu Leu  
115 120 125

Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser Gln Lys Asn Asn Thr  
130 135 140

Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp Gly Ser Val Thr Ala  
145 150 155 160

Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn Lys Trp Lys Ile Asn  
165 170 175

Gln Leu Asp Ala Ala Ile  
180

<210> 71

<211> 1621

<212> DNA

<213> Bacillus licheniformis

<220>



<221> CDS

<222> (271)..(1122)

<400> 71

gcttgatggc agtgcacggg tttggctatt ctgcgcttcc ggcaatgaac gatgcctgga	60
gtgctgtatt cagccgctcg tttgccatat tcacagtttt tgtattggct ggcggattgc	120
tatattttatt gacttgcaaa cgcaaaaaat cttaggatat tcgagtgggtt gggcgggaaa	180
gccagccgt tttttatgct gactcgattt tctgaaacat aatgaaaaga aaatcgtatt	240
tgatgtaaag cttcttgaga ggatgaaaat gat gaa aag aag cat cgg cac ctt	294
Asp Glu Lys Lys His Arg His Leu	
1 5	
tta aat tta cgg act gac aat tta ata ttc gcg agt agg tta agg gaa	342
Leu Asn Leu Arg Thr Asp Asn Leu Ile Phe Ala Ser Arg Leu Arg Glu	
10 15 20	
gcc gat tct tgt gat gca cgg agg tca ttc gaa ttg ccg cga gga att	390
Ala Asp Ser Cys Asp Ala Arg Arg Ser Phe Glu Leu Pro Arg Gly Ile	
25 30 35 40	
tggtgtatcgc agatcttata ttgagccg attcttcatt caccgccctt	438
Trp Val Ser Arg Ser Leu Leu Glu Pro Ile Leu Tyr His His Ala Phe	
45 50 55	
ccgtgcagggtatgtggccgacatcgaaagaaatcggggacagtttgga	486
Pro Cys Arg Val Trp Pro Asp Ile Glu Arg Asn Arg Gly Gln Phe Gly	
60 65 70	
acttgcctgctattatcatatgaaa ctgcttgatcat ttaaatatcaag	534
Thr Cys Leu Leu Leu His Met Lys Leu Leu Asp His Leu Asn Ile Lys	
75 80 85	
aaagttcatgtgggttgcggtgtcatgccggcgggccaagcggaatatgt	582
Lys Val His Val Val Ala Val Ser Ala Gly Gly Pro Ser Gly Ile Cys	
90 95 100	
tttgcatccaaatactctggaaagatgaa tcc ttaattttgcaaagc	630
Phe Ala Ser Lys Tyr Ser Glu Arg Val Glu Ser Leu Ile Leu Gln Ser	
105 110 115 120	
gctgtcacaagcagtggtctgacagcgagagatattgaaatataaagt	678
Ala Val Thr Lys Gln Trp Leu Thr Ala Lys Asp Ile Glu Tyr Lys Val	
125 130 135	
ggtcagatc atctttcggccgcctgttgaaaggccgtatggaaagctg	726
Gly Gln Ile Ile Phe Arg Pro Pro Val Glu Lys Ala Val Trp Lys Leu	
140 145 150	
atatcggcgcttaacaaatcgat tttccggaa tggatc ttt aagaaaatg	774
Ile Ser Ala Leu Asn Asn Arg Phe Pro Glu Trp Ile Phe Lys Lys Met	
155 160 165	
ctatccctctttactacacttctgctgatcaggcg atgctgaaa gtc	822

Leu Ser Ser Phe Thr Thr Leu Pro Ala Asp Gln Ala Met Leu Lys Val	
170 175 180	
acg gag gga gat att gaa gaa atg aga aaa atg aac aac aga cag cgt	870
Thr Glu Gly Asp Ile Glu Glu Met Arg Lys Met Asn Asn Arg Gln Arg	
185 190 195 200	
tca agt cga ggg ttc ttg ctt gat tta aaa aat ata gac gat tta tct	918
Ser Ser Arg Gly Phe Leu Leu Asp Leu Lys Asn Ile Asp Asp Leu Ser	
205 210 215	
ttc cat cat ttg aag gag att tct tgt ccg gta tta att atg cat tgc	966
Phe His His Leu Lys Glu Ile Ser Cys Pro Val Leu Ile Met His Cys	
220 225 230	
cga tat gat cgt gtt gtt cca gcc gag cat gct ttt cat gca aaa aaa	1014
Arg Tyr Asp Arg Val Val Pro Ala Glu His Ala Phe His Ala Lys Lys	
235 240 245	
ctg att cct ttt tca gaa gtc tat cag gca gac agc tgg ggt cat ctc	1062
Leu Ile Pro Phe Ser Glu Val Tyr Gln Ala Asp Ser Trp Gly His Leu	
250 255 260	
att tgg ctg gga aca gag ggt aaa tct gtc tca cag aag gtc atc agc	1110
Ile Trp Leu Gly Thr Glu Gly Lys Ser Val Ser Gln Lys Val Ile Ser	
265 270 275 280	
ttt tta aaa acc acatcatctt gatcataaga tgaataaaaat tttaggatcg	1162
Phe Leu Lys Thr	
cagcctaccc gcaaatagaag tagtgcaatt ttttaatacaa gagcagaatg atctttccga	1222
acagaactga tgaacgtcgt acaagacttg caaataagat gaatgagaaa tcctccctgg	1282
ccggttttcg gagcacaagg gaaacttatg tataagaatc tattccgata gagggacagg	1342
tacgggatga atcattgatt accgttgctt gcgatttccc aggggggaga gagttggtaa	1402
acttgatatc atccgcgggt ttgctttgct tggcattctt ttagcccata gggaagtcgt	1462
ctttggctgt ggatatttca atttgggcct gctgaatgga tatggcgag tttggcttgc	1522
ggcaagcggc agcttcttcc taaactcgcg attgaaacga tgcggctatg caatatggtg	1582
aaacgttgca tgaaaaactt aacattttaa aaatccagc	1621

<210> 72  
 <211> 284  
 <212> PRT  
 <213> Bacillus licheniformis  
  
 <400> 72

Asp Glu Lys Lys His Arg His Leu Leu Asn Leu Arg Thr Asp Asn Leu
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Ile Phe Ala Ser Arg Leu Arg Glu Ala Asp Ser Cys Asp Ala Arg Arg  
 20 25 30

Ser Phe Glu Leu Pro Arg Gly Ile Trp Val Ser Arg Ser Leu Leu Glu  
 35 40 45

Pro Ile Leu Tyr His His Ala Phe Pro Cys Arg Val Trp Pro Asp Ile  
 50 55 60

Glu Arg Asn Arg Gly Gln Phe Gly Thr Cys Leu Leu Leu His Met Lys  
 65 70 75 80

Leu Leu Asp His Leu Asn Ile Lys Lys Val His Val Val Ala Val Ser  
 85 90 95

Ala Gly Gly Pro Ser Gly Ile Cys Phe Ala Ser Lys Tyr Ser Glu Arg  
 100 105 110

Val Glu Ser Leu Ile Leu Gln Ser Ala Val Thr Lys Gln Trp Leu Thr  
 115 120 125

Ala Lys Asp Ile Glu Tyr Lys Val Gly Gln Ile Ile Phe Arg Pro Pro  
 130 135 140

Val Glu Lys Ala Val Trp Lys Leu Ile Ser Ala Leu Asn Asn Arg Phe  
 145 150 155 160

Pro Glu Trp Ile Phe Lys Lys Met Leu Ser Ser Phe Thr Thr Leu Pro  
 165 170 175

Ala Asp Gln Ala Met Leu Lys Val Thr Glu Gly Asp Ile Glu Glu Met  
 180 185 190

Arg Lys Met Asn Asn Arg Gln Arg Ser Ser Arg Gly Phe Leu Leu Asp  
 195 200 205

Leu Lys Asn Ile Asp Asp Leu Ser Phe His His Leu Lys Glu Ile Ser  
 210 215 220

Cys Pro Val Leu Ile Met His Cys Arg Tyr Asp Arg Val Val Pro Ala  
 225 230 235 240

Glu His Ala Phe His Ala Lys Lys Leu Ile Pro Phe Ser Glu Val Tyr  
245 250 255

Gln Ala Asp Ser Trp Gly His Leu Ile Trp Leu Gly Thr Glu Gly Lys  
260 265 270

Ser Val Ser Gln Lys Val Ile Ser Phe Leu Lys Thr  
275 280

<210> 73  
<211> 1630  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (256)..(1131)

<400> 73  
cgctgttcac ccatttggtt tgttctcag cctcttgggc gctcgacat ccggcgagcc 60  
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tttttgcca ttatatgaat tcggccagcg ttgaatattt cctcttttca gggaaatttc 180  
cgaagcggcg attcaaaaat ccgcaaactt atcttacaat agaaaaagtt ctgaatgatc 240  
gagtagggag agatc gtt agt atg aaa gta tcg gtt ctg ttt gtc ttg ctt 291  
Val Ser Met Lys Val Ser Val Leu Phe Val Leu Leu  
1 5 10  
gcg gca att tta tgg gga acg acg gga aca acc cag gca ttt gcg ccg 339  
Ala Ala Ile Leu Trp Gly Thr Thr Gly Thr Thr Gln Ala Phe Ala Pro  
15 20 25  
aaa gag gcg gca cct ctt gtg ttc ggc gct gtc aga atg gct gtc ggc 387  
Lys Glu Ala Ala Pro Leu Val Phe Gly Ala Val Arg Met Ala Val Gly  
30 35 40  
ggc atc acc ctg ctc ttg ttc gcg gct ttc cgc ggt caa ttg aaa cga 435  
Gly Ile Thr Leu Leu Leu Phe Ala Ala Phe Arg Gly Gln Leu Lys Arg  
45 50 55 60  
agc ggc tgg ccc gtt aaa acg ctg atc atc gca gca ttg agc atg gca 483  
Ser Gly Trp Pro Val Lys Thr Leu Ile Ile Ala Ala Leu Ser Met Ala  
65 70 75  
ttt tac cag cct ttc ttt ttt tca gcc gtc agc ctg tca gga atc gcc 531  
Phe Tyr Gln Pro Phe Phe Phe Ser Ala Val Ser Leu Ser Gly Ile Ala  
80 85 90  
gtc gga acg gtc gtc gcc atc ggc agc gct ccg att att gcc ggc tgc 579

Val Gly Thr Val Val Ala Ile Gly Ser Ala Pro Ile Ile Ala Gly Cys	
95 100 105	
ctc gaa tgg ctg gtg ttc aaa aag gtt ccg cag acg aaa tgg tgg atc	627
Leu Glu Trp Leu Val Phe Lys Lys Val Pro Gln Thr Lys Trp Trp Ile	
110 115 120	
gca act gct gca gcg ata gca ggc gta gcc tta tta ttc att ccc tcc	675
Ala Thr Ala Ala Ala Ile Ala Gly Val Ala Leu Phe Ile Pro Ser	
125 130 135 140	
gcc tca tcg ggg ggg agc ttt ctc ggc ata ctg ctc gca ctt ggc gcc	723
Ala Ser Ser Gly Gly Ser Phe Leu Gly Ile Leu Leu Ala Leu Gly Ala	
145 150 155	
ggc ctt tcc ttt gcc gtc tac acg ctg aca agc aag aaa ctc ctg caa	771
Gly Leu Ser Phe Ala Val Tyr Thr Leu Thr Ser Lys Lys Leu Leu Gln	
160 165 170	
aag caa aag ccg gag gct gtc aca ggc acc gta ttc ttt tta agc gct	819
Lys Gln Lys Pro Glu Ala Val Thr Gly Thr Val Phe Phe Leu Ser Ala	
175 180 185	
gta ttg ctt gcc ccg ttg ttg ttt ctg tac gat ctc ggc tgg atc tca	867
Val Leu Leu Ala Pro Leu Leu Phe Leu Tyr Asp Leu Gly Trp Ile Ser	
190 195 200	
tcg gtt cag gga atg gct gtc agc ctc tat atc ggg gtc att gca acc	915
Ser Val Gln Gly Met Ala Val Ser Leu Tyr Ile Gly Val Ile Ala Thr	
205 210 215 220	
gga gcc gcg tac ctg tta ttt acg aca gga ttg gca aaa gtg ccc gcc	963
Gly Ala Ala Tyr Leu Leu Phe Thr Thr Gly Leu Ala Lys Val Pro Ala	
225 230 235	
tca acg gcg gtg acg ctg tcg ctt gct gaa ccg ctt aca gcg tcg ctg	1011
Ser Thr Ala Val Thr Leu Ser Leu Ala Glu Pro Leu Thr Ala Ser Leu	
240 245 250	
ttg gga acc gtg ctt gtc agg gaa tcg ctg cct ctt gtt tcc tgg gcc	1059
Leu Gly Thr Val Leu Val Arg Glu Ser Leu Pro Leu Val Ser Trp Ala	
255 260 265	
ggg atc gcc ctg ctt ctt tta ggc att ttt tat att tcc tat cag ccc	1107
Gly Ile Ala Leu Leu Leu Leu Gly Ile Phe Tyr Ile Ser Tyr Gln Pro	
270 275 280	
aaa aag gat aaa ata aac gct gaa cagatgaaag cgtaaaaaaa acccgcccgg	1161
Lys Lys Asp Lys Ile Asn Ala Glu	
285 290	
ggatatacgg gcgggttttc atgttgctctt gttattcatc caaacccgatg gacaaatatt	1221
ttgttttccaa atacggctcg atgccttcca gtccgctttc gcgtccgata ccgctttcct	1281
tcatgccgcc gaaaggcgcc tgaacggttg acggtccgcc gtcattccag ccgagaatgc	1341

cgtaatcaag gttttcggat aaatagatgc cgcggcggta gttttccgta aagaagtatg 1401  
 ccgctaaacc gtaaggcgta tcattggcga gcttgaccgc ttcgtccagc gttttaaaag 1461  
 acgtaatcgg cgcaacgggg ccgaatgttt cctcatgcat gatcgtcatt gaaggatcaa 1521  
 catccgtcag cactgtcgga tggacaaagt agcatgattt ctcacatcgc ctttcatatt 1581  
 cggcgcgat gagaactttc gcccctttat tcaccgcgtc attgatttg 1630

<210> 74  
 <211> 292  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 74

Val Ser Met Lys Val Ser Val Leu Phe Val Leu Leu Ala Ala Ile Leu  
 1 5 10 15

Trp Gly Thr Thr Gly Thr Thr Gln Ala Phe Ala Pro Lys Glu Ala Ala  
 20 25 30

Pro Leu Val Phe Gly Ala Val Arg Met Ala Val Gly Gly Ile Thr Leu  
 35 40 45

Leu Leu Phe Ala Ala Phe Arg Gly Gln Leu Lys Arg Ser Gly Trp Pro  
 50 55 60

Val Lys Thr Leu Ile Ile Ala Ala Leu Ser Met Ala Phe Tyr Gln Pro  
 65 70 75 80

Phe Phe Phe Ser Ala Val Ser Leu Ser Gly Ile Ala Val Gly Thr Val  
 85 90 95

Val Ala Ile Gly Ser Ala Pro Ile Ile Ala Gly Cys Leu Glu Trp Leu  
 100 105 110

Val Phe Lys Lys Val Pro Gln Thr Lys Trp Trp Ile Ala Thr Ala Ala  
 115 120 125

Ala Ile Ala Gly Val Ala Leu Leu Phe Ile Pro Ser Ala Ser Ser Gly  
 130 135 140

Gly Ser Phe Leu Gly Ile Leu Leu Ala Leu Gly Ala Gly Leu Ser Phe  
 145 150 155 160

Ala Val Tyr Thr Leu Thr Ser Lys Lys Leu Leu Gln Lys Gln Lys Pro  
165 170 175

Glu Ala Val Thr Gly Thr Val Phe Phe Leu Ser Ala Val Leu Leu Ala  
180 185 190

Pro Leu Leu Phe Leu Tyr Asp Leu Gly Trp Ile Ser Ser Val Gln Gly  
195 200 205

Met Ala Val Ser Leu Tyr Ile Gly Val Ile Ala Thr Gly Ala Ala Tyr  
210 215 220

Leu Leu Phe Thr Thr Gly Leu Ala Lys Val Pro Ala Ser Thr Ala Val  
225 230 235 240

Thr Leu Ser Leu Ala Glu Pro Leu Thr Ala Ser Leu Leu Gly Thr Val  
245 250 255

Leu Val Arg Glu Ser Leu Pro Leu Val Ser Trp Ala Gly Ile Ala Leu  
260 265 270

Leu Leu Leu Gly Ile Phe Tyr Ile Ser Tyr Gln Pro Lys Lys Asp Lys  
275 280 285

Ile Asn Ala Glu  
290

<210> 75  
<211> 2140  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501) .. (1637)

<400> 75  
agctgccggg gcaaataagag cgcgctggct tgcagataat gctgctggaa gagatactat 60  
gaatacaagt gattathtag attttaatga agaaaacaaa aacaatgata atggaaaaga 120  
ttacagtaat gcctacactg atatggactg tgaggcgatg actgaagata ttaatcattt 180  
gaaatctgcc aatcctgagg tgtatcaaaa gctgcagaag atggacatta ccgctgcggc 240  
gggatacaga acagaggata ctgtaagttt ttccccttac tataaccgcaa gcggaaaaca 300

taaaataaac agtgatgata tcgtttcggg cgaaagtcaa cacggtgaca tattaggcga	360
tctcattgat aaaaagccag aaattgaagt aagaggttcc ggtgtaacca atcctggaca	420
tatttatgaa attgaagact ctgaatttgt tgacttgatt cgagaggtca acaaaaaaga	480
agcagaatag gagaagggtcg atg aaa aag aaa ggg ttt ata agt ata ttt ttt	533
Met Lys Lys Lys Gly Phe Ile Ser Ile Phe Phe	
1 5 10	
tta ata gtg ttt cta ctg ctc gcc acc acc ggc tgc ggc aaa gat gat	581
Leu Ile Val Phe Leu Leu Leu Ala Thr Thr Gly Cys Gly Lys Asp Asp	
15 20 25	
gtt cag gaa gcc atc tat aaa aaa ggc ttg ccc aaa gaa gac agt cca	629
Val Gln Glu Ala Ile Tyr Lys Lys Gly Leu Pro Lys Glu Asp Ser Pro	
30 35 40	
gca ttt aga gaa ttt atg aga cat gaa ctt gat tta gcg aca gac gca	677
Ala Phe Arg Glu Phe Met Arg His Glu Leu Asp Leu Ala Thr Asp Ala	
45 50 55	
act ctt agt tat caa aat agt aca tat acg att atg cgc agt gat aaa	725
Thr Leu Ser Tyr Gln Asn Ser Thr Tyr Thr Ile Met Arg Ser Asp Lys	
60 65 70 75	
aag ggg cta cgg tac tat caa tat aca gat caa gaa gta gac gat ttt	773
Lys Gly Leu Arg Tyr Tyr Gln Tyr Thr Asp Gln Glu Val Asp Asp Phe	
80 85 90	
tac agt ccc ttt ctt tcg gct aat aaa tat cct gcg aca aaa tta tat	821
Tyr Ser Pro Phe Leu Ser Ala Asn Lys Tyr Pro Ala Thr Lys Leu Tyr	
95 100 105	
gat ttg aaa aca act gaa ttt tta act aaa gaa aaa ctt atc cac aat	869
Asp Leu Lys Thr Thr Glu Phe Leu Thr Lys Glu Lys Leu Ile His Asn	
110 115 120	
aaa ctt gaa tat aat ctg ccg gaa atg aca tta gat aaa aag aat gtt	917
Lys Leu Glu Tyr Asn Leu Pro Glu Met Thr Leu Asp Lys Lys Asn Val	
125 130 135	
cta aaa gtg aaa aca aaa agc gga gaa aaa aaa ata gag ttt cca tca	965
Leu Lys Val Lys Thr Lys Ser Gly Glu Lys Lys Ile Glu Phe Pro Ser	
140 145 150 155	
gcc aag gat aaa aaa gta cat ctg gcg tta gca gct gtt agc aaa gac	1013
Ala Lys Asp Lys Lys Val His Leu Ala Leu Ala Ala Val Ser Lys Asp	
160 165 170	
agc atg ctt ata caa gtg gac gta tat gaa aaa ttt aaa aat ggt gac	1061
Ser Met Leu Ile Gln Val Asp Val Tyr Glu Lys Phe Lys Asn Gly Asp	
175 180 185	
ctt gga gac aga caa ata tat tat ctt ttt tta aaa agt gat ctt tca	1109
Leu Gly Asp Arg Gln Ile Tyr Tyr Leu Phe Leu Lys Ser Asp Leu Ser	



190	195	200	
aaa tac cgg att gtt aaa gaa gag gaa tta aat tca aca att gag tct			1157
Lys Tyr Arg Ile Val Lys Glu Glu Glu Leu Asn Ser Thr Ile Glu Ser			
205	210	215	
ggg aaa ctg aag gaa tac tta tcc gta ttt cca aat gta gcg aag gat			1205
Gly Lys Leu Lys Glu Tyr Leu Ser Val Phe Pro Asn Val Ala Lys Asp			
220	225	230	235
gga gca tat cgt aag tta ttt gat aaa tac att ttt gat gaa aag aaa			1253
Gly Ala Tyr Arg Lys Leu Phe Asp Lys Tyr Ile Phe Asp Glu Lys Lys			
240	245	250	
aac aaa gtt agg aaa atc aaa aac act gat att ctg agc aaa gac ggt			1301
Asn Lys Val Arg Lys Ile Lys Asn Thr Asp Ile Leu Ser Lys Asp Gly			
255	260	265	
aag tat gtt tat att aac gga gca aaa gaa aaa gaa aca aat gta atg			1349
Lys Tyr Val Tyr Ile Asn Gly Ala Lys Glu Lys Glu Thr Asn Val Met			
270	275	280	
cct gat ggt atc caa cag ata caa aca atg gat aat tat cta aaa gga			1397
Pro Asp Gly Ile Gln Gln Ile Gln Thr Met Asp Asn Tyr Leu Lys Gly			
285	290	295	
aat gaa aaa tat gaa gct caa ttt aag att gat ttc aaa caa att gca			1445
Asn Glu Lys Tyr Glu Ala Gln Phe Lys Ile Asp Phe Lys Gln Ile Ala			
300	305	310	315
aaa gag atg gat tta aac gcg ggt gat gcg agg ata gct aat att cat			1493
Lys Glu Met Asp Leu Asn Ala Gly Asp Ala Arg Ile Ala Asn Ile His			
320	325	330	
tat ttt aat aaa gat tat gta gtt ttg tat att tct tat cat ggg aag			1541
Tyr Phe Asn Lys Asp Tyr Val Val Leu Tyr Ile Ser Tyr His Gly Lys			
335	340	345	
aca att ggt aca gca ggt tct gtt aat gta ctt att gat tta caa aaa			1589
Thr Ile Gly Thr Ala Gly Ser Val Asn Val Leu Ile Asp Leu Gln Lys			
350	355	360	
aac aaa caa cag cca acg gct tat tta gtt gat tta gga att gaa tca			1637
Asn Lys Gln Gln Pro Thr Ala Tyr Leu Val Asp Leu Gly Ile Glu Ser			
365	370	375	
tagagggact gaagagtttt tatgcagtcc ttttcttatt tgacaaaggt aggccacaaa			1697
attgggacaa gccttctgct tcctacttcc ttatccaatt taagagaagt tcttgcagaa			1757
agcgtacaat gacgaaagaa tgcagcagcg tttggaacac tcgttaatgc tcgtttcgga			1817
agcggacgga aaaatcgctcg gctttgccaa ctactccttt gtcagagaag gaggggtagc			1877
ctatctcgca gccgtttatt tagctccgga ataccagggg aaaggcatcg gaaccgcatt			1937
attggaagag gggatgaacc atttaaaggg agtgaaaaag atctttgtag aggttgaaaa			1997

agaaaaccgc accggaaaaa actttttacaa ggccaagggt ttgaggatg tcgccgaata 2057  
 tgatgaagat ttcgaagggc atatcctcaa aacagtcaga atggccttgc acgtataatc 2117  
 ccgctttcac ttcgtaactt gga 2140

<210> 76  
 <211> 379  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 76

Met Lys Lys Lys Gly Phe Ile Ser Ile Phe Phe Leu Ile Val Phe Leu  
 1 5 10 15

Leu Leu Ala Thr Thr Gly Cys Gly Lys Asp Asp Val Gln Glu Ala Ile  
 20 25 30

Tyr Lys Lys Gly Leu Pro Lys Glu Asp Ser Pro Ala Phe Arg Glu Phe  
 35 40 45

Met Arg His Glu Leu Asp Leu Ala Thr Asp Ala Thr Leu Ser Tyr Gln  
 50 55 60

Asn Ser Thr Tyr Thr Ile Met Arg Ser Asp Lys Lys Gly Leu Arg Tyr  
 65 70 75 80

Tyr Gln Tyr Thr Asp Gln Glu Val Asp Asp Phe Tyr Ser Pro Phe Leu  
 85 90 95

Ser Ala Asn Lys Tyr Pro Ala Thr Lys Leu Tyr Asp Leu Lys Thr Thr  
 100 105 110

Glu Phe Leu Thr Lys Glu Lys Leu Ile His Asn Lys Leu Glu Tyr Asn  
 115 120 125

Leu Pro Glu Met Thr Leu Asp Lys Lys Asn Val Leu Lys Val Lys Thr  
 130 135 140

Lys Ser Gly Glu Lys Lys Ile Glu Phe Pro Ser Ala Lys Asp Lys Lys  
 145 150 155 160

Val His Leu Ala Leu Ala Ala Val Ser Lys Asp Ser Met Leu Ile Gln  
 165 170 175

Val Asp Val Tyr Glu Lys Phe Lys Asn Gly Asp Leu Gly Asp Arg Gln  
 180 185 190

Ile Tyr Tyr Leu Phe Leu Lys Ser Asp Leu Ser Lys Tyr Arg Ile Val  
 195 200 205

Lys Glu Glu Glu Leu Asn Ser Thr Ile Glu Ser Gly Lys Leu Lys Glu  
 210 215 220

Tyr Leu Ser Val Phe Pro Asn Val Ala Lys Asp Gly Ala Tyr Arg Lys  
 225 230 235 240

Leu Phe Asp Lys Tyr Ile Phe Asp Glu Lys Lys Asn Lys Val Arg Lys  
 245 250 255

Ile Lys Asn Thr Asp Ile Leu Ser Lys Asp Gly Lys Tyr Val Tyr Ile  
 260 265 270

Asn Gly Ala Lys Glu Lys Glu Thr Asn Val Met Pro Asp Gly Ile Gln  
 275 280 285

Gln Ile Gln Thr Met Asp Asn Tyr Leu Lys Gly Asn Glu Lys Tyr Glu  
 290 295 300

Ala Gln Phe Lys Ile Asp Phe Lys Gln Ile Ala Lys Glu Met Asp Leu  
 305 310 315 320

Asn Ala Gly Asp Ala Arg Ile Ala Asn Ile His Tyr Phe Asn Lys Asp  
 325 330 335

Tyr Val Val Leu Tyr Ile Ser Tyr His Gly Lys Thr Ile Gly Thr Ala  
 340 345 350

Gly Ser Val Asn Val Leu Ile Asp Leu Gln Lys Asn Lys Gln Gln Pro  
 355 360 365

Thr Ala Tyr Leu Val Asp Leu Gly Ile Glu Ser  
 370 375

<210> 77  
 <211> 1387  
 <212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(884)

<400> 77

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gttcaaggag tacgagtgac gaacccgtag ttaggaggaa aacaagagtg tctatacgaa 120

atctggatgg aaaagctttt gcagatatga ttctgtacgg cgcacacccat ctgtctcaaa 180

acgcaaattgt agttgatgcg ttaaacgtat ttccggttcc ggacggagat acgggaacga 240

acactaatct gtcgatgaca tccggtgcga aagaagtgga gcaaatcgac accgccaata 300

tcggcaaagt ggcacaaagc ctgtcaaggg ggcttctgat gggggcgcgg ggaaactcgg 360

gcgtcatttt atcccagctg ttcagaggct ttggcaaadc gattgaacag aaatcggaag 420

ttaacgcgaa agaatttgcc gccgcgttcc aggcggaggt ggacaccgcc tacaaggccg 480

tcataaaciaa gcttctacag atg tct acc agc agc att gtc gtt ctc ttg att 533  
Met Ser Thr Ser Ser Ile Val Val Leu Leu Ile  
1 5 10

tgc gcc gcg ctc atc atc tac gcg gtc gct tca tac atc tat cag cag 581  
Cys Ala Ala Leu Ile Ile Tyr Ala Val Ala Ser Tyr Ile Tyr Gln Gln  
15 20 25

cgc att atg aaa acc ttg aca gaa gaa gaa ttc cgg gca ggc tat cgc 629  
Arg Ile Met Lys Thr Leu Thr Glu Glu Glu Phe Arg Ala Gly Tyr Arg  
30 35 40

aaa gcg cag ctc atc gat gtg cgc gag ccg aat gag tat gaa ggc ggc 677  
Lys Ala Gln Leu Ile Asp Val Arg Glu Pro Asn Glu Tyr Glu Gly Gly  
45 50 55

cac att ttg ggt gcg aga aac att ccg ctt tca cag ctt aag caa aga 725  
His Ile Leu Gly Ala Arg Asn Ile Pro Leu Ser Gln Leu Lys Gln Arg  
60 65 70 75

aaa agc gaa atc cgg cct gac aaa ccg gtt tac ctg tac tgc caa aac 773  
Lys Ser Glu Ile Arg Pro Asp Lys Pro Val Tyr Leu Tyr Cys Gln Asn  
80 85 90

aac gtc aga agc gga agg gcc gcc caa acg ctc cgc aaa cac ggc tgt 821  
Asn Val Arg Ser Gly Arg Ala Ala Gln Thr Leu Arg Lys His Gly Cys  
95 100 105

aag gag att tac aac ctg aaa ggc ggg ttc aaa aaa tgg ggc gga aaa 869  
Lys Glu Ile Tyr Asn Leu Lys Gly Gly Phe Lys Lys Trp Gly Gly Lys  
110 115 120

att aaa acg aaa aat taataaccga agctgtctct gctatggaag gcttcagttg 924

Ile Lys Thr Lys Asn  
125

agtcacgcat cctaaagcgg tttaacgttt taggatgttt tttttgcatc cgggaggatt 984  
cggtgatga gcggttatcc ctttcggca aaaataagcc ggcgagatgg gtccgccggc 1044  
tttggtcggtt attttttcaa gtcttcgatt gaattgacat ctttcatata tgcggaacg 1104  
acaaggccaa tttttacgcc tgcacgcta gtaccgatat cttcgtatct gcctttgtat 1164  
ttttcagcat atgttttatt gcgttgccggc agccatgcag caagtgaagc atcgacgctt 1224  
ccattttgca tgccagggtca catcgggcct gcttctactt gggctgagcg tacgggtgtat 1284  
ccctagtctt caagaacttt gcgatgacat tcgtgctcgc attttcgctg tcccatgccca 1344  
catagccgag ctttaattttt tcaccgtccg cttatcgacg ccc 1387

<210> 78  
<211> 128  
<212> PRT  
<213> Bacillus licheniformis

<400> 78

Met Ser Thr Ser Ser Ile Val Val Leu Leu Ile Cys Ala Ala Leu Ile  
1 5 10 15

Ile Tyr Ala Val Ala Ser Tyr Ile Tyr Gln Gln Arg Ile Met Lys Thr  
20 25 30

Leu Thr Glu Glu Glu Phe Arg Ala Gly Tyr Arg Lys Ala Gln Leu Ile  
35 40 45

Asp Val Arg Glu Pro Asn Glu Tyr Glu Gly Gly His Ile Leu Gly Ala  
50 55 60

Arg Asn Ile Pro Leu Ser Gln Leu Lys Gln Arg Lys Ser Glu Ile Arg  
65 70 75 80

Pro Asp Lys Pro Val Tyr Leu Tyr Cys Gln Asn Asn Val Arg Ser Gly  
85 90 95

Arg Ala Ala Gln Thr Leu Arg Lys His Gly Cys Lys Glu Ile Tyr Asn  
100 105 110

Leu Lys Gly Gly Phe Lys Lys Trp Gly Gly Lys Ile Lys Thr Lys Asn  
115 120 125

<210> 79  
 <211> 1486  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(983)

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<400> 79
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cgaacctctt cctacggcac ggtgtttatg aaggctctgc cccctgcaaa agtcatggag 120
cctactttcc ttgagcttga agcctacata gccgggaaaa acggctaaaa gccgcataaa 180
gcggctctta aatggtgtgg attaaggttt ttttttttag gctgtttatt taaacggata 240
tcccgttgta acaactagta tggcttttgc taaaagagt atgaattaca attattgttt 300
cgttcggagg tatttgaaaa atggaaaaca aaatcgaaat tctatctact gtaagcgctcg 360
agcactcaga agacctgtat aaaatcgttg atcttttgaa ccgtacgctc aaacgcgatg 420
atctcatggt cggcctcgct ctcgatgaag aagacaaaaa acaggccatt tttacgattt 480
atcgtactta ggagcagaaa atg ggc aaa aca tta att ttc ata ctg ata 533
          Met Gly Lys Lys Thr Leu Ile Phe Ile Leu Ile
          1              5              10

ttt ggt att atc ttt tta aca gca ctt ctt gcg gga gcg aat gtc tac 581
Phe Gly Ile Ile Phe Leu Thr Ala Leu Leu Ala Gly Ala Asn Val Tyr
          15              20              25

cgt acg gca atg gat cag aaa gaa aac ggc cac gag cag gct gcc gaa 629
Arg Thr Ala Met Asp Gln Lys Glu Asn Gly His Glu Gln Ala Ala Glu
          30              35              40

aca gcc agg cag gaa gcc ggc tta aaa caa gtt gac agc gtg gag acg 677
Thr Ala Arg Gln Glu Ala Gly Leu Lys Gln Val Asp Ser Val Glu Thr
          45              50              55

ttt gtc ggt aaa gaa aag cag tac att gtt aca ggg gca gac aaa aaa 725
Phe Val Gly Lys Glu Lys Gln Tyr Ile Val Thr Gly Ala Asp Lys Lys
60              65              70              75

ggc gac aaa atg tat gtt tgg gtg cct gct gac aaa aag cag aaa acg 773
Gly Asp Lys Met Tyr Val Trp Val Pro Ala Asp Lys Lys Gln Lys Thr
          80              85              90

ctt tac aaa aaa gca tca gcc ggc att acc ggc cgc cag gct gca aaa 821
Leu Tyr Lys Lys Ala Ser Ala Gly Ile Thr Gly Arg Gln Ala Ala Lys
          95              100             105

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gct gtt cag gat gag ggc ctg atg tct gag ctt aaa gag gtg cac ctt 869  
 Ala Val Gln Asp Glu Gly Leu Met Ser Glu Leu Lys Glu Val His Leu  
 110 115 120

gca agg gaa ggc aat gtt cta ttg tgg gaa gtt aca tac tta aat aaa 917  
 Ala Arg Glu Gly Asn Val Leu Leu Trp Glu Val Thr Tyr Leu Asn Lys  
 125 130 135

gat ggg cag tac agt tta agc tat gtg gac ttt ata aac gga aaa att 965  
 Asp Gly Gln Tyr Ser Leu Ser Tyr Val Asp Phe Ile Asn Gly Lys Ile  
 140 145 150 155

cac aaa aat att acg cct tagacgaaac aggggggaaat cgagttgaat 1013  
 His Lys Asn Ile Thr Pro  
 160

ctagctaaaa gagtatcagc gttaacacca tctgcaacat tggcaatcac tgcaaaagca 1073

aaagaattaa aagcggcagg gcacgacgtc atcgggtcttg gggcaggtga gccggatttt 1133

aatacgccctg agcacatcat tgaagcggct gtccgttcga tgaacgaagg acataccaaa 1193

tacacgcctt ccggcgggtct tgcggcgctg aaagacagca tccgcgataa attcaagcgc 1253

gatcaggggaa ttgaatacag ccaatcggaa gttattgtgt gcacaggtgc aaagcatgct 1313

ctttacaccc tatttcaagt gtcctcgcac gaaggggacg aagtgattat tccgactccg 1373

tactgggtca gctatcctga acaagtcaag cttgcaggcg gcaaacctgt gtttgtggaa 1433

ggccttgagg aaaacagctt caagatttct ccggagcagc tcgaaaaagc cgt 1486

<210> 80  
 <211> 161  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 80

Met Gly Lys Lys Thr Leu Ile Phe Ile Leu Ile Phe Gly Ile Ile Phe  
 1 5 10 15

Leu Thr Ala Leu Leu Ala Gly Ala Asn Val Tyr Arg Thr Ala Met Asp  
 20 25 30

Gln Lys Glu Asn Gly His Glu Gln Ala Ala Glu Thr Ala Arg Gln Glu  
 35 40 45

Ala Gly Leu Lys Gln Val Asp Ser Val Glu Thr Phe Val Gly Lys Glu  
 50 55 60

Lys Gln Tyr Ile Val Thr Gly Ala Asp Lys Lys Gly Asp Lys Met Tyr

65

70

75

80

Val Trp Val Pro Ala Asp Lys Lys Gln Lys Thr Leu Tyr Lys Lys Ala  
85 90 95

Ser Ala Gly Ile Thr Gly Arg Gln Ala Ala Lys Ala Val Gln Asp Glu  
100 105 110

Gly Leu Met Ser Glu Leu Lys Glu Val His Leu Ala Arg Glu Gly Asn  
115 120 125

Val Leu Leu Trp Glu Val Thr Tyr Leu Asn Lys Asp Gly Gln Tyr Ser  
130 135 140

Leu Ser Tyr Val Asp Phe Ile Asn Gly Lys Ile His Lys Asn Ile Thr  
145 150 155 160

Pro

<210> 81  
<211> 1993  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(1490)

<400> 81  
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gagatttttc tgccggggcgg aatagcaggg attgccggcc tgatcgcaat tgttgcgagc 120  
ctcttttttag cttcgggaag ctttaagggtc atggccgtct ccattttgat tgcaactgct 180  
gtttcgatag cggcattccat tctattgaca aggggtgttg gtaagcgtat gaaatttttt 240  
aaaaaattga tcttaaccga ctcgacaagc acagaaagcg gatacgtgtc aaatgaaagc 300  
cggcgcgatt taattggcaa aatcggcgtc acgtatacac cgctcagacc gtccggaacg 360  
gtcatcatcg acgatgaacg gcttgatggt gtatctgaag gctcgttcac cgcaaaggat 420  
aagaaagtga aagtgggtaa agtggaaagg tcacgcattg ttgtgagaga attataaatt 480  
acatttttag gaggaatata atg gat ccg tca aca ctg ttt ctt tta ctt att 533  
Met Asp Pro Ser Thr Leu Phe Leu Leu Leu Ile  
1 5 10



atc gca gcc gga atc atc cta cta gct gtc ttc ttt aca ttc gtc ccg	581
Ile Ala Ala Gly Ile Ile Leu Leu Ala Val Phe Phe Thr Phe Val Pro	
15 20 25	
gtc atg ctg tgg atc tcg gct ttg gcc gct ggt gtt aaa atc agc att	629
Val Met Leu Trp Ile Ser Ala Leu Ala Ala Gly Val Lys Ile Ser Ile	
30 35 40	
ttc aca ctg atc gga atg agg ctc cgc cgc gtc att cca aac cgc gtg	677
Phe Thr Leu Ile Gly Met Arg Leu Arg Arg Val Ile Pro Asn Arg Val	
45 50 55	
gtg aac ccg ctc atc aaa gcg cac aaa gcg gga ctt gat gtt gcc atc	725
Val Asn Pro Leu Ile Lys Ala His Lys Ala Gly Leu Asp Val Ala Ile	
60 65 70 75	
aat cag ctg gaa agc cac tat ctt gca ggg ggt aat gtt gac cgg gtc	773
Asn Gln Leu Glu Ser His Tyr Leu Ala Gly Gly Asn Val Asp Arg Val	
80 85 90	
gtc aac gcg ctt atc gct gcc caa cgt gca aac att gaa ctt aca ttc	821
Val Asn Ala Leu Ile Ala Ala Gln Arg Ala Asn Ile Glu Leu Thr Phe	
95 100 105	
gcc aga tgt gcg gcc atc gat tta gcg ggc cgt gac gtg ctt gaa gcc	869
Ala Arg Cys Ala Ala Ile Asp Leu Ala Gly Arg Asp Val Leu Glu Ala	
110 115 120	
gtt caa atg agc gtt aat ccg aaa gtc atc gaa acg ccg ttt att gcc	917
Val Gln Met Ser Val Asn Pro Lys Val Ile Glu Thr Pro Phe Ile Ala	
125 130 135	
ggg gta gca atg gat ggt atc gaa gtg aaa gca aaa gcg aga atc acg	965
Gly Val Ala Met Asp Gly Ile Glu Val Lys Ala Lys Ala Arg Ile Thr	
140 145 150 155	
gtt cgc gct aac atc gac cgc ctt gtc ggg gga gcg ggc gaa gaa acg	1013
Val Arg Ala Asn Ile Asp Arg Leu Val Gly Gly Ala Gly Glu Glu Thr	
160 165 170	
atc att gcc cgt gtc ggc gaa ggg atc gtt tcg aca atc ggt tct tcc	1061
Ile Ile Ala Arg Val Gly Glu Gly Ile Val Ser Thr Ile Gly Ser Ser	
175 180 185	
gat aat cat aaa aaa gtg ctt gaa aac cca gat atg att tca caa acc	1109
Asp Asn His Lys Lys Val Leu Glu Asn Pro Asp Met Ile Ser Gln Thr	
190 195 200	
gta ttg agc aaa ggg ttg gat tca ggt aca gcg ttt gaa att cta tcg	1157
Val Leu Ser Lys Gly Leu Asp Ser Gly Thr Ala Phe Glu Ile Leu Ser	
205 210 215	
atc gat atc gct gac gtt gac atc ggc aaa aac atc gga gcg att ctg	1205
Ile Asp Ile Ala Asp Val Asp Ile Gly Lys Asn Ile Gly Ala Ile Leu	
220 225 230 235	

caa acc gac cag gct gaa gcc gat aaa aac atc gcc cag gcg aaa gcg	1253
Gln Thr Asp Gln Ala Glu Ala Asp Lys Asn Ile Ala Gln Ala Lys Ala	
240 245 250	
gaa gag cgc cgc gcc atg gcg gtt gcg caa gaa cag gaa atg cgc gcc	1301
Glu Glu Arg Arg Ala Met Ala Val Ala Gln Glu Gln Glu Met Arg Ala	
255 260 265	
cgc gtc gaa gaa atg cgc gcc aaa gtc gtc gaa gcc gaa gcc gaa gtg	1349
Arg Val Glu Glu Met Arg Ala Lys Val Val Glu Ala Glu Ala Glu Val	
270 275 280	
ccg ctt gca atg tct gaa gct ctc cgc agc gga aaa atc ggc gtc atg	1397
Pro Leu Ala Met Ser Glu Ala Leu Arg Ser Gly Lys Ile Gly Val Met	
285 290 295	
gac tac ctc aat atg aaa aac atc gac gcc gac act gac atg cgc gat	1445
Asp Tyr Leu Asn Met Lys Asn Ile Asp Ala Asp Thr Asp Met Arg Asp	
300 305 310 315	
tct ttc gga aag atg acg aaa gac caa aat gaa gag gat cat aaa	1490
Ser Phe Gly Lys Met Thr Lys Asp Gln Asn Glu Glu Asp His Lys	
320 325 330	
taaacaagcc cctgtaaaaa ggaggagct cattgcttga tatcctgttc gacaatccga	1550
ttatcatggc ggccatcatc gcagccatth ccttcatatt caacaagctc ggaaaaaacg	1610
atgaaaatga agaagcgaag cgaaaaccgg cgctgaaca gcagaggacg cagacgccga	1670
agccgaaaca gacggcgcag caccgtcctg caaaaaataa aaaccagcgg ccggcagcgg	1730
cagctgcaaa cagcgcagat atggaagcag agctccgcag aatcaaagaa gatgccgagc	1790
gttccatgcc ggccgttgaa cggaccatta aaaagcagag cagccgggtg atcaaccgga	1850
agcaagagct gctcgacatg aataaaaaaaaa caatagttca aggcattgtc ctcaagtgaag	1910
tattcggccc tccgcggtcg agaaagccgc attacacaat gaggcgccgg cctaaaattt	1970
aagtattaga acccccttct cac	1993

<210> 82  
 <211> 330  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 82

Met Asp Pro Ser Thr Leu Phe Leu Leu Leu Ile Ile Ala Ala Gly Ile
1 5 10 15

Ile Leu Leu Ala Val Phe Phe Thr Phe Val Pro Val Met Leu Trp Ile
20 25 30

Ser Ala Leu Ala Ala Gly Val Lys Ile Ser Ile Phe Thr Leu Ile Gly  
 35 40 45  
 Met Arg Leu Arg Arg Val Ile Pro Asn Arg Val Val Asn Pro Leu Ile  
 50 55 60  
 Lys Ala His Lys Ala Gly Leu Asp Val Ala Ile Asn Gln Leu Glu Ser  
 65 70 75 80  
 His Tyr Leu Ala Gly Gly Asn Val Asp Arg Val Val Asn Ala Leu Ile  
 85 90 95  
 Ala Ala Gln Arg Ala Asn Ile Glu Leu Thr Phe Ala Arg Cys Ala Ala  
 100 105 110  
 Ile Asp Leu Ala Gly Arg Asp Val Leu Glu Ala Val Gln Met Ser Val  
 115 120 125  
 Asn Pro Lys Val Ile Glu Thr Pro Phe Ile Ala Gly Val Ala Met Asp  
 130 135 140  
 Gly Ile Glu Val Lys Ala Lys Ala Arg Ile Thr Val Arg Ala Asn Ile  
 145 150 155 160  
 Asp Arg Leu Val Gly Gly Ala Gly Glu Glu Thr Ile Ile Ala Arg Val  
 165 170 175  
 Gly Glu Gly Ile Val Ser Thr Ile Gly Ser Ser Asp Asn His Lys Lys  
 180 185 190  
 Val Leu Glu Asn Pro Asp Met Ile Ser Gln Thr Val Leu Ser Lys Gly  
 195 200 205  
 Leu Asp Ser Gly Thr Ala Phe Glu Ile Leu Ser Ile Asp Ile Ala Asp  
 210 215 220  
 Val Asp Ile Gly Lys Asn Ile Gly Ala Ile Leu Gln Thr Asp Gln Ala  
 225 230 235 240  
 Glu Ala Asp Lys Asn Ile Ala Gln Ala Lys Ala Glu Glu Arg Arg Ala  
 245 250 255

Met Ala Val Ala Gln Glu Gln Glu Met Arg Ala Arg Val Glu Glu Met  
 260 265 270

Arg Ala Lys Val Val Glu Ala Glu Ala Glu Val Pro Leu Ala Met Ser  
 275 280 285

Glu Ala Leu Arg Ser Gly Lys Ile Gly Val Met Asp Tyr Leu Asn Met  
 290 295 300

Lys Asn Ile Asp Ala Asp Thr Asp Met Arg Asp Ser Phe Gly Lys Met  
 305 310 315 320

Thr Lys Asp Gln Asn Glu Glu Asp His Lys  
 325 330

<210> 83  
 <211> 1705  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (308)..(1237)

<400> 83  
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 tggcttaaat tcaccagtaa ggaaaagacc tcattaaaca ttatcgtatt catttggtca 120  
 ctgctgagtt tcggcgtttc gcaatccctt ttagggcttc tctttccatg gtcttttctt 180  
 gtgacggccc tcattgcaat ggagaagtca gttgccgttc ttatcgggtc gattggttgg 240  
 ttcacggcgg ttctgcagct ctttttttct cttctattga aacagatcag gccataccaa 300  
 aaaggag gaa tac aaa atg agt caa gtc gaa ttt gaa ggt gta agt aaa 349  
 Glu Tyr Lys Met Ser Gln Val Glu Phe Glu Gly Val Ser Lys  
 1 5 10  
 cga ata aaa ggc aga cca att gtc caa aat atc aca ttt caa att gcc 397  
 Arg Ile Lys Gly Arg Pro Ile Val Gln Asn Ile Thr Phe Gln Ile Ala  
 15 20 25 30  
 cca ggt aca att ttt ggg ctg ctc ggg cca aac ggc gct ggc aag aca 445  
 Pro Gly Thr Ile Phe Gly Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr  
 35 40 45  
 aca ctt atc aaa atg att gtc ggg atg gca aag ccg aca tca gga gat 493  
 Thr Leu Ile Lys Met Ile Val Gly Met Ala Lys Pro Thr Ser Gly Asp  
 50 55 60

atc cgc atc gac ggc tat tca gtt aaa agc aat tac gag gaa gcg gca Ile Arg Ile Asp Gly Tyr Ser Val Lys Ser Asn Tyr Glu Glu Ala Ala	541
65 70 75	
gcc cga gtc ggt tct gtt gtt gaa aac cca tcc ttt tat gag cac tta Ala Arg Val Gly Ser Val Val Glu Asn Pro Ser Phe Tyr Glu His Leu	589
80 85 90	
aca gga tac caa aac ctt aaa tat ctc ggc gga ttc cac agc cac gtg Thr Gly Tyr Gln Asn Leu Lys Tyr Leu Gly Gly Phe His Ser His Val	637
95 100 105 110	
tca aag gag cgc ata gaa gag atc gtt cag ctt gtt gat ttg aca gga Ser Lys Glu Arg Ile Glu Glu Ile Val Gln Leu Val Asp Leu Thr Gly	685
115 120 125	
agt att cat aaa cca gtt aaa acg tat tca tta ggc atg aaa cag cgt Ser Ile His Lys Pro Val Lys Thr Tyr Ser Leu Gly Met Lys Gln Arg	733
130 135 140	
ttg ggc ctt gcc gtc gcg ctc ttg cat gat ccg gaa ttt ctc att ctc Leu Gly Leu Ala Val Ala Leu Leu His Asp Pro Glu Phe Leu Ile Leu	781
145 150 155	
gat gaa ccg aca aac ggc ctt gat cct cag gga atc att gat ttg cgc Asp Glu Pro Thr Asn Gly Leu Asp Pro Gln Gly Ile Ile Asp Leu Arg	829
160 165 170	
gaa cac ctt cag tac ttg gcg aaa acc ttc aac aaa acg att ttg att Glu His Leu Gln Tyr Leu Ala Lys Thr Phe Asn Lys Thr Ile Leu Ile	877
175 180 185 190	
tcg agt cat ctt ctg tct gag gtt gag atg att tgt gat gaa tac ggc Ser Ser His Leu Leu Ser Glu Val Glu Met Ile Cys Asp Glu Tyr Gly	925
195 200 205	
gtc atg aaa aac gga gaa ctc ctg caa att aag agc aat cac cgc gat Val Met Lys Asn Gly Glu Leu Leu Gln Ile Lys Ser Asn His Arg Asp	973
210 215 220	
acc gat acg gtt cgt tat cgg ctt aca tta aac ggc cac gcc gat gaa Thr Asp Thr Val Arg Tyr Arg Leu Thr Leu Asn Gly His Ala Asp Glu	1021
225 230 235	
gcg gct gac ctg ttg aat gag tac cag tat gca ggc ggt ctc acg gaa Ala Ala Asp Leu Leu Asn Glu Tyr Gln Tyr Ala Gly Gly Leu Thr Glu	1069
240 245 250	
gat aaa aat gag att tat gtc ctt tgc atg gaa gaa gac att atg aaa Asp Lys Asn Glu Ile Tyr Val Leu Cys Met Glu Glu Asp Ile Met Lys	1117
255 260 265 270	
gtc gtt aat ctg tta atg gag aac aaa ata aga gtt ctg cat atg aag Val Val Asn Leu Leu Met Glu Asn Lys Ile Arg Val Leu His Met Lys	1165
275 280 285	
cag gaa aaa cag tcg ata gaa caa agc ttt ctg gaa ttg atc aat aag	1213

Gln Glu Lys Gln Ser Ile Glu Gln Ser Phe Leu Glu Leu Ile Asn Lys  
290 295 300

ggg tta ccg gca tta ggg tct tga aaaatgaact ttacaggctg atggtgacga 1267  
Gly Leu Pro Ala Leu Gly Ser  
305

aaagtacctg gattgtgtta agcttgctgc ttgtcatgac aatcgctgtt gcatggatgg 1327

tcagcaatgg cgaaaaggag aaggagacag gtaactggaa agagcaatta accgttcaaa 1387

acgctcagta tgaaagagaa atgagagagc tgagcccagc gggtcccaaa taccaatttt 1447

taaaagaaga gatcgcggtc aatcaatacc ggcttgagca taatttgccg ccttctgcga 1507

aatacaatgt ttggacgatg ctgaaggagt taaaaccgat cacaacatta atcgcgttga 1567

ttgcaatcgt gctggcagcg aactccatcg cgcttgagca cagcaaagga actattaaat 1627

ttgcgattgc aacaccggtc aagcgttggc attatctatt ggggaaatac ttgtcgatct 1687

tgctcaacac tgtattta 1705

<210> 84  
<211> 309  
<212> PRT  
<213> Bacillus licheniformis

<400> 84

Glu Tyr Lys Met Ser Gln Val Glu Phe Glu Gly Val Ser Lys Arg Ile  
1 5 10 15

Lys Gly Arg Pro Ile Val Gln Asn Ile Thr Phe Gln Ile Ala Pro Gly  
20 25 30

Thr Ile Phe Gly Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr Thr Leu  
35 40 45

Ile Lys Met Ile Val Gly Met Ala Lys Pro Thr Ser Gly Asp Ile Arg  
50 55 60

Ile Asp Gly Tyr Ser Val Lys Ser Asn Tyr Glu Glu Ala Ala Ala Arg  
65 70 75 80

Val Gly Ser Val Val Glu Asn Pro Ser Phe Tyr Glu His Leu Thr Gly  
85 90 95

Tyr Gln Asn Leu Lys Tyr Leu Gly Gly Phe His Ser His Val Ser Lys  
100 105 110

Glu Arg Ile Glu Glu Ile Val Gln Leu Val Asp Leu Thr Gly Ser Ile  
115 120 125

His Lys Pro Val Lys Thr Tyr Ser Leu Gly Met Lys Gln Arg Leu Gly  
130 135 140

Leu Ala Val Ala Leu Leu His Asp Pro Glu Phe Leu Ile Leu Asp Glu  
145 150 155 160

Pro Thr Asn Gly Leu Asp Pro Gln Gly Ile Ile Asp Leu Arg Glu His  
165 170 175

Leu Gln Tyr Leu Ala Lys Thr Phe Asn Lys Thr Ile Leu Ile Ser Ser  
180 185 190

His Leu Leu Ser Glu Val Glu Met Ile Cys Asp Glu Tyr Gly Val Met  
195 200 205

Lys Asn Gly Glu Leu Leu Gln Ile Lys Ser Asn His Arg Asp Thr Asp  
210 215 220

Thr Val Arg Tyr Arg Leu Thr Leu Asn Gly His Ala Asp Glu Ala Ala  
225 230 235 240

Asp Leu Leu Asn Glu Tyr Gln Tyr Ala Gly Gly Leu Thr Glu Asp Lys  
245 250 255

Asn Glu Ile Tyr Val Leu Cys Met Glu Glu Asp Ile Met Lys Val Val  
260 265 270

Asn Leu Leu Met Glu Asn Lys Ile Arg Val Leu His Met Lys Gln Glu  
275 280 285

Lys Gln Ser Ile Glu Gln Ser Phe Leu Glu Leu Ile Asn Lys Gly Leu  
290 295 300

Pro Ala Leu Gly Ser  
305

<210> 85  
<211> 1371  
<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(878)

<400> 85

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tattttttga aagtctccgt cttttctttt ccatctttca cgtatgctgc tttcagtaat 120

gggtgctttgt cggattcgct gtcattcacg taatcaaacc atacgagatc gtatttttga 180

atggattggg catctgcgac ctctgtgaa cgggtctgaag cggatgatga acatcctgat 240

aagggaacgg ctaaaagcat cgcagccgcg gataaagaga tcagtttcga ttttttctact 300

gtgatcatcc tattcatttc ggtttcgctt ttatatacga acgatccggg caaagggtgc 360

atctattcaa aatagattgg cagaaaacag ggcgtaacaa ttgcatttta aacgtaaaca 420

aactgtaaaa taccatttct atgaaaaaag gtataatttg aatgtcagaa aaaaatccca 480

ttcacggagg atatttttat atg aag aag ata ctt ttt tct gtt ttt gtt ttg 533  
Met Lys Lys Ile Leu Phe Ser Val Phe Val Leu  
1 5 10

gca ggc agc ttg cta ttg gct ttt aat ttt gcc ggt gaa gcg agt gct 581  
Ala Gly Ser Leu Leu Ala Phe Asn Phe Ala Gly Glu Ala Ser Ala  
15 20 25

aaa acg aaa aaa gtc agc ggc tat atc act tgg tac aac gga gtg ggc 629  
Lys Thr Lys Lys Val Ser Gly Tyr Ile Thr Trp Tyr Asn Gly Val Gly  
30 35 40

aaa atc ggc gct gac ggc aag agg ctc ggc cat tgg gac tgc gcc aca 677  
Lys Ile Gly Ala Asp Gly Lys Arg Leu Gly His Trp Asp Cys Ala Thr  
45 50 55

aag atg ggc ttc gat gtt ccg aga aaa ggc aca aaa ata aga gcc tat 725  
Lys Met Gly Phe Asp Val Pro Arg Lys Gly Thr Lys Ile Arg Ala Tyr  
60 65 70 75

tca aaa gca aaa ccg cac aaa gtc att aca gtc tat aaa tat gat gtc 773  
Ser Lys Ala Lys Pro His Lys Val Ile Thr Val Tyr Lys Tyr Asp Val  
80 85 90

ggc aga atg ccg ggc gct gtt ttg gat gta agc ccg aaa gct ttt aga 821  
Gly Arg Met Pro Gly Ala Val Leu Asp Val Ser Pro Lys Ala Phe Arg  
95 100 105

gct ttg gga ttt ccg aca agc aaa gga aag gta gcc gga cat tat aca 869  
Ala Leu Gly Phe Pro Thr Ser Lys Gly Lys Val Ala Gly His Tyr Thr  
110 115 120

tat aaa aaa taggagaaat gaagcaagaa aaatcgtttt cttgcttctt 918



Tyr Lys Lys  
125

tcaattggcg gggtcgaata tgaaaaaagt ttcagttggt ttggtggcgg cagtcatttt 978  
agccgcaggc gcatttgccg ccgtccgcta tttcgtcccg gaaaaagcgg agccggcaaa 1038  
gagcggcggg tcagacctgc ttgtatcgat aaccgatcag aagctgatga ccgcttacta 1098  
tgaaaatcaa aataagctgt atgaagaaaa gatgacggat tatccggcta tggcattaga 1158  
ccggaaaaaa cgaattcttt actatacaaa caccgataac agcaatgtga agcatttgat 1218  
caggctggat ttacagtcgg gcaaaaaaac aaccctatat tcaggagatg aatatgtcga 1278  
cgggctcagt ttatcggcgg acggttcgaa gctgttcatt agatacaacc ttgcggagga 1338  
gaggaatttt caccttgctt cctttgattt aaa 1371

<210> 86  
<211> 126  
<212> PRT  
<213> Bacillus licheniformis

<400> 86

Met Lys Lys Ile Leu Phe Ser Val Phe Val Leu Ala Gly Ser Leu Leu  
1 5 10 15

Leu Ala Phe Asn Phe Ala Gly Glu Ala Ser Ala Lys Thr Lys Lys Val  
20 25 30

Ser Gly Tyr Ile Thr Trp Tyr Asn Gly Val Gly Lys Ile Gly Ala Asp  
35 40 45

Gly Lys Arg Leu Gly His Trp Asp Cys Ala Thr Lys Met Gly Phe Asp  
50 55 60

Val Pro Arg Lys Gly Thr Lys Ile Arg Ala Tyr Ser Lys Ala Lys Pro  
65 70 75 80

His Lys Val Ile Thr Val Tyr Lys Tyr Asp Val Gly Arg Met Pro Gly  
85 90 95

Ala Val Leu Asp Val Ser Pro Lys Ala Phe Arg Ala Leu Gly Phe Pro  
100 105 110

Thr Ser Lys Gly Lys Val Ala Gly His Tyr Thr Tyr Lys Lys  
115 120 125

<210> 87  
 <211> 1957  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1454)

<400> 87  
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 gaagtcgcga tccggtcgat tgcacacgaa gactttgtct gttttaagcc gggctatggg 120  
 cttcgatatg tgtttgatca aatgtgccgg ggactgtcca tcagcccgaa gcttgctttt 180  
 gaaggggaag aagtgtcgac gattttggga ctagtatcag cagggctcgg tgtagcaatc 240  
 ctgccgaaaa cggcggagca cgtccattct ccagtggcat tttgccgagt gtcagactac 300  
 cgttctgaga ggacgatcgg tctcgccgtc ctgaaagacc attatttgtc gccggcggca 360  
 cgcaacttta aagaatttgt aattgaatac tatcgccgga acgaacggtc tgatcagccg 420  
 taactcaaat aaggacttct caagatgaca aatatcctgt atattgataa tgataattat 480  
 tatcaattgg aggattaaat atg acg aaa aag caa tat tct tat ata ttc acc 533  
                   Met Thr Lys Lys Gln Tyr Ser Tyr Ile Phe Thr  
                   1                  5                  10  
 ctt tta ctc gct ttc gct gta ttt ctt tca ggc tgt caa agc ggc cag 581  
 Leu Leu Leu Ala Phe Ala Val Phe Leu Ser Gly Cys Gln Ser Gly Gln  
                   15                  20                  25  
 aaa cag gct gca tca gag aaa aat gaa gag aaa aca aga gtg gtg aaa 629  
 Lys Gln Ala Ala Ser Glu Lys Asn Glu Glu Lys Thr Arg Val Val Lys  
                   30                  35                  40  
 acc atc aac gga aat gtc act gta ccg gct aat ccg aag cgc gtc gtg 677  
 Thr Ile Asn Gly Asn Val Thr Val Pro Ala Asn Pro Lys Arg Val Val  
                   45                  50                  55  
 acg att ggc tat gcg gga acc atg ctt gca ttc ggg atc aag ccg ctt 725  
 Thr Ile Gly Tyr Ala Gly Thr Met Leu Ala Phe Gly Ile Lys Pro Leu  
                   60                  65                  70                  75  
 gga gaa acg gga aag tac ctc gga agt cct tat att aaa gat caa gtt 773  
 Gly Glu Thr Gly Lys Tyr Leu Gly Ser Pro Tyr Ile Lys Asp Gln Val  
                   80                  85                  90  
 tca gga ata aag gat atc ggg gga aaa gac ggt ttt tca gta tct gtg 821  
 Ser Gly Ile Lys Asp Ile Gly Gly Lys Asp Gly Phe Ser Val Ser Val  
                   95                  100                  105

gaa aaa gtt ctt gaa ctt aaa ccc gat tta atc gta tcg atg acg aac	869
Glu Lys Val Leu Glu Leu Lys Pro Asp Leu Ile Val Ser Met Thr Asn	
110 115 120	
gat tca aaa gaa tat gaa aag ctg tca aaa atc gct ccc act gtc gtc	917
Asp Ser Lys Glu Tyr Glu Lys Leu Ser Lys Ile Ala Pro Thr Val Val	
125 130 135	
tat ccg ttc ggc aca ttt aaa gat gca cgc gat gaa atg aaa acg ttt	965
Tyr Pro Phe Gly Thr Phe Lys Asp Ala Arg Asp Glu Met Lys Thr Phe	
140 145 150 155	
ggc aag ctg ctc ggc aag gaa aag gaa gct cgg gag tgg acg aaa acg	1013
Gly Lys Leu Leu Gly Lys Glu Lys Glu Ala Arg Glu Trp Thr Lys Thr	
160 165 170	
ttt aat caa aaa atg aaa gcc gcc cgc gcg aaa att aaa gat gca tct	1061
Phe Asn Gln Lys Met Lys Ala Ala Arg Ala Lys Ile Lys Asp Ala Ser	
175 180 185	
gta aaa ggt gaa acg ttc tct tta atc ggc gca tat gca aaa tct tta	1109
Val Lys Gly Glu Thr Phe Ser Leu Ile Gly Ala Tyr Ala Lys Ser Leu	
190 195 200	
tat gtc tac ggg gca tac ggg tat cgg ggc gga gaa gcg atc tat acg	1157
Tyr Val Tyr Gly Ala Tyr Gly Tyr Arg Gly Gly Glu Ala Ile Tyr Thr	
205 210 215	
cag ctg gga ctg acg ccg cct gaa tct gtt aaa aag gat gcc att gat	1205
Gln Leu Gly Leu Thr Pro Pro Glu Ser Val Lys Lys Asp Ala Ile Asp	
220 225 230 235	
aca gct gac gga tat aaa gcc ata tct ttc gag gtc ctg ccg aaa tat	1253
Thr Ala Asp Gly Tyr Lys Ala Ile Ser Phe Glu Val Leu Pro Lys Tyr	
240 245 250	
gcc gga gac tac ata ttt gtc gac gaa tca tac aac gga aag ctt gat	1301
Ala Gly Asp Tyr Ile Phe Val Asp Glu Ser Tyr Asn Gly Lys Leu Asp	
255 260 265	
cag gac aat ccg gtt tgg gca tcg ctt gac gcg gtg aaa aaa ggc aag	1349
Gln Asp Asn Pro Val Trp Ala Ser Leu Asp Ala Val Lys Lys Gly Lys	
270 275 280	
gtc ttt ttc ctc gat ccg gac aga ttt tgg ccg tat gat cca aac gct	1397
Val Phe Phe Leu Asp Pro Asp Arg Phe Trp Pro Tyr Asp Pro Asn Ala	
285 290 295	
gtt cag gca cag gcc gaa gaa atc gcc gac atg att tcc aag aaa gcg	1445
Val Gln Ala Gln Ala Glu Glu Ile Ala Asp Met Ile Ser Lys Lys Ala	
300 305 310 315	
aaa aat aaa tagaaaagcg gggagccgaa aagaatgatc cggcttcccg	1494
Lys Asn Lys	
cttttttcatt tttcataatg ctgaaattga atatccagtg tccggaggta cgtttgcagg	1554

cccgcacatctt ggatggggat gatataggcg gcttcatctg actcattatg gtgggaatgc 1614  
 cataatccccg gcggtgtaat gaaggctttt ccggttaccc agtcaattcg tttcggatca 1674  
 atgatttcct ttgtggccgg atcgattttg cttccgacta atgtatacgt gccgggtgcg 1734  
 gcataggcga caaaatcgag agccaccgac ttgtggctgt gaggagcttg attggagccg 1794  
 ggaggcacga tgccgaacat tgcccacaat acatgggtga tcgtcagcgt ttgatcgaat 1854  
 atttcattgt tcaagagaac ggaaatgcgg ttgcgataac gggcgtcagg agcggcggcc 1914  
 gcttcagcca attttgcttt tgactgttca gcggtgtaga gag 1957

<210> 88  
 <211> 318  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 88

Met Thr Lys Lys Gln Tyr Ser Tyr Ile Phe Thr Leu Leu Leu Ala Phe  
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Ala Val Phe Leu Ser Gly Cys Gln Ser Gly Gln Lys Gln Ala Ala Ser  
 20 25 30

Glu Lys Asn Glu Glu Lys Thr Arg Val Val Lys Thr Ile Asn Gly Asn  
 35 40 45

Val Thr Val Pro Ala Asn Pro Lys Arg Val Val Thr Ile Gly Tyr Ala  
 50 55 60

Gly Thr Met Leu Ala Phe Gly Ile Lys Pro Leu Gly Glu Thr Gly Lys  
 65 70 75 80

Tyr Leu Gly Ser Pro Tyr Ile Lys Asp Gln Val Ser Gly Ile Lys Asp  
 85 90 95

Ile Gly Gly Lys Asp Gly Phe Ser Val Ser Val Glu Lys Val Leu Glu  
 100 105 110

Leu Lys Pro Asp Leu Ile Val Ser Met Thr Asn Asp Ser Lys Glu Tyr  
 115 120 125

Glu Lys Leu Ser Lys Ile Ala Pro Thr Val Val Tyr Pro Phe Gly Thr  
 130 135 140

Phe Lys Asp Ala Arg Asp Glu Met Lys Thr Phe Gly Lys Leu Leu Gly  
 145 150 155 160

Lys Glu Lys Glu Ala Arg Glu Trp Thr Lys Thr Phe Asn Gln Lys Met  
 165 170 175

Lys Ala Ala Arg Ala Lys Ile Lys Asp Ala Ser Val Lys Gly Glu Thr  
 180 185 190

Phe Ser Leu Ile Gly Ala Tyr Ala Lys Ser Leu Tyr Val Tyr Gly Ala  
 195 200 205

Tyr Gly Tyr Arg Gly Gly Glu Ala Ile Tyr Thr Gln Leu Gly Leu Thr  
 210 215 220

Pro Pro Glu Ser Val Lys Lys Asp Ala Ile Asp Thr Ala Asp Gly Tyr  
 225 230 235 240

Lys Ala Ile Ser Phe Glu Val Leu Pro Lys Tyr Ala Gly Asp Tyr Ile  
 245 250 255

Phe Val Asp Glu Ser Tyr Asn Gly Lys Leu Asp Gln Asp Asn Pro Val  
 260 265 270

Trp Ala Ser Leu Asp Ala Val Lys Lys Gly Lys Val Phe Phe Leu Asp  
 275 280 285

Pro Asp Arg Phe Trp Pro Tyr Asp Pro Asn Ala Val Gln Ala Gln Ala  
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Glu Glu Ile Ala Asp Met Ile Ser Lys Lys Ala Lys Asn Lys  
 305 310 315

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<220>  
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 <222> (501) .. (929)

<400> 89

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tcgaacgtcg acctttcaga agaattttcc gaaatgatta tcgcgcagcg cggcttccag	180
tccaatgcga aaatcattac aacctctgat gaaattcttc aggaactcgt caatctgaag	240
cgataggagg gaaggaggcg cctctgtgaa ggcgccctctt gataacacat gatcaaagtt	300
acgcgattaa acggacagcc ctttattctg aatgcactat tcattgagca aattgaatgt	360
tttccggata cgacaattac gctgtccaac ggaaaaaagt ttgttgtcaa agaagatgaa	420
gatacagttg tggatacaat cgtgtcattc tatcaaaaaa tccaaataact ttcttgtgac	480
caaagaattg aggaatctga atg aat aaa aaa ctt cta gga att atg atg acg	533
Met Asn Lys Lys Leu Leu Gly Ile Met Met Thr	
1 5 10	
att att ttg gca att gct gtg ttg gga acc gct gcg ttc ttt gtc atc	581
Ile Ile Leu Ala Ile Ala Val Leu Gly Thr Ala Ala Phe Phe Val Ile	
15 20 25	
aag gga agc gca agt gaa aaa gat caa aac gca gaa cct tcg atc gat	629
Lys Gly Ser Ala Ser Glu Lys Asp Gln Asn Ala Glu Pro Ser Ile Asp	
30 35 40	
gaa gtg gtc gaa tct tca gtt gaa gtc gcc gaa atc acg aca aac ttg	677
Glu Val Val Glu Ser Ser Val Glu Val Ala Glu Ile Thr Thr Asn Leu	
45 50 55	
aaa tca gac aat gta gtc cgt ttg tca atc aag ctt gaa acc gat tcg	725
Lys Ser Asp Asn Val Val Arg Leu Ser Ile Lys Leu Glu Thr Asp Ser	
60 65 70 75	
aaa gag gcg aaa gaa gag ctt gaa aag cgg gat ttc caa att aaa gat	773
Lys Glu Ala Lys Glu Glu Leu Glu Lys Arg Asp Phe Gln Ile Lys Asp	
80 85 90	
tca gtc atc tcc ctt ttg gcg aac acg aac gca gat gag ctt gaa gga	821
Ser Val Ile Ser Leu Leu Ala Asn Thr Asn Ala Asp Glu Leu Glu Gly	
95 100 105	
caa aaa gga aaa gaa aaa ttt aaa gaa cag ctg aaa gaa aag ctg aac	869
Gln Lys Gly Lys Glu Lys Phe Lys Glu Gln Leu Lys Glu Lys Leu Asn	
110 115 120	
acg aac tac atg aaa gag gga aaa gtg aaa act gtg tac att acc tcc	917
Thr Asn Tyr Met Lys Glu Gly Lys Val Lys Thr Val Tyr Ile Thr Ser	
125 130 135	
ttt aat ctg cag taggaacata gatgacagaa ccatggaggt gaaaacagat	969
Phe Asn Leu Gln	
140	
ggcaggagaa gtgctctccc aaaatgaaat cgatgcactg ctttcagcga tatcgaccgg	1029

tgaaatggac gccgacgagc tgaaaaaaga agagtccgtt aaaaaagtaa aagtctatga 1089  
 ctttaaacgg gcgctccgct tttcaaagga tcaaataccgc agcttgacca ggattcacga 1149  
 taactttgca aggctgctaa cgacttattt ctcagctcag ttgagaacct atatccaaat 1209  
 ctcggtcagc tcggttgatc aggttccgta tgaggaattc atcagatcga ttccgaatat 1269  
 gacgatcctc aatctgtttg aggttcgccc tcttgaagga agaatacatga tggagatcaa 1329  
 cccgaccatc gcctatacga tgatggaccg ggtgatgggc gggatcggct cgagccacaa 1389  
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 <211> 143  
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 <213> Bacillus licheniformis

<400> 90

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Glu Lys Asp Gln Asn Ala Glu Pro Ser Ile Asp Glu Val Val Glu Ser  
 35 40 45

Ser Val Glu Val Ala Glu Ile Thr Thr Asn Leu Lys Ser Asp Asn Val  
 50 55 60

Val Arg Leu Ser Ile Lys Leu Glu Thr Asp Ser Lys Glu Ala Lys Glu  
 65 70 75 80

Glu Leu Glu Lys Arg Asp Phe Gln Ile Lys Asp Ser Val Ile Ser Leu  
 85 90 95

Leu Ala Asn Thr Asn Ala Asp Glu Leu Glu Gly Gln Lys Gly Lys Glu  
 100 105 110

Lys Phe Lys Glu Gln Leu Lys Glu Lys Leu Asn Thr Asn Tyr Met Lys  
 115 120 125

Glu Gly Lys Val Lys Thr Val Tyr Ile Thr Ser Phe Asn Leu Gln  
 130 135 140

<210> 91  
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 <222> (488)..(874)

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 cagaatgaat gtcggatggt cgctctctgt tgtaaaagac ggactccgac gtctgaagac 180  
 cgcttttttcg taagcggtcc ggctgaaagc cgggcgcttc taagagcggt tatggatggg 240  
 ttcattcaat tctctttcca gcttttccgc tttttcagct tcttttttgg aatgcttgat 300  
 aatcagccgg aatacagcga tcgcatgat aaagaaaacg gccagcgtaa taaaagaagg 360  
 gatataattct cttttgtctt caggaaaata gagcataaac tgaatcagaa acggcgccat 420  
 ttttcttctt ccctgaaatg atttttttac catttatatta ttatgatacc attaggaggc 480  
 agatgca gtg aac aac caa ttt caa gtc gga gat cgc gta aag ggc ttt 529  
 Val Asn Asn Gln Phe Gln Val Gly Asp Arg Val Lys Gly Phe  
 1 5 10  
 tat aaa aca ggc gtc tac atc ggc gaa att acg gat gtt aaa ccg atg 577  
 Tyr Lys Thr Gly Val Tyr Ile Gly Glu Ile Thr Asp Val Lys Pro Met  
 15 20 25 30  
 cac tac ctg gtc aaa atc ctc gcc gtg ctg acc cat ccg aag cag ggc 625  
 His Tyr Leu Val Lys Ile Leu Ala Val Leu Thr His Pro Lys Gln Gly  
 35 40 45  
 gac ctt cat cat ccc aat cgg gca gac gtc cct ttt ttt cat gaa cga 673  
 Asp Leu His His Pro Asn Arg Ala Asp Val Pro Phe Phe His Glu Arg  
 50 55 60  
 aaa gcg ctc gct tac ggt gaa cag acg aat atc ccg cac cgc atg gtg 721  
 Lys Ala Leu Ala Tyr Gly Glu Gln Thr Asn Ile Pro His Arg Met Val  
 65 70 75  
 aag ccg ttc gat gaa gct gta ccg gat tat gcg gat tcg ctc cgc tca 769  
 Lys Pro Phe Asp Glu Ala Val Pro Asp Tyr Ala Asp Ser Leu Arg Ser  
 80 85 90  
 gct ttg agc cgc tta aaa acg gat ctg caa aac gat tcg tcc gaa tac 817  
 Ala Leu Ser Arg Leu Lys Thr Asp Leu Gln Asn Asp Ser Ser Glu Tyr  
 95 100 105 110



gcg gca aaa tcg ctt gag ctt att cat ggg ctt gaa aaa gaa tat ttc 865  
 Ala Ala Lys Ser Leu Glu Leu Ile His Gly Leu Glu Lys Glu Tyr Phe  
                   115                  120                  125

ctg cac aaa taaccaatc tgtttgtcag attgggtttt ttatgtggcg 914  
 Leu His Lys

tgcggaaga cttttgagag gtcaaccggt tcgccgatcg tcgtcggtt cggattttcc 974  
 aaatacttct tatcccggtc tacgagccga aacaacttat acgttgtcat cgcgtcgtca 1034  
 agcgctttat gctgttttcc cgttcctgaa tcgccgtact cttccgctgc cttccacaaa 1094  
 ttcgtcaatg ttttgtcgcc gaaaaattcc ttgtactcca tggaaagggtc cctcatctct 1154  
 cctttaaacg gaaacggaac atgggtgaac atgcaatttt gcttcagcac tttcatatcc 1214  
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 ttgcagcgcc tcgttaattt agggaaacttc tt 1366

<210> 92  
 <211> 129  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 92

Val Asn Asn Gln Phe Gln Val Gly Asp Arg Val Lys Gly Phe Tyr Lys  
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Thr Gly Val Tyr Ile Gly Glu Ile Thr Asp Val Lys Pro Met His Tyr  
                   20                  25                  30

Leu Val Lys Ile Leu Ala Val Leu Thr His Pro Lys Gln Gly Asp Leu  
                   35                  40                  45

His His Pro Asn Arg Ala Asp Val Pro Phe Phe His Glu Arg Lys Ala  
                   50                  55                  60

Leu Ala Tyr Gly Glu Gln Thr Asn Ile Pro His Arg Met Val Lys Pro  
 65                  70                  75                  80

Phe Asp Glu Ala Val Pro Asp Tyr Ala Asp Ser Leu Arg Ser Ala Leu  
                   85                  90                  95

Ser Arg Leu Lys Thr Asp Leu Gln Asn Asp Ser Ser Glu Tyr Ala Ala

100

105

110

Lys Ser Leu Glu Leu Ile His Gly Leu Glu Lys Glu Tyr Phe Leu His  
 115 120 125

Lys

<210> 93  
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 <212> DNA  
 <213> Bacillus licheniformis

<220>  
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 <222> (501)..(1406)

<400> 93  
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 ctgaaaacgg agaaagcatg gagatccgcg gccgcgatct tttaacaggc ctgccgaaaa 180  
 cgattgaaat cactgaaaaa gaaattacag cggctcttcg cgacactgtg accgccattg 240  
 tcgatgccgt aaaaaatacg cttgaaaaaa ctccgcctga actcgcggct gatattatgg 300  
 accgcggaat cgtccttacg ggaggcggcg cactgctgcg ccacctggac aaagtcatca 360  
 gcgaagaaac gaaaatgccg gttttaattg cggaagaccc tcttgactgt gtagcgatcg 420  
 gaacaggcaa agctctcgag caaattcatc tatttaaagg caaaaattaa ggacacaggg 480  
 aatagaagag gtgtataatc atg ccg cag ttt ttt aca aat aaa cgg ttg atg 533  
 Met Pro Gln Phe Phe Thr Asn Lys Arg Leu Met  
 1 5 10  
 ctt tta ctc ctt tgt atc atc att tta gtg gca atg att gga ttt tcg 581  
 Leu Leu Leu Leu Cys Ile Ile Ile Leu Val Ala Met Ile Gly Phe Ser  
 15 20 25  
 tta aag aat gac cgg aat gca act tgg ccc gaa aaa ttt att ggc gat 629  
 Leu Lys Asn Asp Arg Asn Ala Thr Trp Pro Glu Lys Phe Ile Gly Asp  
 30 35 40  
 aca act ggt gta ttc cag acg att ttt cat acg ccc gct caa ttt ttt 677  
 Thr Thr Gly Val Phe Gln Thr Ile Phe His Thr Pro Ala Gln Phe Phe  
 45 50 55  
 gcg ggc ttc ttt gaa aat atc gaa gac tta aaa aat acg tac agc gaa 725  
 Ala Gly Phe Phe Glu Asn Ile Glu Asp Leu Lys Asn Thr Tyr Ser Glu  
 60 65 70 75

aat gag cgc ctg cgg aaa aag ctc gac ggc cag aca caa tac gag gca	773
Asn Glu Arg Leu Arg Lys Lys Leu Asp Gly Gln Thr Gln Tyr Glu Ala	
80 85 90	
aag ctg cag gag ctt gaa aat gaa aat aag tct tta aga aaa gag ctc	821
Lys Leu Gln Glu Leu Glu Asn Glu Asn Lys Ser Leu Arg Lys Glu Leu	
95 100 105	
ggc cat ctg aaa tca att aaa gac tac acg ccg att ctg gcg acc gtt	869
Gly His Leu Lys Ser Ile Lys Asp Tyr Thr Pro Ile Leu Ala Thr Val	
110 115 120	
atc gcc aga aat ccc gat aag tat gag tgg tgg aac ctg att acg atc	917
Ile Ala Arg Asn Pro Asp Lys Tyr Glu Trp Trp Asn Leu Ile Thr Ile	
125 130 135	
aac aaa ggt tca aag cac ggc gtt gag aag gat atg gcg gta aca gat	965
Asn Lys Gly Ser Lys His Gly Val Glu Lys Asp Met Ala Val Thr Asp	
140 145 150 155	
gaa aac ggc aac ttg atc gga aaa atc aaa agc aca aaa gtg aac aat	1013
Glu Asn Gly Asn Leu Ile Gly Lys Ile Lys Ser Thr Lys Val Asn Asn	
160 165 170	
ttc act tcc acc gtc cag ctt tta agc gca aca gac aga aac aac aga	1061
Phe Thr Ser Thr Val Gln Leu Leu Ser Ala Thr Asp Arg Asn Asn Arg	
175 180 185	
atc tcc aca gtt atc gct gca gat aaa ggc aag aaa acg gtg aac gga	1109
Ile Ser Thr Val Ile Ala Ala Asp Lys Gly Lys Lys Thr Val Asn Gly	
190 195 200	
atc atc aac ggc tac gac tca gat aaa aag gcg ctt tcc atg gaa atc	1157
Ile Ile Asn Gly Tyr Asp Ser Asp Lys Lys Ala Leu Ser Met Glu Ile	
205 210 215	
atc gag cct gat gaa gac agg gaa gtg aaa aaa ggt gac ctc gtc gaa	1205
Ile Glu Pro Asp Glu Asp Arg Glu Val Lys Lys Gly Asp Leu Val Glu	
220 225 230 235	
act tcc ggt gcg ggc ggc gtt ttt cct aaa ggc ctg aca atc gga aaa	1253
Thr Ser Gly Ala Gly Gly Val Phe Pro Lys Gly Leu Thr Ile Gly Lys	
240 245 250	
gtg aca gag gtt gaa cca gat tcc tac ggt ttg acg aaa atc gct tat	1301
Val Thr Glu Val Glu Pro Asp Ser Tyr Gly Leu Thr Lys Ile Ala Tyr	
255 260 265	
gta gag ccg gca gcc gat atg tat aac ctt gat aac gtc atc gtc gtc	1349
Val Glu Pro Ala Ala Asp Met Tyr Asn Leu Asp Asn Val Ile Val Val	
270 275 280	
gac aga acg ctt gat acg gtg gat gtc gac aag atg gac gat gag gag	1397
Asp Arg Thr Leu Asp Thr Val Asp Val Asp Lys Met Asp Asp Glu Glu	
285 290 295	

gaa ggg tgg tgaacgctt ccttcttccc gtggtcatga tgtttgtttt 1446  
 Glu Gly Ser  
 300

agtatctgac agcgtctatg cggattttgt caacttgcct tttgtgacgg aagaacagca 1506  
 gctcatcccg cgttttctgc tgcttgtctt agtttttatg acggcttatg tcaatcagcc 1566  
 ttttgccatt acatatggat ttattttcgg actgttatat gatattaatt acaccgacct 1626  
 tttaggtgta tatatgtttg gttttgccgg tatttgctat ttatcgtcaa aagcgttcaa 1686  
 agtattgcag acaaacgcgc tggtcgtcat ttttatttcg ctgctcgccg tctgtgttct 1746  
 tgaattttac caatatggcg tgcagatgct gatacgctccg gaaattatgc cgttccatca 1806  
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<210> 94  
 <211> 302  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 94

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 20 25 30

Asn Ala Thr Trp Pro Glu Lys Phe Ile Gly Asp Thr Thr Gly Val Phe  
 35 40 45

Gln Thr Ile Phe His Thr Pro Ala Gln Phe Phe Ala Gly Phe Phe Glu  
 50 55 60

Asn Ile Glu Asp Leu Lys Asn Thr Tyr Ser Glu Asn Glu Arg Leu Arg  
 65 70 75 80

Lys Lys Leu Asp Gly Gln Thr Gln Tyr Glu Ala Lys Leu Gln Glu Leu  
 85 90 95

Glu Asn Glu Asn Lys Ser Leu Arg Lys Glu Leu Gly His Leu Lys Ser  
 100 105 110

Ile Lys Asp Tyr Thr Pro Ile Leu Ala Thr Val Ile Ala Arg Asn Pro

115

120

125

Asp Lys Tyr Glu Trp Trp Asn Leu Ile Thr Ile Asn Lys Gly Ser Lys  
 130 135 140

His Gly Val Glu Lys Asp Met Ala Val Thr Asp Glu Asn Gly Asn Leu  
 145 150 155 160

Ile Gly Lys Ile Lys Ser Thr Lys Val Asn Asn Phe Thr Ser Thr Val  
 165 170 175

Gln Leu Leu Ser Ala Thr Asp Arg Asn Asn Arg Ile Ser Thr Val Ile  
 180 185 190

Ala Ala Asp Lys Gly Lys Lys Thr Val Asn Gly Ile Ile Asn Gly Tyr  
 195 200 205

Asp Ser Asp Lys Lys Ala Leu Ser Met Glu Ile Ile Glu Pro Asp Glu  
 210 215 220

Asp Arg Glu Val Lys Lys Gly Asp Leu Val Glu Thr Ser Gly Ala Gly  
 225 230 235 240

Gly Val Phe Pro Lys Gly Leu Thr Ile Gly Lys Val Thr Glu Val Glu  
 245 250 255

Pro Asp Ser Tyr Gly Leu Thr Lys Ile Ala Tyr Val Glu Pro Ala Ala  
 260 265 270

Asp Met Tyr Asn Leu Asp Asn Val Ile Val Val Asp Arg Thr Leu Asp  
 275 280 285

Thr Val Asp Val Asp Lys Met Asp Asp Glu Glu Glu Gly Ser  
 290 295 300

<210> 95  
 <211> 1450  
 <212> DNA  
 <213> Bacillus licheniformis

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 <222> (121)..(951)

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atg aca cat agc gca tta aag cat tta gat tat cac aat tgg gcg aat 168  
Met Thr His Ser Ala Leu Lys His Leu Asp Tyr His Asn Trp Ala Asn  
1 5 10 15  
caa agg gtg ctc acc cac ctg aaa agc ctg cct gaa gag ctg ttc acc 216  
Gln Arg Val Leu Thr His Leu Lys Ser Leu Pro Glu Glu Leu Phe Thr  
20 25 30  
cgg gaa atc aaa agc gtt ttt caa act gta tct gag gtt gtt acc cat 264  
Arg Glu Ile Lys Ser Val Phe Gln Thr Val Ser Glu Val Val Thr His  
35 40 45  
atg tgc ggc gct gac gac ctt agg ctg aaa gat acc acc ctc tta acc 312  
Met Cys Gly Ala Asp Asp Leu Arg Leu Lys Asp Thr Thr Leu Leu Thr  
50 55 60  
aga aag tgt ggg gga aag tat acc cgc aga acc gtt caa aaa atg aag 360  
Arg Lys Cys Gly Gly Lys Tyr Thr Arg Arg Thr Val Gln Lys Met Lys  
65 70 75 80  
cca aag ttt agg ttg cag tgt cag ttt aag aag aag cgc caa aag tac 408  
Pro Lys Phe Arg Leu Gln Cys Gln Phe Lys Lys Lys Arg Gln Lys Tyr  
85 90 95  
att tgt ggt gaa agg aat aat att ggg cgg aac act gtc aat ggt aat 456  
Ile Cys Gly Glu Arg Asn Asn Ile Gly Arg Asn Thr Val Asn Gly Asn  
100 105 110  
ttt aaa gca agc cga ttt aat gaa aaa tgg gta acc gac att acc tac 504  
Phe Lys Ala Ser Arg Phe Asn Glu Lys Trp Val Thr Asp Ile Thr Tyr  
115 120 125  
tta cat tat ggc tcc gat atg tta tat tta tca acg att atg gac tta 552  
Leu His Tyr Gly Ser Asp Met Leu Tyr Leu Ser Thr Ile Met Asp Leu  
130 135 140  
tat aac aac gaa ata gtg gct tac aaa ata ggt acg agc caa gat att 600  
Tyr Asn Asn Glu Ile Val Ala Tyr Lys Ile Gly Thr Ser Gln Asp Ile  
145 150 155 160  
aac cta gta tta gac aca ttg agg gaa gct gta gaa tta cgt aaa cca 648  
Asn Leu Val Leu Asp Thr Leu Arg Glu Ala Val Glu Leu Arg Lys Pro  
165 170 175  
gta ggg tta ctt ctt cat agc gac cag gga tct gtc tat act tca cat 696  
Val Gly Leu Leu Leu His Ser Asp Gln Gly Ser Val Tyr Thr Ser His  
180 185 190  
gca' tat cag aat ttg gcc aaa gaa aaa ggc att acc aca agc atg tct 744  
Ala Tyr Gln Asn Leu Ala Lys Glu Lys Gly Ile Thr Thr Ser Met Ser  
195 200 205

cga aaa gga aac tgc cat gat aat gcc gtc att gaa tcc ttt cac tcc 792  
 Arg Lys Gly Asn Cys His Asp Asn Ala Val Ile Glu Ser Phe His Ser  
 210 215 220

tcg cta aag tcg gaa gga ttt aac gct caa agt aga gca tct ata tcc 840  
 Ser Leu Lys Ser Glu Gly Phe Asn Ala Gln Ser Arg Ala Ser Ile Ser  
 225 230 235 240

aat tct aaa gta gta caa att gta aat caa tac atg tat cga tat aat 888  
 Asn Ser Lys Val Val Gln Ile Val Asn Gln Tyr Met Tyr Arg Tyr Asn  
 245 250 255

cat gta cga att cag gca aaa tta aac tac ctg tcc cca ctg gaa tac 936  
 His Val Arg Ile Gln Ala Lys Leu Asn Tyr Leu Ser Pro Leu Glu Tyr  
 260 265 270

agg gga cag gca gca taggtgtttt ttctaagtct cattttaacg ggtcagttca 991  
 Arg Gly Gln Ala Ala  
 275

tctttacatg ccgggttttt gctttattca ggctgcttcg cgtccgcttc aagccgggcc 1051

actgctccag gcgacgcttt ttccaccgct ctggcggcta tgcgtaagc ctcttcatac 1111

tgatatgcgt aaaaacagtt ttctgcttct ttcagctggt cggaaaggat acggtcctgg 1171

cttctgaagc ggttgccata ttgaatgatg cgttcgatca gcaaaaccag ttcaaccagt 1231

tcgtccgtct ttgttttcac ttccgtgaca agctgttccg cctcttgaag acgttcgttc 1291

accgcatcca tgttcagcgg cagctcattc aactgttctg tcactttctg cacagtcgtc 1351

tgcgactgtc ggatcttttc gggtatggcc tccgggatgc ctggaacatt gcttttctcc 1411

aggctgcgcg ccgtatcctt gattgtctgc ttcaattgc 1450

<210> 96

<211> 277

<212> PRT

<213> Bacillus licheniformis

<400> 96

Met Thr His Ser Ala Leu Lys His Leu Asp Tyr His Asn Trp Ala Asn  
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Gln Arg Val Leu Thr His Leu Lys Ser Leu Pro Glu Glu Leu Phe Thr  
 20 25 30

Arg Glu Ile Lys Ser Val Phe Gln Thr Val Ser Glu Val Val Thr His  
 35 40 45

Met Cys Gly Ala Asp Asp Leu Arg Leu Lys Asp Thr Thr Leu Leu Thr

50

55

60

Arg Lys Cys Gly Gly Lys Tyr Thr Arg Arg Thr Val Gln Lys Met Lys  
 65 70 75 80

Pro Lys Phe Arg Leu Gln Cys Gln Phe Lys Lys Lys Arg Gln Lys Tyr  
 85 90 95

Ile Cys Gly Glu Arg Asn Asn Ile Gly Arg Asn Thr Val Asn Gly Asn  
 100 105 110

Phe Lys Ala Ser Arg Phe Asn Glu Lys Trp Val Thr Asp Ile Thr Tyr  
 115 120 125

Leu His Tyr Gly Ser Asp Met Leu Tyr Leu Ser Thr Ile Met Asp Leu  
 130 135 140

Tyr Asn Asn Glu Ile Val Ala Tyr Lys Ile Gly Thr Ser Gln Asp Ile  
 145 150 155 160

Asn Leu Val Leu Asp Thr Leu Arg Glu Ala Val Glu Leu Arg Lys Pro  
 165 170 175

Val Gly Leu Leu Leu His Ser Asp Gln Gly Ser Val Tyr Thr Ser His  
 180 185 190

Ala Tyr Gln Asn Leu Ala Lys Glu Lys Gly Ile Thr Thr Ser Met Ser  
 195 200 205

Arg Lys Gly Asn Cys His Asp Asn Ala Val Ile Glu Ser Phe His Ser  
 210 215 220

Ser Leu Lys Ser Glu Gly Phe Asn Ala Gln Ser Arg Ala Ser Ile Ser  
 225 230 235 240

Asn Ser Lys Val Val Gln Ile Val Asn Gln Tyr Met Tyr Arg Tyr Asn  
 245 250 255

His Val Arg Ile Gln Ala Lys Leu Asn Tyr Leu Ser Pro Leu Glu Tyr  
 260 265 270

Arg Gly Gln Ala Ala  
 275



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<210> 97
<211> 2312
<212> DNA
<213> Bacillus licheniformis
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110 115 120	
cgc ggg gat tct ccg aga tcc gcc ctc ggg ctt gct gtc gca gac gac	917
Arg Gly Asp Ser Pro Arg Ser Ala Leu Gly Leu Ala Val Ala Asp Asp	
125 130 135	
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Ile Glu Gly Pro Tyr Lys Asn Lys Gly Ile Phe Leu Lys Ser Gly Met	
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Asp Gly Ile Ser Asn Asp Gly Thr Pro Tyr Asp Ala Thr Lys His Pro	
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Met Val Tyr Gly Ser Tyr Ser Gly Gly Ile Phe Ile Leu Glu Met Asp	
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Lys Lys Thr Gly Phe Pro Leu Pro Gly Gln Gly Tyr Gly Lys Lys Leu	
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Ile Gly Gly Asn His Ser Arg Ile Glu Gly Ala Tyr Ile Leu Tyr His	
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Pro Glu Thr Gln Tyr Tyr Tyr Leu Tyr Met Ser Phe Gly Gly Leu Ala	
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Gly Pro Tyr Tyr Asp Ala Glu Gly His Ala Met Ile Asp Val Arg Gly	
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Pro Gly His Asn Ser Ala Phe Tyr Asp Glu Lys Ser Gly Lys Ser Tyr	
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Trp	Asp	Ala	Ala	Ser	Glu	Arg	Lys	Val	Met	Thr	Phe	Ser	Ala	Leu	Ser		
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Ala Phe Tyr Asp Glu Lys Ser Gly Lys Ser Tyr Leu Ile Phe His Thr  
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Arg Phe Pro Gly Arg Gly Glu Glu His Glu Val Arg Val His Gln Leu  
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Tyr Ile Ala Val Val Met Ser Lys Asp Gly Ser Tyr Asp Gly Trp Gly	
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His Thr Ser Val Ser Gly Gly Thr Leu Phe Pro Asp Leu Lys Pro Glu	
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Arg Glu Val Leu Asn Lys Glu Glu Gly Val Trp His Thr Ser Val Ser  
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Gly Gly Thr Leu Phe Pro Asp Leu Lys Pro Glu Leu Ala Leu Pro Val  
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Val	Asn	Val	Tyr	Met	Thr	Arg	Asn	Asp	Asp	Ser	Phe	Val	Ser	Leu	Gln	
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Gly Asp Tyr Phe Val Leu Arg Glu Asn Lys Gln Pro Ala Ala Leu Phe			
475	480	485	
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Glu Leu Gly Tyr Leu Ser His Pro Gln Glu Glu Ala Val Val Ser Thr			
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Asn Ala Tyr Arg Glu Arg Val Thr Asp Gly Ile Arg Ser Gly Leu Glu			
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Gln Lys Gly Trp Val Val Ser Trp Leu Ile Lys Lys Lys Ser Gln Val  
85 90 95

Ser Ser Gly Ser Asp Ser Ala Ser Gly Lys Val Thr Ser Ser Glu Ala  
100 105 110

Asn Leu Arg Ile Arg Lys Gly Pro Gly Thr Ser Tyr Glu Val Gln Gly  
115 120 125

Val Phe Pro Glu Gly Glu Gln Ala Asp Leu Leu Lys Thr Asp Gly Lys  
130 135 140

Trp Ile Lys Ile Ser Tyr Gln Asn Ile Thr Gly Trp Val Tyr Ser Asp  
145 150 155 160

Tyr Val Asn Gln Gly Ser Gly Ala Lys Gln Ser Gln Ser Ser Ser Ser  
165 170 175

His Ala Ser Ser Ser Lys Ser Gly Thr Val Gly Val Ser Thr Leu Asn  
180 185 190

Val Arg Ser Thr Ala Ser His Gln Gly Arg Ile Ile Ala Thr Leu Gln  
195 200 205

Arg Asn Ala Ser Val Thr Ile Leu Asn Glu Gln His Gly Trp Tyr Glu  
210 215 220

Ile Glu Phe Asn Gly Gln Lys Gly Trp Ala Ala Ser His Tyr Ile Leu  
225 230 235 240

Glu Gly Asn Lys Gln Asn Ser Gly Thr Ser Gly Thr Ser Ser Ser Ser  
245 250 255

Glu Ala Lys Arg Gln Gly Thr Ile Val Tyr Glu Ser Thr Asn Val Arg  
260 265 270

Ser Gly Ala Ser Thr Ser Ser Ala Ile Val Lys Arg Thr Gly Lys Gly  
 275 280 285

Glu Ser Tyr Pro Ile Val Ser Thr Lys Gly Asp Trp Tyr Glu Ile Lys  
 290 295 300

Leu Ser Asn Gly Asp Ser Ala Tyr Val Ala Ser Trp Val Val Gln Thr  
 305 310 315 320

Val Asp Gln Ala Gly Ser Ala Gly Asp Ser Lys Ser Ala Ala Pro Pro  
 325 330 335

Leu Ala Lys Arg Ser Ser Ser Gly Gly Thr Ile Lys Asn Lys Thr Val  
 340 345 350

Val Ile Asp Ala Gly His Gly Gly His Asp Ser Gly Thr Ile Gly Thr  
 355 360 365

Arg Gly Thr Leu Glu Lys Arg Leu Thr Ile Lys Thr Ala Thr Leu Leu  
 370 375 380

Ala Ala Lys Leu Arg Ala Asp Gly Val Asn Val Tyr Met Thr Arg Asn  
 385 390 395 400

Asp Asp Ser Phe Val Ser Leu Gln Ser Arg Val Ala Thr Ser His Tyr  
 405 410 415

Arg Asn Ala Asp Ala Phe Ile Ser Ile His Tyr Asp Ser Phe Pro Asn  
 420 425 430

Ala Ser Val Arg Gly Asn Thr Ala Tyr Tyr Tyr Ser Pro Ser Lys Asp  
 435 440 445

Arg Lys Leu Ala Ala Asp Val Gln Ser Glu Ile Glu Arg His Ser Pro  
 450 455 460

Leu Pro Ser Arg Gly Val Leu Phe Gly Asp Tyr Phe Val Leu Arg Glu  
 465 470 475 480

Asn Lys Gln Pro Ala Ala Leu Phe Glu Leu Gly Tyr Leu Ser His Pro  
 485 490 495

Gln Glu Glu Ala Val Val Ser Thr Asn Ala Tyr Arg Glu Arg Val Thr

Asp Gly Ile Arg Ser Gly Leu Glu Asn Tyr Phe Asp  
 515 520

<210> 103  
 <211> 1774  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (516)..(1271)

<400> 103  
 gtgccgctgc tgttgaaaaa cgaagctttt ttaaaggaca ttttcccgga tatgccggaa 60  
 gaggatctgg cgcaattgaa agacgatctg gcgattgaaa tcagaacgga ttcacttttc 120  
 aacttaagct acacagggcc tgataaacag gaaacattgg atacttttagg aaaaattaaa 180  
 gatgcctata tgaaaggcga taaggcgctg ttctcaaaaa gagaagaagt cattgaaaag 240  
 aatattaagg cgcttgaaga cgaaacagtc agcgctgatt ccaaagttga caaacagcgg 300  
 tttttgtatg agcttgaaac aagcaagctt gatatgaagg ctgctgaaga aattgagccg 360  
 ttgatcgtgc ttgataacca ggctgccggc atgtcgctta agaaaagagc ggtgctgggc 420  
 gtactgatcg gtttagcgct gtcatttttc atcattgtca ttccggaagt tttcagagaa 480  
 cggttaaattt ttaattgggg atgtggatca ggacc atg acg agg caa aaa cct 533  
 Met Thr Arg Gln Lys Pro  
 1 5  
 tta atc tct gtc att acg cct tcc tat aac gcg gag gaa ttt atc gaa 581  
 Leu Ile Ser Val Ile Thr Pro Ser Tyr Asn Ala Glu Glu Phe Ile Glu  
 10 15 20  
 aaa acc att aag tcc gtc tta aat cag acg ttt tcc gac tgg gaa atg 629  
 Lys Thr Ile Lys Ser Val Leu Asn Gln Thr Phe Ser Asp Trp Glu Met  
 25 30 35  
 atc att gcc gat gat tgc tca aca gat ggg aca aga gac att ttg aag 677  
 Ile Ile Ala Asp Asp Cys Ser Thr Asp Gly Thr Arg Asp Ile Leu Lys  
 40 45 50  
 cgc tat gaa gaa gat gat gag cgg atc cat gcc att ttt ctg aaa gag 725  
 Arg Tyr Glu Glu Asp Asp Glu Arg Ile His Ala Ile Phe Leu Lys Glu  
 55 60 65 70  
 aat caa ggt gct gca gcg gcg cga aat gcg gcg ctc agc aaa gcc gaa 773  
 Asn Gln Gly Ala Ala Ala Ala Arg Asn Ala Ala Leu Ser Lys Ala Glu  
 75 80 85

ggg cgc tat gtc gcc ttt ttg gac agc gat gat gtt tgg aaa gca gaa	821
Gly Arg Tyr Val Ala Phe Leu Asp Ser Asp Asp Val Trp Lys Ala Glu	
90 95 100	
aag ctg gat aag cag ctc gcc ttc atg aga aag cat cag cat gct ttc	869
Lys Leu Asp Lys Gln Leu Ala Phe Met Arg Lys His Gln His Ala Phe	
105 110 115	
tca ttt acg gca tac gag ctg atc agc caa gac ggc gaa ccg ctt cat	917
Ser Phe Thr Ala Tyr Glu Leu Ile Ser Gln Asp Gly Glu Pro Leu His	
120 125 130	
aaa acc att cat gca ccc gta agc ctt aca tat gat gat gta tta aaa	965
Lys Thr Ile His Ala Pro Val Ser Leu Thr Tyr Asp Asp Val Leu Lys	
135 140 145 150	
aat acg atc atc ggc tgc ttg acg gtg atg att gac aga gaa caa acg	1013
Asn Thr Ile Ile Gly Cys Leu Thr Val Met Ile Asp Arg Glu Gln Thr	
155 160 165	
ggg gat atc cgg atg ccg aat att aga acc cgc cag gat ttg gcg aca	1061
Gly Asp Ile Arg Met Pro Asn Ile Arg Thr Arg Gln Asp Leu Ala Thr	
170 175 180	
tgg ctg tcc gta tta aag cgg ggg ttc aag gca tat gga ctg aac gaa	1109
Trp Leu Ser Val Leu Lys Arg Gly Phe Lys Ala Tyr Gly Leu Asn Glu	
185 190 195	
ccc ctc gcg gaa tac cgc atc gtt gaa aca tcg atc tcc aga aac aag	1157
Pro Leu Ala Glu Tyr Arg Ile Val Glu Thr Ser Ile Ser Arg Asn Lys	
200 205 210	
tgg aag gcg gcg cga aaa acc tgg tac gta tac agg gaa atc gaa cga	1205
Trp Lys Ala Ala Arg Lys Thr Trp Tyr Val Tyr Arg Glu Ile Glu Arg	
215 220 225 230	
ctt cac ttg atg aaa gcg aca tgg tgc ttt ttc cat tac gct aag aac	1253
Leu His Leu Met Lys Ala Thr Trp Cys Phe Phe His Tyr Ala Lys Asn	
235 240 245	
gca gta atg aaa aga tta taacggcatt gacagaaaag gtgattgaaa	1301
Ala Val Met Lys Arg Leu	
250	
gtgaaagcag atcaattcat acacgtcata gtagcgacag gtgaatgggg gcaggatcag	1361
ctaagataca gaaggcaccg ccttgctgag tttttagcag gccgcaagga gacgaaggaa	1421
gtcattttggg tttgtccgtc tgaaaatcct tcccgtgaga cttttacatt gcttgacaac	1481
ggaatcaagc aatttgagcgt caaagatttt ttgaaaaaga aaatattcag gtttgcccg	1541
tacaaagatg ttttctatca aagcaagctg aagccgctgc ttgaccggct gaaagaagac	1601
gttcagggag aaaagggtgtg cttatggtac accttccccg gctttccgct gctgtcgtcg	1661



ctttatcaat gggatcaggt catctatgac tgcagcgacc tgtgggcggc cccgatcagc 1721  
 ggtagccaaa gccttgtctc aggattcagg caaaagggtca tttttgaagc tga 1774

<210> 104  
 <211> 252  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 104

Met Thr Arg Gln Lys Pro Leu Ile Ser Val Ile Thr Pro Ser Tyr Asn  
 1 5 10 15

Ala Glu Glu Phe Ile Glu Lys Thr Ile Lys Ser Val Leu Asn Gln Thr  
 20 25 30

Phe Ser Asp Trp Glu Met Ile Ile Ala Asp Asp Cys Ser Thr Asp Gly  
 35 40 45

Thr Arg Asp Ile Leu Lys Arg Tyr Glu Glu Asp Asp Glu Arg Ile His  
 50 55 60

Ala Ile Phe Leu Lys Glu Asn Gln Gly Ala Ala Ala Arg Asn Ala  
 65 70 75 80

Ala Leu Ser Lys Ala Glu Gly Arg Tyr Val Ala Phe Leu Asp Ser Asp  
 85 90 95

Asp Val Trp Lys Ala Glu Lys Leu Asp Lys Gln Leu Ala Phe Met Arg  
 100 105 110

Lys His Gln His Ala Phe Ser Phe Thr Ala Tyr Glu Leu Ile Ser Gln  
 115 120 125

Asp Gly Glu Pro Leu His Lys Thr Ile His Ala Pro Val Ser Leu Thr  
 130 135 140

Tyr Asp Asp Val Leu Lys Asn Thr Ile Ile Gly Cys Leu Thr Val Met  
 145 150 155 160

Ile Asp Arg Glu Gln Thr Gly Asp Ile Arg Met Pro Asn Ile Arg Thr  
 165 170 175

Arg Gln Asp Leu Ala Thr Trp Leu Ser Val Leu Lys Arg Gly Phe Lys

180

185

190

Ala Tyr Gly Leu Asn Glu Pro Leu Ala Glu Tyr Arg Ile Val Glu Thr  
 195 200 205

Ser Ile Ser Arg Asn Lys Trp Lys Ala Ala Arg Lys Thr Trp Tyr Val  
 210 215 220

Tyr Arg Glu Ile Glu Arg Leu His Leu Met Lys Ala Thr Trp Cys Phe  
 225 230 235 240

Phe His Tyr Ala Lys Asn Ala Val Met Lys Arg Leu  
 245 250

&lt;210&gt; 105

&lt;211&gt; 1309

&lt;212&gt; DNA

&lt;213&gt; Bacillus licheniformis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (485)..(808)

&lt;400&gt; 105

tgatgaagcg gtgaaccgct ttaaagatat accgaaagag cgccgcgtcc ttgtgacaag 60

cgaaggggct tttaaattatt tcgcttcggc ctacggcgctc gacgcgcagt atatttggga 120

aatcaacacc gaaaatgaag gaactcccgg tcagatgaaa aaaatcgtcg acacagtgaa 180

gaaaaaggac gtccccggcct tattcgtgga gacaagcggt gacccgcgga gcatggaaa 240

cctttcagcc gaaacggggcg tgccgattaa agcaaaagtc ttcaccgatt cgatcgga 300

gcccgggtga agcgggagat tcctattata agatgatgaa agaaaacctt gaccggatcc 360

atcaaggcct cgccgaataa ccaatgaact gctgtacagg atgtacagca gtttttttct 420

tatgtttttc cgatttttaa gcagggtaca acgaagggaa aacgaggaaa aaggagtgtg 480

tttc gtg aaa tct gga tat gag gaa tgc atc aaa gcc tgc cga gaa tgt 529

Val Lys Ser Gly Tyr Glu Glu Cys Ile Lys Ala Cys Arg Glu Cys  
 1 5 10 15

ctt gaa gcc tgc aac cac tgc ttt gac aaa tgt ctg atg gaa gaa gag 577

Leu Glu Ala Cys Asn His Cys Phe Asp Lys Cys Leu Met Glu Glu Glu  
 20 25 30

gct ggg atg atg gcc gaa tgc atc cgt ctt gac cgg gaa tgc gcg gag 625

Ala Gly Met Met Ala Glu Cys Ile Arg Leu Asp Arg Glu Cys Ala Glu  
 35 40 45

atg tgc ggt tac gca att caa gcc atg acg cgc aac agc ccg tat gcc 673  
Met Cys Gly Tyr Ala Ile Gln Ala Met Thr Arg Asn Ser Pro Tyr Ala  
50 55 60

gaa gat att tgc cag ctt tgc gca aag gtt tgc gaa gct tgc ggc aat 721  
Glu Asp Ile Cys Gln Leu Cys Ala Lys Val Cys Glu Ala Cys Gly Asn  
65 70 75

gaa tgc agc cag cac aag cat gac cac tgc caa ttt tgc gct gaa agc 769  
Glu Cys Ser Gln His Lys His Asp His Cys Gln Phe Cys Ala Glu Ser  
80 85 90 95

tgc ttt gca tgc gcg gaa gcg tgc aga aaa atg gct tct taacttgaaa 818  
Cys Phe Ala Cys Ala Glu Ala Cys Arg Lys Met Ala Ser  
100 105

catccggccc tcgagccgga tattttttatg taggaaatgt ttatttttttc tccttcccc 878

tttctaaact gatacaatat gactataaaa ggggggtttta tcatgaaaga cagcgtgttt 938

caaatgactt ctgacacata tcaatctctc agcgattcag aacggcattt gctcgagtac 998

atztatcagc acttagacgt catcgccact ttatcgattg taaaattaag cgaggatgca 1058

aatgtttcaa cagccacgat tgtcagggtta atgaaaaaac tcggatatga cggctacact 1118

tcttttaagt atgcattaaa agaaaaacac cacctcggac acgctccgct gatggatgat 1178

atcgacagcc aaattaaaca ggccgtgcta aagaatgaaa gagaagttct ggatacgatt 1238

aagatgcttg atatcgggtt gatcgaagat gccattcaaa aaatcagcaa tgccgaaaaa 1298

gtttacatct t 1309

<210> 106

<211> 108

<212> PRT

<213> Bacillus licheniformis

<400> 106

Val Lys Ser Gly Tyr Glu Glu Cys Ile Lys Ala Cys Arg Glu Cys Leu  
1 5 10 15

Glu Ala Cys Asn His Cys Phe Asp Lys Cys Leu Met Glu Glu Glu Ala  
20 25 30

Gly Met Met Ala Glu Cys Ile Arg Leu Asp Arg Glu Cys Ala Glu Met  
35 40 45

Cys Gly Tyr Ala Ile Gln Ala Met Thr Arg Asn Ser Pro Tyr Ala Glu  
50 55 60

Asp Ile Cys Gln Leu Cys Ala Lys Val Cys Glu Ala Cys Gly Asn Glu  
65 70 75 80

Cys Ser Gln His Lys His Asp His Cys Gln Phe Cys Ala Glu Ser Cys  
85 90 95

Phe Ala Cys Ala Glu Ala Cys Arg Lys Met Ala Ser  
100 105

<210> 107  
<211> 1561  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (284)..(1060)

<400> 107  
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ctcgggatct tcaccggata tgtactatgg catccttttg ccaataaaatt aaagcggaaa 120  
tccaaacagg aagtcaaagt ccgcgaagtt atgattgaag gcatcctttc gatcttgtaa 180  
ggccaggctc caaaagtcac tgaacaaaag cttttgatgt acgtttctcc aagcgaacgc 240  
tccagcatcg tcatcccaga tggagacaaa ggggacagca gca atg gct aga aaa 295  
Met Ala Arg Lys  
1  
aag aag cac aaa aaa gac cat gaa gaa cac gtg gat gag tct tgg ctc 343  
Lys Lys His Lys Lys Asp His Glu Glu His Val Asp Glu Ser Trp Leu  
5 10 15 20  
atc cca tat gca gac ttg ctg aca ctg ctt ttg gcc ctg ttc atc gta 391  
Ile Pro Tyr Ala Asp Leu Leu Thr Leu Leu Leu Ala Leu Phe Ile Val  
25 30 35  
ctg ttt gcc atg agc tcg atc gac gcc aag aag ttc gat atg ctg tca 439  
Leu Phe Ala Met Ser Ser Ile Asp Ala Lys Lys Phe Asp Met Leu Ser  
40 45 50  
aaa tca ttt aat gcc gta ttt acc ggc gga aca gga atg atg gat tat 487  
Lys Ser Phe Asn Ala Val Phe Thr Gly Gly Thr Gly Met Met Asp Tyr  
55 60 65  
tcc agc ttc acc gag ccg aaa acg agc aca acc gaa gat gga aaa agc 535  
Ser Ser Phe Thr Glu Pro Lys Thr Ser Thr Thr Glu Asp Gly Lys Ser  
70 75 80

cct gac cag gca aaa gat ctc tcc gaa gct caa aaa gaa aaa gac aag	583
Pro Asp Gln Ala Lys Asp Leu Ser Glu Ala Gln Lys Glu Lys Asp Lys	
85 90 95 100	
cag tcg ctg aaa aaa att cag gag cag gtc aac cgg ttt att aaa gag	631
Gln Ser Leu Lys Lys Ile Gln Glu Gln Val Asn Arg Phe Ile Lys Glu	
105 110 115	
aag aat ctt caa aaa cag gtc aat acg aag ctg aca gac gag ggc ctc	679
Lys Asn Leu Gln Lys Gln Val Asn Thr Lys Leu Thr Asp Glu Gly Leu	
120 125 130	
ctc ctt tcc atc gag gat aat atc ttt ttc gat tcc gga aaa gcg gag	727
Leu Leu Ser Ile Glu Asp Asn Ile Phe Phe Asp Ser Gly Lys Ala Glu	
135 140 145	
atc cgc cag cag gac att ccg ctg gcc aag gaa gta tcc gac ctt ctc	775
Ile Arg Gln Gln Asp Ile Pro Leu Ala Lys Glu Val Ser Asp Leu Leu	
150 155 160	
gta ttg aac ccg ccc cgc aat atc gta atc agc ggg cat acg gac aat	823
Val Leu Asn Pro Pro Arg Asn Ile Val Ile Ser Gly His Thr Asp Asn	
165 170 175 180	
gtg ccg att cga aat tct caa ttt aaa tca aat tgg cat tta agc gtg	871
Val Pro Ile Arg Asn Ser Gln Phe Lys Ser Asn Trp His Leu Ser Val	
185 190 195	
atg cgg gct gtc aat ttc atg ggg ctt tta atc gaa aat cca aag ctt	919
Met Arg Ala Val Asn Phe Met Gly Leu Leu Ile Glu Asn Pro Lys Leu	
200 205 210	
gac gcc aag atc ttc agc gcg aaa ggc tac ggg gaa ttt aaa ccg atc	967
Asp Ala Lys Ile Phe Ser Ala Lys Gly Tyr Gly Glu Phe Lys Pro Ile	
215 220 225	
gct tca aat gac acc gaa gaa gga aga aga aaa aac aga cgc gtt gaa	1015
Ala Ser Asn Asp Thr Glu Glu Gly Arg Arg Lys Asn Arg Arg Val Glu	
230 235 240	
atc ctt atc ctg ccg atc ggc cag gaa aat ctg aat aaa aaa gaa	1060
Ile Leu Ile Leu Pro Ile Gly Gln Glu Asn Leu Asn Lys Lys Glu	
245 250 255	
taaggaagct gtcttttggc agcttcctta ctctttgccc ttataaatat ttcttgcatt	1120
cagtccgact tttttcagca tttcgatgca ggcttctttc tcctcatcgc ttaatacgct	1180
gatcatgttg tgcagctctt ctgcatgacc cggaataatc ttctcgagga gctcgggtgcc	1240
tttatctgta atttgcgcat aggtcaccct gcggtctgtc gtacaggctc ttctcgtgat	1300
cagctgcttt tgctcaagct tgtcaaccac atatgtaata ctcccgtcg ccagaagaat	1360
cttatcccct atttgctgaa ggggctgatc ccctttatga tagaggagtt ctaaaacggc	1420
aaactcgggt ggattcagac catgatgatg aatatgttta ttcatatgat cattaatgga	1480

tctgtacgct cgagataata caataaataa cttcaaggac tgttcctggt ctctattact 1540  
 catatcactc atctccaaag a 1561

<210> 108  
 <211> 259  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 108

Met Ala Arg Lys Lys Lys His Lys Lys Asp His Glu Glu His Val Asp  
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Glu Ser Trp Leu Ile Pro Tyr Ala Asp Leu Leu Thr Leu Leu Leu Ala  
 20 25 30

Leu Phe Ile Val Leu Phe Ala Met Ser Ser Ile Asp Ala Lys Lys Phe  
 35 40 45

Asp Met Leu Ser Lys Ser Phe Asn Ala Val Phe Thr Gly Gly Thr Gly  
 50 55 60

Met Met Asp Tyr Ser Ser Phe Thr Glu Pro Lys Thr Ser Thr Thr Glu  
 65 70 75 80

Asp Gly Lys Ser Pro Asp Gln Ala Lys Asp Leu Ser Glu Ala Gln Lys  
 85 90 95

Glu Lys Asp Lys Gln Ser Leu Lys Lys Ile Gln Glu Gln Val Asn Arg  
 100 105 110

Phe Ile Lys Glu Lys Asn Leu Gln Lys Gln Val Asn Thr Lys Leu Thr  
 115 120 125

Asp Glu Gly Leu Leu Leu Ser Ile Glu Asp Asn Ile Phe Phe Asp Ser  
 130 135 140

Gly Lys Ala Glu Ile Arg Gln Gln Asp Ile Pro Leu Ala Lys Glu Val  
 145 150 155 160

Ser Asp Leu Leu Val Leu Asn Pro Pro Arg Asn Ile Val Ile Ser Gly  
 165 170 175

His Thr Asp Asn Val Pro Ile Arg Asn Ser Gln Phe Lys Ser Asn Trp  
 180 185 190

His Leu Ser Val Met Arg Ala Val Asn Phe Met Gly Leu Leu Ile Glu  
 195 200 205

Asn Pro Lys Leu Asp Ala Lys Ile Phe Ser Ala Lys Gly Tyr Gly Glu  
 210 215 220

Phe Lys Pro Ile Ala Ser Asn Asp Thr Glu Glu Gly Arg Arg Lys Asn  
 225 230 235 240

Arg Arg Val Glu Ile Leu Ile Leu Pro Ile Gly Gln Glu Asn Leu Asn  
 245 250 255

Lys Lys Glu

<210> 109  
 <211> 1735  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1232)

<400> 109  
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 tgcgggcaaa acatttttaa tagatccgat gctggctgaa aaaggcgctt accctccttt 120  
 cccgaactca gcaagacaag agcaaaacaa ccctttggtc agcctgcctg tgccaaccga 180  
 cgagctcgtc aagaatacag acgcagtcac cgtcactcat tcggacccgg atttctctcc 240  
 tataaactag aagcctcatg ttgaaaaagt attttatatt gaaaaagaat tctatctggg 300  
 acctcgccgg gagcaggaaa gaggatcact gaaacatcaa tgaattatat tgtaaaaaat 360  
 cagaatttta tataaaatca aactttatca gtaaaaaaac tgtaacgaaa ttcgcatcaa 420  
 tctgtcatag cggtgacatt ttgctgtggt acgattttcc ctgttagttt caaaagggct 480  
 aacaaggagg gatttaactt atg aag aag aca atc atg tcc ttg gct gca gcc 533  
 Met Lys Lys Thr Ile Met Ser Leu Ala Ala Ala  
 1 5 10  
 gcg gct atg tcg gcg act gca ttc gga gcg act gcc tca gca aaa gaa 581  
 Ala Ala Met Ser Ala Thr Ala Phe Gly Ala Thr Ala Ser Ala Lys Glu

15	20	25	
atc gaa gtt caa aaa gga gac acg ctc tgg ggg att tct caa aac tac Ile Glu Val Gln Lys Gly Asp Thr Leu Trp Gly Ile Ser Gln Asn Tyr 30 35 40			629
gga atg aac ctc aag gac tta aaa aaa tgg aat cag ctt tca tca gat Gly Met Asn Leu Lys Asp Leu Lys Lys Trp Asn Gln Leu Ser Ser Asp 45 50 55			677
ctg att ttt cca ggt caa aag ctg aac att tct tct caa gaa gaa aaa Leu Ile Phe Pro Gly Gln Lys Leu Asn Ile Ser Ser Gln Glu Glu Lys 60 65 70 75			725
tct gaa gaa aag cag tac acc gtt cag cca ggg gac acg ctc tca aaa Ser Glu Glu Lys Gln Tyr Thr Val Gln Pro Gly Asp Thr Leu Ser Lys 80 85 90			773
atc gca aaa gag ttc ggt gtg act gta agc gat ctt caa aaa cgg aac Ile Ala Lys Glu Phe Gly Val Thr Val Ser Asp Leu Gln Lys Arg Asn 95 100 105			821
aac ctg aag tca gac ttg att att gca ggg caa acg att gca ata aac Asn Leu Lys Ser Asp Leu Ile Ile Ala Gly Gln Thr Ile Ala Ile Asn 110 115 120			869
gga gaa gcg gca gct gca gca gcg cct gtg aaa caa gag tcc gct cca Gly Glu Ala Ala Ala Ala Ala Pro Val Lys Gln Glu Ser Ala Pro 125 130 135			917
aaa caa aat gat cag cct gtc aac gta caa aag gaa atc aca gtg acc Lys Gln Asn Asp Gln Pro Val Asn Val Gln Lys Glu Ile Thr Val Thr 140 145 150 155			965
gca act gcg tat acg gca aat gac ggg ggc att tca ggc atc aca aaa Ala Thr Ala Tyr Thr Ala Asn Asp Gly Gly Ile Ser Gly Ile Thr Lys 160 165 170			1013
acg gga gtc gac ctg aat gcg aac cgc aat gcg aaa gtc atc gcg gtt Thr Gly Val Asp Leu Asn Ala Asn Arg Asn Ala Lys Val Ile Ala Val 175 180 185			1061
gat cca agc gtg att ccg ctc ggc acg aaa gta tat gtg gaa ggc tat Asp Pro Ser Val Ile Pro Leu Gly Thr Lys Val Tyr Val Glu Gly Tyr 190 195 200			1109
ggc gaa gcg acg gct gaa gac acc ggc ggc gcc att aaa ggc cat aaa Gly Glu Ala Thr Ala Glu Asp Thr Gly Gly Ala Ile Lys Gly His Lys 205 210 215			1157
ata gac gta ttt att cca gat aaa aaa gac gct ttc aat tgg ggc gtc Ile Asp Val Phe Ile Pro Asp Lys Lys Asp Ala Phe Asn Trp Gly Val 220 225 230 235			1205
aaa acc gta aag gtt aaa att tta aac tgatataaaa aatgcaggag Lys Thr Val Lys Val Lys Ile Leu Asn 240			1252



gcgttaattg cctcctgcat ttttttgtcg aacgatgttt atgctgcatg ctgttccgcg 1312  
 cgtctgcttt ttacaaaaac cgaaatcgca agagcggcgg ctgcaaaggc gatggctacg 1372  
 aaataaacca tatgaacgcc ttctgtcatg ccttgcattg gcagctcctg acggctgcct 1432  
 ccggaagagt gcgcgataaa gcgattcgaa acggttgta ggcgcgtcgt atacaatgcc 1492  
 ggaccgattg cccctgaaac ttgattaact gtattcatta tcgccgaacc atgcgggtaa 1552  
 agcggtttgg gcacctgatt caaacggagc gtcataatcg gagccattgt caacccgacg 1612  
 ccgagtgtaa agccggcgta gagcatcatt ccgaccgcca tcggcgtatc gcttgaaata 1672  
 ttcgtaaaca gcgaaaggac ggcaatcaca atgatcaatc cggtgatcaa cagcgggtta 1732  
 aag 1735

<210> 110  
 <211> 244  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 110

Met Lys Lys Thr Ile Met Ser Leu Ala Ala Ala Ala Met Ser Ala  
 1 5 10 15

Thr Ala Phe Gly Ala Thr Ala Ser Ala Lys Glu Ile Glu Val Gln Lys  
 20 25 30

Gly Asp Thr Leu Trp Gly Ile Ser Gln Asn Tyr Gly Met Asn Leu Lys  
 35 40 45

Asp Leu Lys Lys Trp Asn Gln Leu Ser Ser Asp Leu Ile Phe Pro Gly  
 50 55 60

Gln Lys Leu Asn Ile Ser Ser Gln Glu Glu Lys Ser Glu Glu Lys Gln  
 65 70 75 80

Tyr Thr Val Gln Pro Gly Asp Thr Leu Ser Lys Ile Ala Lys Glu Phe  
 85 90 95

Gly Val Thr Val Ser Asp Leu Gln Lys Arg Asn Asn Leu Lys Ser Asp  
 100 105 110

Leu Ile Ile Ala Gly Gln Thr Ile Ala Ile Asn Gly Glu Ala Ala Ala  
 115 120 125

Ala Ala Ala Pro Val Lys Gln Glu Ser Ala Pro Lys Gln Asn Asp Gln  
 130 135 140

Pro Val Asn Val Gln Lys Glu Ile Thr Val Thr Ala Thr Ala Tyr Thr  
 145 150 155 160

Ala Asn Asp Gly Gly Ile Ser Gly Ile Thr Lys Thr Gly Val Asp Leu  
 165 170 175

Asn Ala Asn Arg Asn Ala Lys Val Ile Ala Val Asp Pro Ser Val Ile  
 180 185 190

Pro Leu Gly Thr Lys Val Tyr Val Glu Gly Tyr Gly Glu Ala Thr Ala  
 195 200 205

Glu Asp Thr Gly Gly Ala Ile Lys Gly His Lys Ile Asp Val Phe Ile  
 210 215 220

Pro Asp Lys Lys Asp Ala Phe Asn Trp Gly Val Lys Thr Val Lys Val  
 225 230 235 240

Lys Ile Leu Asn

<210> 111  
 <211> 1731  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
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 <222> (507) .. (1274)

<400> 111  
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 agaatatcct acaggcaagc gcaaaaaaca atgattcaag aggaaatcaa tcgttttgaa 180  
 cgaccatata aaataagagc attctttttt aagcaacgtc tttggtttct tcggccgctt 240  
 ttgcatcagc cccgctggac gtttaaaaga aagaagaaaa gccggaaggg gatatacataa 300  
 gctgagatgc gagattattc agaaaagccc ggatgtatgg cccagctgg aagagtga 360

tcaaggggaa cggttttttaa gatcatggac cagcagtatg ccattatctt attttcga	420
gcaaataaaa gacgttttct gtttaaagaa aacgtctttt tgcatacaagc cgtcttatca	480
taacaaaaaac agattggaga atgcac atg atc tcg tgg ctc agt ctg gct tcg	533
Met Ile Ser Trp Leu Ser Leu Ala Ser	
1 5	
gcc gct ttc atc ggc ctt gct gct tta gtg tgg aga atg tca gcc atc	581
Ala Ala Phe Ile Gly Leu Ala Ala Leu Val Trp Arg Met Ser Ala Ile	
10 15 20 25	
gcg cgc gaa aac cgg gtg ttg aag gct gaa ttt tca ctc ggg cgc ctg	629
Ala Arg Glu Asn Arg Val Leu Lys Ala Glu Phe Ser Leu Gly Arg Leu	
30 35 40	
aaa aag gaa ttg aat gtc ttt ttt att tca gat att cat agg cgg aca	677
Lys Lys Glu Leu Asn Val Phe Phe Ile Ser Asp Ile His Arg Arg Thr	
45 50 55	
gtc agc gaa gac att att tgt gaa gtg aaa gaa cgc ggg gtt cag ctc	725
Val Ser Glu Asp Ile Ile Cys Glu Val Lys Glu Arg Gly Val Gln Leu	
60 65 70	
gtc atc atc ggc ggc gac tta gca gag ggc ggc gtc cct tat acg aga	773
Val Ile Ile Gly Gly Asp Leu Ala Glu Gly Gly Val Pro Tyr Thr Arg	
75 80 85	
att gaa gaa aat atc aaa agg ctt tca agt ttg gga aaa acg tat ttt	821
Ile Glu Glu Asn Ile Lys Arg Leu Ser Ser Leu Gly Lys Thr Tyr Phe	
90 95 100 105	
gta tgg gga aat aac gat tat gaa gtt gat cag gaa agg ctg ctg gaa	869
Val Trp Gly Asn Asn Asp Tyr Glu Val Asp Gln Glu Arg Leu Leu Glu	
110 115 120	
ata ttc aag aca tac ggt gta acg cct ttg cgc aat gct tcg gta ttg	917
Ile Phe Lys Thr Tyr Gly Val Thr Pro Leu Arg Asn Ala Ser Val Leu	
125 130 135	
cat gac cat caa gga caa act gtc aat att tgc gga gtg gat gac atc	965
His Asp His Gln Gly Gln Thr Val Asn Ile Cys Gly Val Asp Asp Ile	
140 145 150	
aga ctc gaa ttg gat gat tac ccg gca gct ctc ggc ggc gtg cag ccg	1013
Arg Leu Glu Leu Asp Asp Tyr Pro Ala Ala Leu Gly Gly Val Gln Pro	
155 160 165	
ggt ttt ccg act gtc ctt gtg tca cat aat ccg gag att cat cat caa	1061
Gly Phe Pro Thr Val Leu Val Ser His Asn Pro Glu Ile His His Gln	
170 175 180 185	
ata cag gag gcg gac ggt att gac ctg ata ttg agc ggt cat acc cac	1109
Ile Gln Glu Ala Asp Gly Ile Asp Leu Ile Leu Ser Gly His Thr His	
190 195 200	
gga gga cag att cgc ttc ggc aga ttc ggg ctc tgt gaa atc gga gga	1157

Gly Gly Gln Ile Arg Phe Gly Arg Phe Gly Leu Cys Glu Ile Gly Gly  
 205 210 215  
 acc ggc act gtt ttc aag gct ccg tac ttg atc agc aac ggc tat gga 1205  
 Thr Gly Thr Val Phe Lys Ala Pro Tyr Leu Ile Ser Asn Gly Tyr Gly  
 220 225 230  
 acg tcg aag ctt cct gcg ggg atc cta ggc gtg ccc gcg atc gcc atg 1253  
 Thr Ser Lys Leu Pro Ala Gly Ile Leu Gly Val Pro Ala Ile Ala Met  
 235 240 245  
 gct tat gtc gga gag gaa ttt gatccgcgag ggctcggcaa aatgatggg 1304  
 Ala Tyr Val Gly Glu Glu Phe  
 250 255  
 ctatacatta gcggcacaag cctcggagga atgagcggaa ggcttttgac cggccttttg 1364  
 acagacttgt tcagctggcg cgcggcgcta ggaatcatcg gggcattatc agtactatta 1424  
 agctatttgt tttggatttt gctgccccgg ccgcagcact ccgctaagcg aaaaacaagt 1484  
 gtgaaaaaag cgagcttggc ctacggcgcc gtcttgatga acaaacggct gctgtcaatc 1544  
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 cagttgatgg gacctccgta cagactctct caaactgtca tcgggttcat ctttatcggt 1664  
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 ccgttga 1731  
  
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 <212> PRT  
 <213> Bacillus licheniformis  
  
 <400> 112  
  
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 20 25 30  
  
 Lys Ala Glu Phe Ser Leu Gly Arg Leu Lys Lys Glu Leu Asn Val Phe  
 35 40 45  
  
 Phe Ile Ser Asp Ile His Arg Arg Thr Val Ser Glu Asp Ile Ile Cys  
 50 55 60  
  
 Glu Val Lys Glu Arg Gly Val Gln Leu Val Ile Ile Gly Gly Asp Leu  
 65 70 75 80

Ala Glu Gly Gly Val Pro Tyr Thr Arg Ile Glu Glu Asn Ile Lys Arg  
85 90 95

Leu Ser Ser Leu Gly Lys Thr Tyr Phe Val Trp Gly Asn Asn Asp Tyr  
100 105 110

Glu Val Asp Gln Glu Arg Leu Leu Glu Ile Phe Lys Thr Tyr Gly Val  
115 120 125

Thr Pro Leu Arg Asn Ala Ser Val Leu His Asp His Gln Gly Gln Thr  
130 135 140

Val Asn Ile Cys Gly Val Asp Asp Ile Arg Leu Glu Leu Asp Asp Tyr  
145 150 155 160

Pro Ala Ala Leu Gly Gly Val Gln Pro Gly Phe Pro Thr Val Leu Val  
165 170 175

Ser His Asn Pro Glu Ile His His Gln Ile Gln Glu Ala Asp Gly Ile  
180 185 190

Asp Leu Ile Leu Ser Gly His Thr His Gly Gly Gln Ile Arg Phe Gly  
195 200 205

Arg Phe Gly Leu Cys Glu Ile Gly Gly Thr Gly Thr Val Phe Lys Ala  
210 215 220

Pro Tyr Leu Ile Ser Asn Gly Tyr Gly Thr Ser Lys Leu Pro Ala Gly  
225 230 235 240

Ile Leu Gly Val Pro Ala Ile Ala Met Ala Tyr Val Gly Glu Glu Phe  
245 250 255

<210> 113  
<211> 1722  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (540) .. (788)

<400> 113

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acataaaaaa gctcttcccg ataaggaaga gcttgatata ttcaatctcc tccttatctt 120  
caagagcacg aacatgctct taaggattta gcaccattct gtcatagaca gcggttgccg 180  
ggtttcacag ggccagtccc tccaccactc ttgataagga aaaccttttt atgcgatttt 240  
ttaatagttt taatattaat actttttata aaaatgtcaa tgggtttaaa aaaactcttc 300  
gtttttttca ttttcttctt ctgcggttaa actggagggc gtatcgaatc aatgtgtgaa 360  
tttttcgtca ggacagccgt tcaaacagtc aacaagatgc tgaacaaaca gaataaatta 420  
gaattttttt caatttttat ttccaaaaac agaaactttt tattgagttc accggtctat 480  
aatgtgtacc tgatttcaaa atgggtatta taaaaaatga cagattaagg agggttttt 539  
atg aac aaa aaa aca gtg ttt aaa gcg ttc gga atg ttg atg aca ggg 587  
Met Asn Lys Lys Thr Val Phe Lys Ala Phe Gly Met Leu Met Thr Gly  
1 5 10 15  
gta ttg ttt ttt gcg ctg tac agt gcg gcc gca ctt cct tct gca cac 635  
Val Leu Phe Phe Ala Leu Tyr Ser Ala Ala Ala Leu Pro Ser Ala His  
20 25 30  
gcg gca aac gaa aaa aaa ccg acg gtc acg agc cat acg tac aaa aac 683  
Ala Ala Asn Glu Lys Lys Pro Thr Val Thr Ser His Thr Tyr Lys Asn  
35 40 45  
att aag gct ttg aaa tac ccg caa gtt tca aat gta agc ccc aaa tct 731  
Ile Lys Ala Leu Lys Tyr Pro Gln Val Ser Asn Val Ser Pro Lys Ser  
50 55 60  
ctc caa aac aag atc aac aaa gat ttt aaa cat tat att gag cag tcc 779  
Leu Gln Asn Lys Ile Asn Lys Asp Phe Lys His Tyr Ile Glu Gln Ser  
65 70 75 80  
tac aaa gat tagtaaaaaa caagaaagac ggccaacagc acggatacca 828  
Tyr Lys Asp  
aacggattat caaacgtcct ttgaagtga ataccggacc ggccaaaagc tgagcatcct 888  
gacaagcaat tacgtctatt ccggcggagc gcacggaaat acggcagtcc gctctttcaa 948  
ctatgacctt gtctctaaaa aacgggtgta tttatccgac atcctaaata caaaatcgaa 1008  
aatggataag acaaaaaacat acatttaca ctatattcaa aaacacagcg acattttctt 1068  
tccggatgtg aagaagaaag acatcgtcct cggtaaaaac acggccttct attacactaa 1128  
cgacggcatt gcgatcgtct tccaacaata cgatgtcgcc ccttatgccg ccggaaatcc 1188  
ggtcgttgca gttccgaaaa cgggtgtatc ataaataaca accggggggt tagtccttgt 1248  
gcatcgctg tgacccgaac ccgaaaaaac ggaagaagag ctgaatctga tcgtcgactt 1308

tggcgtaacg gtgaaagatg taacgattga acatccggtc tacggagact taacagcttc 1368  
 gatcagggtc agcacaagaa aagaagtcgc ggatttcgtc aaaaaaatct cttcgacaaa 1428  
 cgccgcttat ctgtctcagc tgacaaacgg catccatctc cacacattgg aggagatga 1488  
 tgaagagaag atcgaacaag cttgcggcgc cctgcaaaaa gcgggcatcc tcattcccga 1548  
 ataaaagaaa aggtcctttg ccgttatcag cgcaaaggac ctttctttta tagtgtatat 1608  
 gcgttgtagg caccgagcat tttcaccttg cagcccaaag cttcaagctc agctattgca 1668  
 cctggaatca gcacgtcatc cagggccatt tcaatatcaa taatgaagaa ataa 1722

<210> 114  
 <211> 83  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 114

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 1 5 10 15

Val Leu Phe Phe Ala Leu Tyr Ser Ala Ala Ala Leu Pro Ser Ala His  
 20 25 30

Ala Ala Asn Glu Lys Lys Pro Thr Val Thr Ser His Thr Tyr Lys Asn  
 35 40 45

Ile Lys Ala Leu Lys Tyr Pro Gln Val Ser Asn Val Ser Pro Lys Ser  
 50 55 60

Leu Gln Asn Lys Ile Asn Lys Asp Phe Lys His Tyr Ile Glu Gln Ser  
 65 70 75 80

Tyr Lys Asp

<210> 115  
 <211> 1705  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (507)..(1202)

<400> 115  
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tagaaaacta ccctgaaaaa gggcggcagg aaaaagtcgt tctcccctct ctagtgcgca 180  
gaaaggggtac gaaagcaata tttaaagacg gcatttttga agtgatgttc ttaaaaaatg 240  
aggactttta cctgtctgaa atcgacatca cgttttgaaa acggccagct tgaaaaagca 300  
ggctgttttt tttcttctg tatcatctta acactactcc tcaaggatga tcatctcatt 360  
tgccctgacat tcggccgcgc ctttaaattt tgacagtgtt agtcattatt ccttaaaaag 420  
tctctgtaac tatttcctct ttccggctgtt gtcgatttgt ccttataatg ataatgggtc 480  
tcaatttata aaacaggagg atgtat atg aaa aag aaa atc agc ata ttg atc 533  
Met Lys Lys Lys Ile Ser Ile Leu Ile  
1 5  
aca gca atg ttt ttg aca atc ctt tgt ttt tcg cct caa gct tcc gct 581  
Thr Ala Met Phe Leu Thr Ile Leu Cys Phe Ser Pro Gln Ala Ser Ala  
10 15 20 25  
gcg tac aac tca ctg cat acg ggc tat gcc act tat acg ggg tcg ggc 629  
Ala Tyr Asn Ser Leu His Thr Gly Tyr Ala Thr Tyr Thr Gly Ser Gly  
30 35 40  
tac tcc ggc ggc gca ttg ctt ttg gac cct att ccg tcc aat atg aag 677  
Tyr Ser Gly Gly Ala Leu Leu Leu Asp Pro Ile Pro Ser Asn Met Lys  
45 50 55  
atc acc gct tta aat ccg aca gat atg aat tac cgc ggt gtg aaa gct 725  
Ile Thr Ala Leu Asn Pro Thr Asp Met Asn Tyr Arg Gly Val Lys Ala  
60 65 70  
gct ctt gcc ggc gcc tat ctg cgg gtt gaa ggg ccg aaa gga aaa acg 773  
Ala Leu Ala Gly Ala Tyr Leu Arg Val Glu Gly Pro Lys Gly Lys Thr  
75 80 85  
acc gtc tat gtt acc gat ctg tat cct gaa gga gcg ccg gga gcc ctt 821  
Thr Val Tyr Val Thr Asp Leu Tyr Pro Glu Gly Ala Pro Gly Ala Leu  
90 95 100 105  
gac ctt tca ccg aac gct ttt cgc gag atc ggc gat atg aaa gac ggc 869  
Asp Leu Ser Pro Asn Ala Phe Arg Glu Ile Gly Asp Met Lys Asp Gly  
110 115 120  
aaa atc gac att aaa tgg cgt ata gtc aaa gcg ccg att acc ggc aat 917  
Lys Ile Asp Ile Lys Trp Arg Ile Val Lys Ala Pro Ile Thr Gly Asn  
125 130 135  
ttc act tac cgg atc aaa gaa ggc agc agc caa tgg tgg gcg gcg atc 965  
Phe Thr Tyr Arg Ile Lys Glu Gly Ser Ser Gln Trp Trp Ala Ala Ile  
140 145 150



caa gtc aga aac cac aaa tat ccc gtc atg aaa atg gaa tat tac aaa 1013  
 Gln Val Arg Asn His Lys Tyr Pro Val Met Lys Met Glu Tyr Tyr Lys  
 155 160 165

gac gga aag tgg atc aac atg gag aaa acg gat tac aac cat ttc gtc 1061  
 Asp Gly Lys Trp Ile Asn Met Glu Lys Thr Asp Tyr Asn His Phe Val  
 170 175 180 185

agc acc aat ctc ggg aca agt ccg ctt aaa gtc agg atc aca gat atc 1109  
 Ser Thr Asn Leu Gly Thr Ser Pro Leu Lys Val Arg Ile Thr Asp Ile  
 190 195 200

cga gga aaa gtc gtc aaa gac acg ata aaa aag ctt ccg gaa aac ggg 1157  
 Arg Gly Lys Val Val Lys Asp Thr Ile Lys Lys Leu Pro Glu Asn Gly  
 205 210 215

acg tca agc gca tat acc gta ccg gga aaa gta cag ttc cct gac 1202  
 Thr Ser Ser Ala Tyr Thr Val Pro Gly Lys Val Gln Phe Pro Asp  
 220 225 230

tgatcgatcc ggaaagaatg agacggcggc caaaggcgaa aagattcgca ggctttggcc 1262

gccgcttcat attgacatcc ggcatttaga cgccagcaac aattggctta ttgatcaata 1322

gcccggtcct gtcctctgt atggagctgc gcccggaaca cctccgtacg gaaaagcccc 1382

aggagctgcc ccgtagccgt aataaggcgc gccgccgtaa ggtcccgggt atggcggcgg 1442

gtaagcgtaa ggtcttgggt agttaaaaat cgcgcttccg agaaatccgc ccagcaatcc 1502

gccgacaagc ggcgctccaa aacccagaa taacgggaat ctggccgggt atccggcagg 1562

acctgatctc gaataaagca tatgagggtt cattggcttt taccctcctt tatgtctgcc 1622

tatagtaaag gtattcataa agtcgggaaa cgtttgggct attcttcata aatcattttt 1682

tttgtcattc cgccgtccac cgt 1705

<210> 116

<211> 232

<212> PRT

<213> Bacillus licheniformis

<400> 116

Met Lys Lys Lys Ile Ser Ile Leu Ile Thr Ala Met Phe Leu Thr Ile  
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Leu Cys Phe Ser Pro Gln Ala Ser Ala Ala Tyr Asn Ser Leu His Thr  
 20 25 30

Gly Tyr Ala Thr Tyr Thr Gly Ser Gly Tyr Ser Gly Gly Ala Leu Leu  
 35 40 45

Leu Asp Pro Ile Pro Ser Asn Met Lys Ile Thr Ala Leu Asn Pro Thr  
 50 55 60

Asp Met Asn Tyr Arg Gly Val Lys Ala Ala Leu Ala Gly Ala Tyr Leu  
 65 70 75 80

Arg Val Glu Gly Pro Lys Gly Lys Thr Thr Val Tyr Val Thr Asp Leu  
 85 90 95

Tyr Pro Glu Gly Ala Pro Gly Ala Leu Asp Leu Ser Pro Asn Ala Phe  
 100 105 110

Arg Glu Ile Gly Asp Met Lys Asp Gly Lys Ile Asp Ile Lys Trp Arg  
 115 120 125

Ile Val Lys Ala Pro Ile Thr Gly Asn Phe Thr Tyr Arg Ile Lys Glu  
 130 135 140

Gly Ser Ser Gln Trp Trp Ala Ala Ile Gln Val Arg Asn His Lys Tyr  
 145 150 155 160

Pro Val Met Lys Met Glu Tyr Tyr Lys Asp Gly Lys Trp Ile Asn Met  
 165 170 175

Glu Lys Thr Asp Tyr Asn His Phe Val Ser Thr Asn Leu Gly Thr Ser  
 180 185 190

Pro Leu Lys Val Arg Ile Thr Asp Ile Arg Gly Lys Val Val Lys Asp  
 195 200 205

Thr Ile Lys Lys Leu Pro Glu Asn Gly Thr Ser Ser Ala Tyr Thr Val  
 210 215 220

Pro Gly Lys Val Gln Phe Pro Asp  
 225 230

<210> 117  
 <211> 1687  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS

<222> (501)..(1184)

<400> 117

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tacaaaggaa cagccgtatc caatgcagat gaatttttaa ataaatacat ggcgaaaaaa	180
taaaacaaaa gacgtctgcc tcttggcggc gtctttttga atatcatcga aatttggcat	240
tcccatgaat ttgatgcacg ctaaattatt atacaaatat ttctaaaaac atgtgccgga	300
gggcttgctg aacagcgtca aaaggccgca aacgccgtat caacaatagg ggtcacaggt	360
tataaagtct attttatata cttgttgtat gatgaattga ataacgagga aaaggagaca	420
tgccctattt atttctccct ggtgttcttc tacgataata atgtgttaac gactttat	480
cagaaagggg aaaggagaa atg aag aag aag atg aca ttg ggc att ttg acc	533
Met Lys Lys Lys Met Thr Leu Gly Ile Leu Thr	
1 5 10	
gct atg gtt ctc agt ctt ggt tgc cct gct ttt gca gct gag aaa aaa	581
Ala Met Val Leu Ser Leu Gly Ser Pro Ala Phe Ala Ala Glu Lys Lys	
15 20 25	
cag gag gta aca gtt gcc gaa gat gcg ccc aac gtt gcg att atg ctt	629
Gln Glu Val Thr Val Ala Glu Asp Ala Pro Asn Val Ala Ile Met Leu	
30 35 40	
gat gca agc ggc agc atg gct aaa aag atc ggc ggg gtc tca aaa tac	677
Asp Ala Ser Gly Ser Met Ala Lys Lys Ile Gly Gly Val Ser Lys Tyr	
45 50 55	
gag ctt gcc aaa aat gaa gcg ttc agc ttt ggt tcc aag ctt gaa aat	725
Glu Leu Ala Lys Asn Glu Ala Phe Ser Phe Gly Ser Lys Leu Glu Asn	
60 65 70 75	
gca aac gtg ctc atg aga gtt ttc ggt tca gag gga aac aat aaa aat	773
Ala Asn Val Leu Met Arg Val Phe Gly Ser Glu Gly Asn Asn Lys Asn	
80 85 90	
tcc gga aaa gtg cag tcc tgc aat gca atc aga ggg gtg tac ggc ttc	821
Ser Gly Lys Val Gln Ser Cys Asn Ala Ile Arg Gly Val Tyr Gly Phe	
95 100 105	
caa acg tat gac gag caa agc ttc cgc aat tcc tta aac ggc atc gga	869
Gln Thr Tyr Asp Glu Gln Ser Phe Arg Asn Ser Leu Asn Gly Ile Gly	
110 115 120	
ccg acc gga tgg aca ccg atc gca aac gcg ctg caa gat gca aaa aac	917
Pro Thr Gly Trp Thr Pro Ile Ala Asn Ala Leu Gln Asp Ala Lys Asn	
125 130 135	
gcg ctt gac cag ctg gac aac aac ggg aaa aac gtc gtc tat ctg ctg	965
Ala Leu Asp Gln Leu Asp Asn Asn Gly Lys Asn Val Val Tyr Leu Leu	

140	145	150	155	
aca gac ggt gag gaa aca tgc gga ggc aat ccg gta aaa gtc gca aca				1013
Thr Asp Gly Glu Glu Thr Cys Gly Gly Asn Pro Val Lys Val Ala Thr				
	160	165	170	
gaa ctg cgc aaa tcc aat gcg gtt gtc aac gtg atc ggc ttt gat tat				1061
Glu Leu Arg Lys Ser Asn Ala Val Val Asn Val Ile Gly Phe Asp Tyr				
	175	180	185	
gaa gga gac ttc cac gga caa ttg acc agt atc gca gca gct ggc ggc				1109
Glu Gly Asp Phe His Gly Gln Leu Thr Ser Ile Ala Ala Ala Gly Gly				
	190	195	200	
ggt gaa tat ttc cag gca aaa act aaa aat gac atc aaa aga att ttt				1157
Gly Glu Tyr Phe Gln Ala Lys Thr Lys Asn Asp Ile Lys Arg Ile Phe				
	205	210	215	
act cag gaa gca att gag ctt tct aaa taaactggaa aaaagctgtg				1204
Thr Gln Glu Ala Ile Glu Leu Ser Lys				
	220	225		
gacatgtttc cgcagctttc cttttgtgat gaaaagattg tcaaaagtca agaaaaatac				1264
tttacaaata ttaagttatt gtgtcagagc gttgaaccct gctgcgtcct ttggaggggt				1324
tatttgtcgt aacggtagct ttattgggat gaaatcgcc ttttagcaga cttttttgat				1384
aggtcttaag tgaatgcgtc gatcgattat cgtaaggatt atgaagaatt tgtgaatttg				1444
aaaaggagat ccggcctatt tatttctatc aagccttctt ttacgatgtt ggtggacttg				1504
atctcatgcy gaagatcggc ccgaaaaaac aaatgcggaa aggaaagtga gaaggttgaa				1564
aaagaggttt gctctgttga caacgttcac catgcttttg tcattggcgc cggcagcagc				1624
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gct				1687

<210> 118  
 <211> 228  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 118

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Leu Gly Ser Pro Ala Phe Ala Ala Glu Lys Lys Gln Glu Val Thr Val
20 25 30

Ala Glu Asp Ala Pro Asn Val Ala Ile Met Leu Asp Ala Ser Gly Ser

35

40

45

Met Ala Lys Lys Ile Gly Gly Val Ser Lys Tyr Glu Leu Ala Lys Asn  
 50 55 60

Glu Ala Phe Ser Phe Gly Ser Lys Leu Glu Asn Ala Asn Val Leu Met  
 65 70 75 80

Arg Val Phe Gly Ser Glu Gly Asn Asn Lys Asn Ser Gly Lys Val Gln  
 85 90 95

Ser Cys Asn Ala Ile Arg Gly Val Tyr Gly Phe Gln Thr Tyr Asp Glu  
 100 105 110

Gln Ser Phe Arg Asn Ser Leu Asn Gly Ile Gly Pro Thr Gly Trp Thr  
 115 120 125

Pro Ile Ala Asn Ala Leu Gln Asp Ala Lys Asn Ala Leu Asp Gln Leu  
 130 135 140

Asp Asn Asn Gly Lys Asn Val Val Tyr Leu Leu Thr Asp Gly Glu Glu  
 145 150 155 160

Thr Cys Gly Gly Asn Pro Val Lys Val Ala Thr Glu Leu Arg Lys Ser  
 165 170 175

Asn Ala Val Val Asn Val Ile Gly Phe Asp Tyr Glu Gly Asp Phe His  
 180 185 190

Gly Gln Leu Thr Ser Ile Ala Ala Ala Gly Gly Gly Glu Tyr Phe Gln  
 195 200 205

Ala Lys Thr Lys Asn Asp Ile Lys Arg Ile Phe Thr Gln Glu Ala Ile  
 210 215 220

Glu Leu Ser Lys  
 225

<210> 119

<211> 1428

<212> DNA

<213> Bacillus licheniformis

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<220>
<221> CDS
<222> (501)..(944)

<400> 119
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tccgccggaa ggctgaacga actgatggaa gaagctcaga aagaagcggtt ttgcggtgcg      120
cttggcgagt atcatccgta tttttgggca tcaaagcttc atttttatat tacgtctggt      180
ccgttttaca attttcctta tacgttcggc tacttggttt cgcttggcatt ttacgcgcaa      240
gcgctgaaag aggggtgcggc atttgaagaa aaatatattg ctctcttaaa agatacagcc      300
tccatgtctg ttgaagaact ggccatgaag catctcggcg ccgatctgac gaagcgggat      360
ttctgggaag cggccattca gccggctgtc cgagatgcag aagcattttt agcgatgaca      420
taaatgcttc cgcttagatt gaatgagttt ccgcaaagtg gacatagcta aggataatgt      480
gcatagagga gatgaacggg atg aat caa ttt cgg atg gcc gtt atc gct ctc      533
                Met Asn Gln Phe Arg Met Ala Val Ile Ala Leu
                  1                5                10

gtc ctg atc ctg atg acc ggc tgc ggc tcc ata gcg gaa gaa cat gcg      581
Val Leu Ile Leu Met Thr Gly Cys Gly Ser Ile Ala Glu Glu His Ala
                15                20                25

gaa ggc aag gag gcc gtt ccc gat aac gcc cct gtt tca gat gtg aaa      629
Glu Gly Lys Glu Ala Val Pro Asp Asn Ala Pro Val Ser Asp Val Lys
                30                35                40

agc gtg cct tac gct gca ttt gca ttg gaa gtg aac tat ggc cat gga      677
Ser Val Pro Tyr Ala Ala Phe Ala Leu Glu Val Asn Tyr Gly His Gly
                45                50                55

aag cac aat acg ttt gaa gcc gta tac gac aaa cag gag cgg gaa gaa      725
Lys His Asn Thr Phe Glu Ala Val Tyr Asp Lys Gln Glu Arg Glu Glu
        60                65                70                75

gca tcg att aaa gac tat ctg aac gga gcg gac cgc gaa ggg gag gaa      773
Ala Ser Ile Lys Asp Tyr Leu Asn Gly Ala Asp Arg Glu Gly Glu Glu
                80                85                90

gct tta aac gaa atg aaa atg gtt tta agc gag ctt tcg atc gcc aaa      821
Ala Leu Asn Glu Met Lys Met Val Leu Ser Glu Leu Ser Ile Ala Lys
                95                100                105

tcc gat cca gag cag gac gtg atc agc aat gtg ctc gag gcc ttc aat      869
Ser Asp Pro Glu Gln Asp Val Ile Ser Asn Val Leu Glu Ala Phe Asn
        110                115                120

ctt gac gaa caa tat gac cgg ttt cag ctg cgg gtg aaa tgg cct gat      917
Leu Asp Glu Gln Tyr Asp Arg Phe Gln Leu Arg Val Lys Trp Pro Asp
        125                130                135

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ggc acg tcc aga atc tat aac gga aaa taaacaaaag agcattttcca 964  
 Gly Thr Ser Arg Ile Tyr Asn Gly Lys  
 140 145

aactggaaat gctctttttt gcttaagatt ttaaaaagta tttttcgatg tcatcaagga 1024  
 acagatacgc tgctttttacg ccgccggccg tcgtccagat cgcacgcgctg acttcatggg 1084  
 cgtttccggt ttttacagcg ttcaattttt tccacagcgg atcgcttgtc caatcgtttt 1144  
 gccatgtttc agcttctttt ttgctttcgg cagggtttata tgtgaaatag aacaggacat 1204  
 ctccgtccat atcagggatc gattctttat tttccgtcat aaaaacaaat ttgtcgtctt 1264  
 gttttctaaa cagttttttcc tgttttttccg gatacttgaa tccgagctga tccaggataa 1324  
 ttcccgggaa agaattcttta tagtaaatcc ttgattggcc ggccataaat ctgattaccg 1384  
 acacccggtt cttttttctgg tcgccgagct tgtcgcttaa ttcg 1428

<210> 120  
 <211> 148  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 120

Met Asn Gln Phe Arg Met Ala Val Ile Ala Leu Val Leu Ile Leu Met  
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Thr Gly Cys Gly Ser Ile Ala Glu Glu His Ala Glu Gly Lys Glu Ala  
 20 25 30

Val Pro Asp Asn Ala Pro Val Ser Asp Val Lys Ser Val Pro Tyr Ala  
 35 40 45

Ala Phe Ala Leu Glu Val Asn Tyr Gly His Gly Lys His Asn Thr Phe  
 50 55 60

Glu Ala Val Tyr Asp Lys Gln Glu Arg Glu Glu Ala Ser Ile Lys Asp  
 65 70 75 80

Tyr Leu Asn Gly Ala Asp Arg Glu Gly Glu Glu Ala Leu Asn Glu Met  
 85 90 95

Lys Met Val Leu Ser Glu Leu Ser Ile Ala Lys Ser Asp Pro Glu Gln  
 100 105 110

Asp Val Ile Ser Asn Val Leu Glu Ala Phe Asn Leu Asp Glu Gln Tyr

115

120

125

Asp Arg Phe Gln Leu Arg Val Lys Trp Pro Asp Gly Thr Ser Arg Ile  
 130 135 140

Tyr Asn Gly Lys  
 145

<210> 121  
 <211> 1589  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1109)

<400> 121  
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 accaaatttta taaagtgaac taggataaac tatgtctctt tagggaggtg aaacatatga 120  
 gcggaggttta cggacacgga agcgggttttg ctttaattgt tgttctgttc attctcttaa 180  
 tcatcatcgg cgccagctgg ttcggcggtg gatatggagg ctactaaaaa gtccgtttta 240  
 aaagtcagca ataacttatg accttctcct tattttacat gttctcctcc tgcttaccgt 300  
 tgttgactcc atcatgaaag gctctttttt aaaaaagagc ctttttttaa tgcaatacag 360  
 ataccgaacc tctcctgctg ctgaatgtta atagaaaatt aatgtttttt tcaaaaagag 420  
 acatgatttt cattctatta atgctattat ttttccatcc tattaataaaa taggaaaatt 480  
 aagagagggga gtgttggttat atg ttt aaa act aag ttc aag aaa aca att ggg 533  
 Met Phe Lys Thr Lys Phe Lys Lys Thr Ile Gly  
 1 5 10  
 att gga ctc gtt gcc gct gcc tgt ttg att tcc gcg tcg gcg gca agc 581  
 Ile Gly Leu Val Ala Ala Ala Cys Leu Ile Ser Ala Ser Ala Ala Ser  
 15 20 25  
 gct gcg tcg caa aat gaa agc gat gtt aaa gtg aaa ctg gac gat cag 629  
 Ala Ala Ser Gln Asn Glu Ser Asp Val Lys Val Lys Leu Asp Asp Gln  
 30 35 40  
 cag cgg aat caa tat acg gtc aaa tct ttc cac tac tta acc gtt gac 677  
 Gln Arg Asn Gln Tyr Thr Val Lys Ser Phe His Tyr Leu Thr Val Asp  
 45 50 55  
 gga aaa aat gtg gat tcg tcg gct caa gcc aac gcc aaa tcc gtc aga 725  
 Gly Lys Asn Val Asp Ser Ser Ala Gln Ala Asn Ala Lys Ser Val Arg  
 60 65 70 75



gat gtc aaa gta acc atg gtt ctg ccc aag cag aat aag aac ggc gat 773  
 Asp Val Lys Val Thr Met Val Leu Pro Lys Gln Asn Lys Asn Gly Asp  
                   80                                  85                                  90

ttg ctt gcg tat gga ttt acg agc aag gtt act tta gaa gcc ttt atc 821  
 Leu Leu Ala Tyr Gly Phe Thr Ser Lys Val Thr Leu Glu Ala Phe Ile  
                   95                                  100                                  105

gcg aaa gac aag cag agg ctt gag aag caa ttc aaa cct tct gcc agc 869  
 Ala Lys Asp Lys Gln Arg Leu Glu Lys Gln Phe Lys Pro Ser Ala Ser  
                   110                                  115                                  120

ggt ccc tgc tgt acc gat ttc tat gaa tat aaa aat aaa ggc ggg cag 917  
 Gly Pro Cys Cys Thr Asp Phe Tyr Glu Tyr Lys Asn Lys Gly Gly Gln  
                   125                                  130                                  135

tat att tac tgg aga gac gga ttt aaa aac ttg cca tcc agc tgg aat 965  
 Tyr Ile Tyr Trp Arg Asp Gly Phe Lys Asn Leu Pro Ser Ser Trp Asn  
                   140                                  145                                  150                                  155

gac aga att tca tcg tta agt acg gcg tct cct tca tca agc tat tca 1013  
 Asp Arg Ile Ser Ser Leu Ser Thr Ala Ser Pro Ser Ser Ser Tyr Ser  
                   160                                  165                                  170

acg acg ctg tgg gag cat act tca act caa gga tac ggc aaa ggc gtt 1061  
 Thr Thr Leu Trp Glu His Thr Ser Thr Gln Gly Tyr Gly Lys Gly Val  
                   175                                  180                                  185

ttg ttt aga cat tcc gat tgg tac ggc act aat tcg agc tcg gca ccc 1109  
 Leu Phe Arg His Ser Asp Trp Tyr Gly Thr Asn Ser Ser Ser Ala Pro  
                   190                                  195                                  200

tgataaatta ctttttttttg cgatgccggt gttgttgatc ggttcatcat gaccgataca 1169

gctgatgaca tggatggtag tcatattccc cgggagccgt ttaacatcag attctgccgc 1229

ctgctttaaa aatgccttga gatctgtatc cgctttttgt tcgttcaggt gcaggagttt 1289

aacatacata tcatagatca gctgttttgt cagttcagac atagtcaatg gacagtccct 1349

tcttttttatt ttccggttaa caaaatattt taatagttta tttcaggatt tgtcaatatt 1409

atgataagggt gaaatcagat aacaaatgtg ttttgtttat catgaaacaa caccaaaaag 1469

gagaatcgct gatgaatatt gaaggaatag agatggaagt tcgctgcaca ggcgatgtat 1529

gttcagatgc ccttgaattt ttgagacgcc ataaccacga aaaaacagcc gaacattcga 1589

<210> 122

<211> 203

<212> PRT

<213> Bacillus licheniformis

<400> 122

Met Phe Lys Thr Lys Phe Lys Lys Thr Ile Gly Ile Gly Leu Val Ala  
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Ala Ala Cys Leu Ile Ser Ala Ser Ala Ala Ser Ala Ala Ser Gln Asn  
 20 25 30

Glu Ser Asp Val Lys Val Lys Leu Asp Asp Gln Gln Arg Asn Gln Tyr  
 35 40 45

Thr Val Lys Ser Phe His Tyr Leu Thr Val Asp Gly Lys Asn Val Asp  
 50 55 60

Ser Ser Ala Gln Ala Asn Ala Lys Ser Val Arg Asp Val Lys Val Thr  
 65 70 75 80

Met Val Leu Pro Lys Gln Asn Lys Asn Gly Asp Leu Leu Ala Tyr Gly  
 85 90 95

Phe Thr Ser Lys Val Thr Leu Glu Ala Phe Ile Ala Lys Asp Lys Gln  
 100 105 110

Arg Leu Glu Lys Gln Phe Lys Pro Ser Ala Ser Gly Pro Cys Cys Thr  
 115 120 125

Asp Phe Tyr Glu Tyr Lys Asn Lys Gly Gly Gln Tyr Ile Tyr Trp Arg  
 130 135 140

Asp Gly Phe Lys Asn Leu Pro Ser Ser Trp Asn Asp Arg Ile Ser Ser  
 145 150 155 160

Leu Ser Thr Ala Ser Pro Ser Ser Ser Tyr Ser Thr Thr Leu Trp Glu  
 165 170 175

His Thr Ser Thr Gln Gly Tyr Gly Lys Gly Val Leu Phe Arg His Ser  
 180 185 190

Asp Trp Tyr Gly Thr Asn Ser Ser Ser Ala Pro  
 195 200

<210> 123

<211> 1522

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1019)

<400> 123

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aagacgaaaa ggcgcgtttc gggtttggat acgtctgaaa gcagcgctct tgaagtcggt	180
tcaaacaaag cgcggcataa tccgtttaag gcattcatga taaagaatgt ccagacatga	240
tcggcgagtg caaaaccggc gaacacgaac gtccagccga aaatcgagac gagcatgatg	300
gttttccggc cgaacctgtc tgataagtac ccgccataaa agcttgccgc aattccgac	360
agagagctcg ctgcaatgac agtccccgca aagccggaag aggcgccttt cacttggtgc	420
aaataaattg ctaaaaaagg gatgactcat ggcgtgttcc tcatgcgctt taaggtaagg	480
caaaaaagaa ggtgatattg atg tac agc cga agc aag ttc aaa atc ggt tta	533
Met Tyr Ser Arg Ser Lys Phe Lys Ile Gly Leu	
1 5 10	
ttg ctt att gga agt ctg ctg gcc gcg ctc agc ttt cac ctg gag gcc	581
Leu Leu Ile Gly Ser Leu Leu Ala Ala Leu Ser Phe His Leu Glu Ala	
15 20 25	
ttg gcc gaa aag ccg gct aaa gtt caa atc cag ctt gaa aag gtt tat	629
Leu Ala Glu Lys Pro Ala Lys Val Gln Ile Gln Leu Glu Lys Val Tyr	
30 35 40	
ctg gac gga gac gtt gga att gag aat aaa gta gag gcc gct cgc aca	677
Leu Asp Gly Asp Val Gly Ile Glu Asn Lys Val Glu Ala Ala Arg Thr	
45 50 55	
ctg gaa gac ttt aaa gct gct tat aaa ggg tgg cag ctc atc gat cag	725
Leu Glu Asp Phe Lys Ala Ala Tyr Lys Gly Trp Gln Leu Ile Asp Gln	
60 65 70 75	
aaa aag ggg ttt att ctg ttt cgc aaa cag gtg gac gac att tct ccc	773
Lys Lys Gly Phe Ile Leu Phe Arg Lys Gln Val Asp Asp Ile Ser Pro	
80 85 90	
ctc agc aaa aca aac ggt tat atc gga gtg act gaa gat ggc gtg att	821
Leu Ser Lys Thr Asn Gly Tyr Ile Gly Val Thr Glu Asp Gly Val Ile	
95 100 105	
tcg act ttt cac ggt cgc ccg ggc atc tta tca gaa ccc att caa tcg	869
Ser Thr Phe His Gly Arg Pro Gly Ile Leu Ser Glu Pro Ile Gln Ser	
110 115 120	
ttt ttt cag att gat ata aag ccg ctg gaa agc ccg atg gcg gat gat	917
Phe Phe Gln Ile Asp Ile Lys Arg Leu Glu Ser Arg Met Ala Asp Asp	
125 130 135	

ctg cgc aaa ggg ata cca tac cgc acg aaa aag gaa ttt gaa cat gtc 965  
 Leu Arg Lys Gly Ile Pro Tyr Arg Thr Lys Lys Glu Phe Glu His Val  
 140 145 150 155

att gaa gcc gta aaa tca tcc gga agc caa cat cat gta gaa gat atg 1013  
 Ile Glu Ala Val Lys Ser Ser Gly Ser Gln His His Val Glu Asp Met  
 160 165 170

aag aca tgacgctggt atgtcttttt tcagctgcag acagaagctt ttttagcgaa 1069  
 Lys Thr

catatgttaa ctttttctatt ctagctttgc ctgttttgtg ttacaatgaa gagcagtcaa 1129

agagggtgaat gaacgttgat cgaattcgtg aaagggacga ttgattatgt atcgccccaa 1189

tatattgtca ttgaaaacgg cgggatcggc tatcagatct tcacgccaaa tccgtttatt 1249

tataagaaaa acagcaaaga aacaatctat acataccatt atgtaagaga agacacgaat 1309

gcgctgtacg gcttttcgac aagggaagaa aaaatgctgt ttacgaaaat gctgaatgtt 1369

acgggggatcg gccccaaaagg agcgcttgcg atcctcgctt ccggcgatcc gggagcggtg 1429

attgaagcga tcgagaatga ggacgaagca tttctcgtca aatttcccgg cgtaggcaaa 1489

aaaacggcaa ggcagatcat ccttgacctg aaa 1522

<210> 124

<211> 173

<212> PRT

<213> Bacillus licheniformis

<400> 124

Met Tyr Ser Arg Ser Lys Phe Lys Ile Gly Leu Leu Leu Ile Gly Ser  
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Leu Leu Ala Ala Leu Ser Phe His Leu Glu Ala Leu Ala Glu Lys Pro  
 20 25 30

Ala Lys Val Gln Ile Gln Leu Glu Lys Val Tyr Leu Asp Gly Asp Val  
 35 40 45

Gly Ile Glu Asn Lys Val Glu Ala Ala Arg Thr Leu Glu Asp Phe Lys  
 50 55 60

Ala Ala Tyr Lys Gly Trp Gln Leu Ile Asp Gln Lys Lys Gly Phe Ile  
 65 70 75 80

Leu Phe Arg Lys Gln Val Asp Asp Ile Ser Pro Leu Ser Lys Thr Asn  
85 90 95

Gly Tyr Ile Gly Val Thr Glu Asp Gly Val Ile Ser Thr Phe His Gly  
100 105 110

Arg Pro Gly Ile Leu Ser Glu Pro Ile Gln Ser Phe Phe Gln Ile Asp  
115 120 125

Ile Lys Arg Leu Glu Ser Arg Met Ala Asp Asp Leu Arg Lys Gly Ile  
130 135 140

Pro Tyr Arg Thr Lys Lys Glu Phe Glu His Val Ile Glu Ala Val Lys  
145 150 155 160

Ser Ser Gly Ser Gln His His Val Glu Asp Met Lys Thr  
165 170

<210> 125  
<211> 1492  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(989)

<400> 125  
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ggcgctcgttt taccttaaaa tgttggtggcc gtattttttta ttccactttt ttgcgatgcc 180  
ttttcaggcc tgtttaatcg gaatggggtt ggccaaagat gctttttatc ataacgtttg 240  
ggccagtgtc ttatcgtttt tgatgatgta tgttctcggg tccatgcaga ctttgcagat 300  
gacggggatc attcttgcca tgaataccgg tatgattttg ctgacggcgc tgcattatgt 360  
gacgatttgc aaggagctgg gcgtcacgct ttttttgaca aacaaatccc gatctccgag 420  
aattgaaagc cgctgatgga tcctcttcat agtttttagct tttgcgggga agctaattatt 480  
aaaaaagaag gggagttccc atg cga aga atc agt ctc att tac ccg ctc atc 533  
Met Arg Arg Ile Ser Leu Ile Tyr Pro Leu Ile  
1 5 10  
ctg ctg ttt ttt acc ggg tta ttc gta ttt cag ccg cag gca tct gca 581  
Leu Leu Phe Phe Thr Gly Leu Phe Val Phe Gln Pro Gln Ala Ser Ala

15	20	25	
aaa caa gct tcg ccg gca gtc atg cag atg aac acg gtc gaa ggt cag			629
Lys Gln Ala Ser Pro Ala Val Met Gln Met Asn Thr Val Glu Gly Gln			
30	35	40	
cgc gtc gtc att ccc gcc gaa ggc cag aag acg atc gtt cat ttt tgg			677
Arg Val Val Ile Pro Ala Glu Gly Gln Lys Thr Ile Val His Phe Trp			
45	50	55	
acg acc tgg tgc ccg cca tgc cgt gaa gag ctt ccg cga ttc caa tcc			725
Thr Thr Trp Cys Pro Pro Cys Arg Glu Glu Leu Pro Arg Phe Gln Ser			
60	65	70	75
tac tat gaa agc aag caa tcc ggc gtc aag ctc gtg acc gtt aat tta			773
Tyr Tyr Glu Ser Lys Gln Ser Gly Val Lys Leu Val Thr Val Asn Leu			
80	85	90	
ctg aat gcc gaa aag aac gaa cag aag gta aaa cag ttt att aaa gca			821
Leu Asn Ala Glu Lys Asn Glu Gln Lys Val Lys Gln Phe Ile Lys Ala			
95	100	105	
aac aag ctg aca ttt ccg atc gtt ttt gac aaa aag ggt gag atg atg			869
Asn Lys Leu Thr Phe Pro Ile Val Phe Asp Lys Lys Gly Glu Met Met			
110	115	120	
aaa gca tat aaa gtc atg aca att cct acg act ttt ttc ttt aat gaa			917
Lys Ala Tyr Lys Val Met Thr Ile Pro Thr Thr Phe Phe Phe Asn Glu			
125	130	135	
aaa gga gag ctg gag aaa acg ttt gtc ggc ccc att act gta gaa cag			965
Lys Gly Glu Leu Glu Lys Thr Phe Val Gly Pro Ile Thr Val Glu Gln			
140	145	150	155
atg aag gaa tgg gca ggg aaa agc tgagccggga gttcagcttt ttttaaaatg			1019
Met Lys Glu Trp Ala Gly Lys Ser			
160			
taaatgataa ttaatatcat aaagaaatta taataattat tatttgaaaa cgtaggatgt			1079
cgctgtataa tgagaaatag aaaaggggtgt gtccaatgga caagtagcag tcataccctt			1139
tatataaata aaatacttaa tgtttatgct gccgatgagg cggcaatttg ttttttaaga			1199
aggaaaattga cgatgaatta cattctcaat tagggaggat attggagatg caattagaga			1259
tcgggaagca atcgagcaa aaccgtcaca cgttgcaatt tgaaaattgg aggcagcacg			1319
gggaattgat agctgcgctt ttgtcgggtt tgttgattct tgcaggctgg ctgttgccg			1379
gcaatgaaac attgtccggt gttctgttta ttttagcttt ttgtatcggc ggctttgcta			1439
aagcgaaaga aggtatacaa gaaacgctgt cggaaaaaac gctgaatgtt gaa			1492
<210>	126		
<211>	163		

<212> PRT

<213> Bacillus licheniformis

<400> 126

Met Arg Arg Ile Ser Leu Ile Tyr Pro Leu Ile Leu Leu Phe Phe Thr  
1 5 10 15

Gly Leu Phe Val Phe Gln Pro Gln Ala Ser Ala Lys Gln Ala Ser Pro  
20 25 30

Ala Val Met Gln Met Asn Thr Val Glu Gly Gln Arg Val Val Ile Pro  
35 40 45

Ala Glu Gly Gln Lys Thr Ile Val His Phe Trp Thr Thr Trp Cys Pro  
50 55 60

Pro Cys Arg Glu Glu Leu Pro Arg Phe Gln Ser Tyr Tyr Glu Ser Lys  
65 70 75 80

Gln Ser Gly Val Lys Leu Val Thr Val Asn Leu Leu Asn Ala Glu Lys  
85 90 95

Asn Glu Gln Lys Val Lys Gln Phe Ile Lys Ala Asn Lys Leu Thr Phe  
100 105 110

Pro Ile Val Phe Asp Lys Lys Gly Glu Met Met Lys Ala Tyr Lys Val  
115 120 125

Met Thr Ile Pro Thr Thr Phe Phe Phe Asn Glu Lys Gly Glu Leu Glu  
130 135 140

Lys Thr Phe Val Gly Pro Ile Thr Val Glu Gln Met Lys Glu Trp Ala  
145 150 155 160

Gly Lys Ser

<210> 127

<211> 1477

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501) .. (974)

<400> 127

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cgacgatgcc tttaaaaaaaa gaaagaaaca ctttgattta accgaagacc tctgcgacct	180
gcttgaagct ttccggagtc tcaaccttga agtgatcgtc gttgatcaga cttccccctgt	240
tatcaaacgg aatggacttt attgtgtgaa agttctcatc ccgggcctga ttccgatgac	300
attcggacag cgcttcatcc gcctggaagg gcttgagaga attttcaccg tgccgaagaa	360
gctcggcttt gcggaagagc cgtaagacc agaacagctg aacctgcacc cgcacccggt	420
cccttaaaat ttaagagaat atattttttc cgattgttct gctttatgat taaagcagaa	480
cttttttaggc ggtgggtaat atg aaa cag gaa tac aag cgg ccg gtg ctt ttc	533
Met Lys Gln Glu Tyr Lys Arg Pro Val Leu Phe	
1 5 10	
atc gcc tcc ctt ttc atg gcc ttt tgc gcc gtt tat ttc ggc ggg agg	581
Ile Ala Ser Leu Phe Met Ala Phe Cys Ala Val Tyr Phe Gly Gly Arg	
15 20 25	
ctg atc ggt ttt tat atg gcg gaa tac cca aaa tgg aac ggc caa agc	629
Leu Ile Gly Phe Tyr Met Ala Glu Tyr Pro Lys Trp Asn Gly Gln Ser	
30 35 40	
gcc gac gga aat tgg gag gcc gtg atc aaa aag ata gat ggc cgc gcg	677
Ala Asp Gly Asn Trp Glu Ala Val Ile Lys Lys Ile Asp Gly Arg Ala	
45 50 55	
ctg ttc ggc gga gag ctc tac tgg aca ggc gac cgc ggc aag ctg gac	725
Leu Phe Gly Gly Glu Leu Tyr Trp Thr Gly Asp Arg Gly Lys Leu Asp	
60 65 70 75	
gat aca tat ttg gaa aaa ttg gtc gta aag ttt ggt gat gaa atc gtt	773
Asp Thr Tyr Leu Glu Lys Leu Val Val Lys Phe Gly Asp Glu Ile Val	
80 85 90	
ttg aac gcc caa atc gaa acg ccg gtg aaa gat tac gcg gga ggc aaa	821
Leu Asn Ala Gln Ile Glu Thr Pro Val Lys Asp Tyr Ala Gly Gly Lys	
95 100 105	
ttc ccc ggc gga ggg tca aaa gaa caa tcc gtt tct ttt ttg gaa ggg	869
Phe Pro Gly Gly Gly Ser Lys Glu Gln Ser Val Ser Phe Leu Glu Gly	
110 115 120	
ctt gaa gaa gct gaa atc gcc ggc cgc gag gtg acg gtt caa ttg gat	917
Leu Glu Glu Ala Glu Ile Ala Gly Arg Glu Val Thr Val Gln Leu Asp	
125 130 135	
tgg aga gag ggc aaa caa gcg tcc cat aca gga ttt acg ctt gat aaa	965
Trp Arg Glu Gly Lys Gln Ala Ser His Thr Gly Phe Thr Leu Asp Lys	



140                      145                      150                      155

agc tca tgg taaaaggcgg aatatcgatt atattccgcc tacctcaatt                      1014  
 Ser Ser Trp

ttgcttcgca tcgtcagctc ttcttcgagg cccaaatccc gaaatccggt cacactcttc                      1074  
 ggaagggttca cgttcgggtgc attcgtcatc caagtgtatg gctcaatata aagcagatca                      1134  
 tcctgatcag atgtaccggt aaacacaacc cagtgcctaa aatggccgct gcattgatag                      1194  
 cgtacgcgaa tgccggcgag gctgtccgca atgacggcgg tgctgtttcc ttcttggtct                      1254  
 tgctcagccg ccaatatatc atcaagcctt tcacccgctg ccatttttcc cgctttgaac                      1314  
 tcctctgtca cccgatactc gccagtcggc agcatgcggt ctgtcagcgt ccaatgcttt                      1374  
 gaggcaggaa gagtaaacag gcacttttct ttatcccctg attcgtttta aggatagcgg                      1434  
 aaagatgtgt gataccccaa tccgatcggc atcggatctt gac                      1477

<210> 128  
 <211> 158  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 128

Met Lys Gln Glu Tyr Lys Arg Pro Val Leu Phe Ile Ala Ser Leu Phe  
 1                      5                      10                      15

Met Ala Phe Cys Ala Val Tyr Phe Gly Gly Arg Leu Ile Gly Phe Tyr  
                     20                      25                      30

Met Ala Glu Tyr Pro Lys Trp Asn Gly Gln Ser Ala Asp Gly Asn Trp  
                     35                      40                      45

Glu Ala Val Ile Lys Lys Ile Asp Gly Arg Ala Leu Phe Gly Gly Glu  
                     50                      55                      60

Leu Tyr Trp Thr Gly Asp Arg Gly Lys Leu Asp Asp Thr Tyr Leu Glu  
 65                      70                      75                      80

Lys Leu Val Val Lys Phe Gly Asp Glu Ile Val Leu Asn Ala Gln Ile  
                     85                      90                      95

Glu Thr Pro Val Lys Asp Tyr Ala Gly Gly Lys Phe Pro Gly Gly Gly  
                     100                      105                      110

Ser Lys Glu Gln Ser Val Ser Phe Leu Glu Gly Leu Glu Glu Ala Glu  
 115 120 125

Ile Ala Gly Arg Glu Val Thr Val Gln Leu Asp Trp Arg Glu Gly Lys  
 130 135 140

Gln Ala Ser His Thr Gly Phe Thr Leu Asp Lys Ser Ser Trp  
 145 150 155

<210> 129  
 <211> 1219  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (812)..(1114)

<400> 129  
 gaccgctcgt taactcagcc tgcttgcac agcgcagatc ttctgcagct actctcgagg 60  
 cacgaggaaa ccaaccgctt cacgggggaa accaaccgct tcacgaggaa accaaccgct 120  
 tcacgaggaa accaaccgct tcacgaggaa accaaccgct tcacgaggaa accaaccgct 180  
 tcacgaggaa acctaccgct tcacgaggaa accaaccact tcacgaggaa accaacactc 240  
 gagagctggg tctcattata cagcaciaat tcgatatctg gtttcaattg cctgggcttt 300  
 agatgcaata ggaactgtcc ttggcccttg aaaccacagg ttagcgaggc ctcatatac 360  
 cgtattctca ataaactctc taatggttga atcagaatag attttctgtc gcattcatca 420  
 cttatcgtca tctgttcgcg tgtactgcgt tccctaatac acgtggaacc acgtgctgaa 480  
 cagtggacta tctctcgctc tctccataac ctggcttata cttcgcgcg ggtcttaaaa 540  
 catgctctcc tataagcagc tttgggtaat gtctgcttat tccatcacc tcgcaaccgt 600  
 gttttttgca attatggacg cgctggaggc ggtggttcca agtcagttcc tcctgaactg 660  
 gtttgtgaac tttatcatgc tgtttctcgc cattaaagaa acgccggctt ctaaagcagc 720  
 gaggtaaagc gggcaggagc aaatttgttg tcatgttga agagggacaa gcgtaacata 780  
 ataaaaaatg cacgaaatgg ggacaaatca g atg aaa cgt gtc att gtg ctg 832  
 Met Lys Arg Val Ile Val Leu  
 1 5  
 ttt tcg att ttg ctc gcc ctg ttc att gtt tat tat gac ttg aaa tca 880  
 Phe Ser Ile Leu Leu Ala Leu Phe Ile Val Tyr Tyr Asp Leu Lys Ser  
 10 15 20

ggc acc atc cct caa aac gcc tta ccg gct tca acc atg gca gcg gaa 928  
 Gly Thr Ile Pro Gln Asn Ala Leu Pro Ala Ser Thr Met Ala Ala Glu  
 25 30 35

gct ccg gct gca agc ctg caa tat aag tcc gtt acg gta aag ccc gga 976  
 Ala Pro Ala Ala Ser Leu Gln Tyr Lys Ser Val Thr Val Lys Pro Gly  
 40 45 50 55

caa acg gta ttt tca atc atc ggg aac agc gcc gtt ccg gct gac aaa 1024  
 Gln Thr Val Phe Ser Ile Ile Gly Asn Ser Ala Val Pro Ala Asp Lys  
 60 65 70

ata gcc gaa gat ttt gaa gag ttg aat ccg aat gtt gag gcg ggc cgc 1072  
 Ile Ala Glu Asp Phe Glu Glu Leu Asn Pro Asn Val Glu Ala Gly Arg  
 75 80 85

att caa gca ggt gtc acc tac aag ttt ccc gtt tat cct gat 1114  
 Ile Gln Ala Gly Val Thr Tyr Lys Phe Pro Val Tyr Pro Asp  
 90 95 100

taagcgttaa tttcttgta gtttcatgaa cgggctgtta caataagact tgtaaagcat 1174

ttggtataag aaaaggagca accgcctccg aattatactt aagga 1219

<210> 130

<211> 101

<212> PRT

<213> Bacillus licheniformis

<400> 130

Met Lys Arg Val Ile Val Leu Phe Ser Ile Leu Leu Ala Leu Phe Ile  
 1 5 10 15

Val Tyr Tyr Asp Leu Lys Ser Gly Thr Ile Pro Gln Asn Ala Leu Pro  
 20 25 30

Ala Ser Thr Met Ala Ala Glu Ala Pro Ala Ala Ser Leu Gln Tyr Lys  
 35 40 45

Ser Val Thr Val Lys Pro Gly Gln Thr Val Phe Ser Ile Ile Gly Asn  
 50 55 60

Ser Ala Val Pro Ala Asp Lys Ile Ala Glu Asp Phe Glu Glu Leu Asn  
 65 70 75 80

Pro Asn Val Glu Ala Gly Arg Ile Gln Ala Gly Val Thr Tyr Lys Phe  
 85 90 95

Pro Val Tyr Pro Asp  
100

<210> 131  
<211> 1381  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(878)

<400> 131  
ctttatatgc gacacaccag atgctccggt tgtaacgact cccgccagggt gaacgaatgc 60  
taccgcacccc gccggtgcga tgccgaaggc aagcagcaat gatgacgatg tcaccccgta 120  
cgccatccct aaggcgccat ctatcagctg cgcaaataat cctatcaaga caaacacaat 180  
cagcttttttc atgttggcct ccacttcaa ttggtttatt tttattgtta aatataatct 240  
atactatgcc tacctgtaaa gtgcgagttt tataaaatat aaattttttg tatttttcat 300  
cgacaccagc aaaaaagagc atatgcatgc aaaatgagcg cctatcccc ggtcctttgt 360  
cttaatgaaa gacagtttat ggatgctgct tgcaaaaaat gcatcgtgca gaaaaggcgt 420  
cggggagtaa cgcctcattc gtttcattgg caatgatgat ataatcccc atgtaatgac 480  
ttcaaaagga ggctcaagcc atg aaa ttc agc aaa atc ggt gcc tta ctg ctc 533  
Met Lys Phe Ser Lys Ile Gly Ala Leu Leu Leu  
1 5 10  
act ttg gcg tgt ttg ctt ttg cct ttt tct tcg gcg act gca gca ggt 581  
Thr Leu Ala Cys Leu Leu Leu Pro Phe Ser Ser Ala Thr Ala Ala Gly  
15 20 25  
gcc ggt gta tgg gat aat atc ggc aca tac ggc atg acg tcg caa act 629  
Ala Gly Val Trp Asp Asn Ile Gly Thr Tyr Gly Met Thr Ser Gln Thr  
30 35 40  
ccg atc atc aaa tca agc gga ggg gaa ttt tat ttt cac aac aac agc 677  
Pro Ile Ile Lys Ser Ser Gly Gly Glu Phe Tyr Phe His Asn Asn Ser  
45 50 55  
ttt tac ggc ttt aca ttt acg ctg tat gaa gtt gac ggg gcg gga agc 725  
Phe Tyr Gly Phe Thr Phe Thr Leu Tyr Glu Val Asp Gly Ala Gly Ser  
60 65 70 75  
acg cct gaa atc gca aga aaa aat ttc tac gtc gga ccg aaa agc aac 773  
Thr Pro Glu Ile Ala Arg Lys Asn Phe Tyr Val Gly Pro Lys Ser Asn  
80 85 90  
agt ccg gcg atc gat gtc agc agt ttt gca gat ggt gcg aat aaa caa 821  
Ser Pro Ala Ile Asp Val Ser Ser Phe Ala Asp Gly Ala Asn Lys Gln

95	100	105	
gca gaa ctc gtc ctg ttt aaa ggg aat gat aca tat atc acc gtt act			869
Ala Glu Leu Val Leu Phe Lys Gly Asn Asp Thr Tyr Ile Thr Val Thr			
110	115	120	
tgt tat gat tgaatgtccc ataaacagca agcccgccgt ttacagccgg			918
Cys Tyr Asp			
125			
cggggtttttt tgatcaagtt ccctccttat acctataggc acaaaaaagt gcctatatga			978
cttaaaaagtg cgtacttccg ttttggtgtc ttctgttcca taatcataat tgatgttttg			1038
tttgacattg ttctgtttat aatgaaaaga aaacggaggg atcaatgatg aacttggatt			1098
tacgggggaaa aagagcgttg gtgaccggat cgacgtccgg aatcggcaaa gcgattgccg			1158
cttcacttgc gaaagaaggt gcgtctgtca tcattaacgg acgccggcaa gaaaaggtca			1218
accaaacaat agacgaattg aaaggccaat ttcccgaggc tgttcttcaa gcggcccctt			1278
atgaccttgg cactgaaaaa ggggtgtcaaa gcctattagc agcattcccg gatgttgata			1338
ttctggtcaa taatttaggg atctttgaac cggcggaata ttt			1381

<210> 132  
 <211> 126  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 132

Met Lys Phe Ser Lys Ile Gly Ala Leu Leu Leu Thr Leu Ala Cys Leu
1 5 10 15

Leu Leu Pro Phe Ser Ser Ala Thr Ala Ala Gly Ala Gly Val Trp Asp
20 25 30

Asn Ile Gly Thr Tyr Gly Met Thr Ser Gln Thr Pro Ile Ile Lys Ser
35 40 45

Ser Gly Gly Glu Phe Tyr Phe His Asn Asn Ser Phe Tyr Gly Phe Thr
50 55 60

Phe Thr Leu Tyr Glu Val Asp Gly Ala Gly Ser Thr Pro Glu Ile Ala
65 70 75 80

Arg Lys Asn Phe Tyr Val Gly Pro Lys Ser Asn Ser Pro Ala Ile Asp
85 90 95

Val Ser Ser Phe Ala Asp Gly Ala Asn Lys Gln Ala Glu Leu Val Leu  
 100 105 110

Phe Lys Gly Asn Asp Thr Tyr Ile Thr Val Thr Cys Tyr Asp  
 115 120 125

<210> 133  
 <211> 1581  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (601)..(978)

<400> 133  
 gaattttccg gaagctgaaa caccctgat atatataacc ataaattaaa cagcataggc 60  
 ggattgtgcg agttcctcca cattcggagt atttctgaat gatagagcca cacggtccac 120  
 gttctcactg gctaaccgga tcaaatgatc ttcaggagtc agcataatac atccagttca 180  
 ggtagataag atttgaattt ggtgacttgc ttttgttctt cttctttcat tttctgacta 240  
 atccaaactg gaaaaagcag gtcttttaac agattaggag gtttctgaca tgcaccattc 300  
 ggtcactaac cgaatgcagt aaaggacact gtggtgcttg ccagccatta gggatttgag 360  
 gaggtgatca aaatgctagg tgacagtatt tcgtcgaagt ggacaagtcg tgaccaaag 420  
 acctcggatc gagggttggt catggaggaa aaaattgatg tctggtgaca aagaggagtc 480  
 atgatcatgg caccgccaac gagggaaaaa actcttcccg catcgacacg gtatgtgggc 540  
 ggtgacaaac taacttatag agtaaattta ttagtcgaat gaaagaggag gaatgaaata 600  
 atg aaa aat cat ttg tat gag aaa aaa aag agg aaa cct ttg act cgg 648  
 Met Lys Asn His Leu Tyr Glu Lys Lys Lys Arg Lys Pro Leu Thr Arg  
 1 5 10 15  
 aca att aaa gcg acg ctc gcc gtg ttg aca atg tcc atc gct ttg gtg 696  
 Thr Ile Lys Ala Thr Leu Ala Val Leu Thr Met Ser Ile Ala Leu Val  
 20 25 30  
 gga ggc gct acg gtg cct tca ttt gca tgg gtg aat ccg ggt tat cac 744  
 Gly Gly Ala Thr Val Pro Ser Phe Ala Trp Val Asn Pro Gly Tyr His  
 35 40 45  
 tac cag tac cca tcg gaa ggt ggt aca tgg agg tat gga ttc gta aac 792  
 Tyr Gln Tyr Pro Ser Glu Gly Gly Thr Trp Arg Tyr Gly Phe Val Asn  
 50 55 60  
 gcc ggg ctc cgt tca gag tac aac cac ccg aca aag gtc cac ggc tcg 840



Tyr Gln Tyr Pro Ser Glu Gly Gly Thr Trp Arg Tyr Gly Phe Val Asn  
 50 55 60

Ala Gly Leu Arg Ser Glu Tyr Asn His Pro Thr Lys Val His Gly Ser  
 65 70 75 80

Thr Val Gln Lys Leu Ile Asp Gly Lys Val Asp Lys Thr Asn Arg Ser  
 85 90 95

Ile Asp Thr Ala Ala Gly Arg Tyr Ser Asn Ala Tyr Val Gly Ala Ile  
 100 105 110

Asn Ser Pro Gly Leu Lys Gly Arg Tyr Tyr Tyr Arg Thr Asn  
 115 120 125

<210> 135  
 <211> 1357  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(854)

<400> 135  
 aggtctcttc tagtccccgcc catcatcggg tctacacgtg agggaatatc gagctctaac 60  
 atgagcggat gacatat tttt attcaagcga cacaatatat tgcgctgttt ctctccgtgt 120  
 ttgacgcaaa agagaagatt tgcttttcga cgtctctaata attttcaaag agcaccgctt 180  
 cagccgctga aagcgcagcc tctgagattt cccagctcag ccgaacgggt tcatgatccg 240  
 gcgaagttat ttttaaaata tcgttacaaa acgaagaatc gcctcgaata ctatgttgaa 300  
 aagggttttt cccgatgatt gtccttttca ccgcgcgccc tcccgttaag ccttggttatg 360  
 tatctatcct attggaaatg gccccgcagg cgcaacgaaa ataaaattct tcgacaaaat 420  
 ttttat ttttt tgcattaact ccttttgaag caagcgtttt tatggtataa aaaagaagga 480  
 gaaaattaga attgaagggtg atg aac gtg gaa att gct atc att gcg ctg ctc 533  
 Met Asn Val Glu Ile Ala Ile Ile Ala Leu Leu  
 1 5 10  
 gtt gtc agt att gcg ctg att gca ttc tca tat ttt caa aga gaa ccg 581  
 Val Val Ser Ile Ala Leu Ile Ala Phe Ser Tyr Phe Gln Arg Glu Pro  
 15 20 25  
 atc aag gaa gtt gaa cag gag ttg gaa acc ctt cag ctg tcc gcc atg 629  
 Ile Lys Glu Val Glu Gln Glu Leu Glu Thr Leu Gln Leu Ser Ala Met



30	35	40	
cag gaa atc tat aaa ctg aaa aag aag atg acc gtg ctt gag gaa gag			677
Gln Glu Ile Tyr Lys Leu Lys Lys Lys Met Thr Val Leu Glu Glu Glu			
45	50	55	
ctc ctc gat tca aat gtg gtc gtc cgc aga ccg aat gcc gga atc agc			725
Leu Leu Asp Ser Asn Val Val Val Arg Arg Pro Asn Ala Gly Ile Ser			
60	65	70	75
cag cat att gcg aag cag att ctt tca aaa tat caa aac ggc atg tct			773
Gln His Ile Ala Lys Gln Ile Leu Ser Lys Tyr Gln Asn Gly Met Ser			
80	85	90	
gta gac gcc atc gca aaa gct gag cac gta tct gtc gaa gat gtc aaa			821
Val Asp Ala Ile Ala Lys Ala Glu His Val Ser Val Glu Asp Val Lys			
95	100	105	
gcg atc att aaa gac tat gag agg gtg ctt gta tgaccagaca gagtgtacaa			874
Ala Ile Ile Lys Asp Tyr Glu Arg Val Leu Val			
110	115		
gcatttgccc ggagaatgga ttgtggctac cgccgttctt gcaagcgcatt tttatttgaa			934
cggtataatac gacccgattt acctgtgcca tgccaagatt ctccgtcagc atcagactgt			994
ccgttctaag gccttcgata aagtagcgct ccattcgaata ccaaataacg tagattaaga			1054
acagttcgcc tctctttaa ttcgcttttc ttaaaagaag cagaacaacg actcccgtaa			1114
agctccacag cgattcatat aaaaaggtag gctggtagta ttgtccgtca atatacattt			1174
gattgatgat aaaatcaggc aggtggaggt tttctaaaaa cgctcttgag accgcctcac			1234
cggtgcgcttc ctggttcata aagtttcccc agcgtccgat cgcttgacca agcagaatgc			1294
ttggagcagc gatattcagcc agcttccaaa acgaaagccc cttgactttc gcataaatga			1354
ttc			1357

<210> 136

<211> 118

<212> PRT

<213> Bacillus licheniformis

<400> 136

Met Asn Val Glu Ile Ala Ile Ile Ala Leu Leu Val Val Ser Ile Ala
1 5 10 15

Leu Ile Ala Phe Ser Tyr Phe Gln Arg Glu Pro Ile Lys Glu Val Glu
20 25 30

Gln Glu Leu Glu Thr Leu Gln Leu Ser Ala Met Gln Glu Ile Tyr Lys

35

40

45

Leu Lys Lys Lys Met Thr Val Leu Glu Glu Glu Leu Leu Asp Ser Asn  
 50 55 60

Val Val Val Arg Arg Pro Asn Ala Gly Ile Ser Gln His Ile Ala Lys  
 65 70 75 80

Gln Ile Leu Ser Lys Tyr Gln Asn Gly Met Ser Val Asp Ala Ile Ala  
 85 90 95

Lys Ala Glu His Val Ser Val Glu Asp Val Lys Ala Ile Ile Lys Asp  
 100 105 110

Tyr Glu Arg Val Leu Val  
 115

<210> 137

<211> 1297

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501) .. (794)

<400> 137

aggcaacatc gactcgattt cgtcactttt cggctacaca gtcagcatgt caaaagcaaa 60

gccgaccaat agtgagttca tcgcatggt cgcagacaag ctgagactgg agcataaggc 120

ttcttaaacg ttgatatgac gcagttttaa cgaagattta accgtcgaat tttcgacctg 180

tttctaacga atagtttatc gtaattccga tgaatttttc gcccatattg cgatgaaatt 240

gtgctacgat ccgaagggtt taatacagta tttgaagggc ctcgttttta taaacgaggc 300

cgtttttttg cccgcaaagt tactgtttgc gatgtaagat caaaaagggtg aatcatttca 360

gcacagtgtg tattgtgtaa agtcaccta aaagcttatc tattgattcc gaaatattgt 420

aatttgatca ctttttggac atacctgcat gttatatgat gaaatagaaa tgaaataaat 480

ggaaaaggag ttgttttaaa atg aag gtc aat aaa tta tta act ggt acg act 533  
 Met Lys Val Asn Lys Leu Leu Thr Gly Thr Thr  
 1 5 10

ctg gct gtt ggt tta ctt att tct gca gcg ccg gta ttt gct gca tcg 581  
 Leu Ala Val Gly Leu Leu Ile Ser Ala Ala Pro Val Phe Ala Ala Ser  
 15 20 25

cat tca tct gag gtg att gca cat ccg act gct caa tat atc aat tgt 629  
 His Ser Ser Glu Val Ile Ala His Pro Thr Ala Gln Tyr Ile Asn Cys  
           30                          35                          40

cca agt gac ttg cca agc tca ttc aaa agc agt aaa tca tca aaa tgt 677  
 Pro Ser Asp Leu Pro Ser Ser Phe Lys Ser Ser Lys Ser Ser Lys Cys  
           45                          50                          55

gta aaa tca tct tct gga gtt ttc agt aac aaa ttt tct gat agc gat 725  
 Val Lys Ser Ser Ser Gly Val Phe Ser Asn Lys Phe Ser Asp Ser Asp  
           60                          65                          70                          75

gga aca tgg tat ttc aaa ggg aaa ttt tac agt aat gtt ttt aat act 773  
 Gly Thr Trp Tyr Phe Lys Gly Lys Phe Tyr Ser Asn Val Phe Asn Thr  
                           80                          85                          90

tgg gtt ggt ttt tat gaa gga tgaacccaaaa aaggggggct cccctttttt 824  
 Trp Val Gly Phe Tyr Glu Gly  
                           95

tttgttttcc ttttagtatc aagtaggaaa tagatggcgg agaattgaaa actcttcgaa 884

gagccgatct cgagttaaaa gtatgaaata agcgggtggt atgatgatct ttacgaaaac 944

agatcttcgc tatccggtga attttttcgg gccagggttg aggattaacc attacggatt 1004

gctcatcgta aacagcaatg caaaaatagg tgcaaactgt gacattcatc aaggggttaa 1064

tatcggacaa aatcacgctc gccgcgatgt tcccacaatc ggagacaatg tctggatcgg 1124

gccgggggca aagctctttg gcgacattca cattgctgac ggcatatcaa ttggcgcaaa 1184

cgccgtggtc aacaaatctt tcaactgagga aaatattaca atagccggca tgcttgccaa 1244

aaagattaaa gaggcgccgt caaataaaga ccggaagcaa gctgttcagc ggc 1297

<210> 138

<211> 98

<212> PRT

<213> Bacillus licheniformis

<400> 138

Met Lys Val Asn Lys Leu Leu Thr Gly Thr Thr Leu Ala Val Gly Leu  
 1                          5                          10                          15

Leu Ile Ser Ala Ala Pro Val Phe Ala Ala Ser His Ser Ser Glu Val  
           20                          25                          30

Ile Ala His Pro Thr Ala Gln Tyr Ile Asn Cys Pro Ser Asp Leu Pro  
           35                          40                          45

Ser Ser Phe Lys Ser Ser Lys Ser Ser Lys Cys Val Lys Ser Ser Ser  
 50 55 60

Gly Val Phe Ser Asn Lys Phe Ser Asp Ser Asp Gly Thr Trp Tyr Phe  
 65 70 75 80

Lys Gly Lys Phe Tyr Ser Asn Val Phe Asn Thr Trp Val Gly Phe Tyr  
 85 90 95

Glu Gly

<210> 139  
 <211> 1261  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(836)

<400> 139  
 tcattaacat tttccggtcc gtcccggttta tcatttttaatt gggttgcttta attccagtgat 60  
 caaggctgat tgtagggacg tcgatcggca catcggcagc gattgttccc ttgacttttt 120  
 atgcgggggcc ttacatcgct agactcgtcg agaactctct gcttgaagtg gatccgggag 180  
 tcattgaagc cgctgaagca atgggagcga ctccgagaca gatcatcttc aggtttctga 240  
 ttccagaagc gtcggttcg cttgtgctga gttttacggt ggcaacggtc ggattggctg 300  
 gggcgctcggc gatggctggt gcgattggtg caggcgggtct tggggatttg gcgatcacat 360  
 acggctatca aagatttgac acgctgacga tgatcatcac gggtgcaatt ctcgatcatcg 420  
 tagtgcaagg attgcagaca tccggaacg ttctgtcaaa aaaattgaga agaagataga 480  
 cagagagggga gacggctatt atg aaa aaa ttt gca tgt gtt gtg atc ttc ctg 533  
 Met Lys Lys Phe Ala Cys Val Val Ile Phe Leu  
 1 5 10  
 ctg ctt gcg gca gtg atc gcg ggg tgc gcg gca gac tct gat gcg aaa 581  
 Leu Leu Ala Ala Val Ile Ala Gly Cys Ala Ala Asp Ser Asp Ala Lys  
 15 20 25  
 acc att aaa atc ggc atc agc gga acg gat acg aga att tgg gac ttt 629  
 Thr Ile Lys Ile Gly Ile Ser Gly Thr Asp Thr Arg Ile Trp Asp Phe  
 30 35 40  
 gtg aag aaa aaa gcc gaa aaa gaa ggc tta aag ctt gaa atc gtc aaa 677  
 Val Lys Lys Lys Ala Glu Lys Glu Gly Leu Lys Leu Glu Ile Val Lys

45	50	55	
tac tcc gac tat gtt cag cca aac cag gct ttg gcg agc ggc gac att			725
Tyr Ser Asp Tyr Val Gln Pro Asn Gln Ala Leu Ala Ser Gly Asp Ile			
60	65	70	75
gac cgc caa cgc ttt tca gac gat atc cta ctt tca tgc att caa aaa			773
Asp Arg Gln Arg Phe Ser Asp Asp Ile Leu Leu Ser Cys Ile Gln Lys			
	80	85	90
gga acg caa cct tta att atc gcc ggt cgg cac aac gac acc agg tcg			821
Gly Thr Gln Pro Leu Ile Ile Ala Gly Arg His Asn Asp Thr Arg Ser			
	95	100	105
ggg ggg gga gga aga ataaataaac acggggccctt ttggttgata agtccccggc			876
Gly Gly Gly Gly Arg			
	110		
attacaagcc cgaccattcc cattgctgat ccgcgttttt cctttgggaa aatcaataaa			936
agcaccgtct gcatcaatgg catcataatg ccggcgccag ccgcctgcac gacgcgcccc			996
gcaatcagcg ccggaaagct gaatgacaag gcgcagatca gcgtgccggc cgtaaataaa			1056
gacattgccg ccatgaacag ctttctcggt gtgaattttt caattaataaa agccgtaact			1116
ggaatcatga tcccattcac gagcataaaa acggtcgtca gccattgggc aagccccggc			1176
gtaatgttta agtccctcat aatcggaggc agagccctga tgaatcccct aatgattttg			1236
gtaaaaaatca ttaagttaag gtgga			1261
<210>	140		
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<212>	PRT		
<213>	Bacillus licheniformis		
<400>	140		
Met Lys Lys Phe Ala Cys Val Val Ile Phe Leu Leu Leu Ala Ala Val			
1	5	10	15
Ile Ala Gly Cys Ala Ala Asp Ser Asp Ala Lys Thr Ile Lys Ile Gly			
	20	25	30
Ile Ser Gly Thr Asp Thr Arg Ile Trp Asp Phe Val Lys Lys Lys Ala			
	35	40	45
Glu Lys Glu Gly Leu Lys Leu Glu Ile Val Lys Tyr Ser Asp Tyr Val			
	50	55	60
Gln Pro Asn Gln Ala Leu Ala Ser Gly Asp Ile Asp Arg Gln Arg Phe			

65

70

75

80

Ser Asp Asp Ile Leu Leu Ser Cys Ile Gln Lys Gly Thr Gln Pro Leu  
85 90 95

Ile Ile Ala Gly Arg His Asn Asp Thr Arg Ser Gly Gly Gly Gly Arg  
100 105 110

&lt;210&gt; 141

&lt;211&gt; 1426

&lt;212&gt; DNA

&lt;213&gt; Bacillus licheniformis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (507) .. (923)

&lt;400&gt; 141

atcgtcaagt ttgcctgcaa tggaaggcaa gaatttcttg gaatattcga tcaccttgcc 60

gtcaatatcg acaagcgtcg cttttttcac gctcggatgc ttcaaaattt cacggataac 120

gccgccgtct ccgccgccga ccacaagcac atgctcagga ttcggatgcg taaacagggg 180

cacgtgcgcc accatttcgt ggtagacaaa ttcattcttt tcagatgtca tgaccatgcc 240

gtccaaaaac agcatgttgc cgaattcttc agtctcggcc atttcgagct tttgaaaatc 300

tgtctgctct gtatgtaaag tcctgttgat tttcattgta ataccgaaat ttttcgtttg 360

cttctctgta taccaaagtc cgctcaaagc gtcattcttc tttcgtgata agctgtattt 420

caatctattt ttctcgcttg cggcggcgat tattctgcac tgaagcatcg gcttttgcct 480

aaggaaaaag tatagaggaa ttgcag gtg att gta aag acg gat cga ttc att 533

Val Ile Val Lys Thr Asp Arg Phe Ile

1

5

ttc acg agt cat tcc aag tcc att ata ttc cca atc gcc agt ttt tct 581

Phe Thr Ser His Ser Lys Ser Ile Ile Phe Pro Ile Ala Ser Phe Ser

10

15

20

25

ttt ata ttg gct aag cta agc aca gat gtg cat acc tgt gcg ctt ttg 629

Phe Ile Leu Ala Lys Leu Ser Thr Asp Val His Thr Cys Ala Leu Leu

30

35

40

gag gtg tgc tca ttt gca gag cac tca act gct caa att gta tat atc 677

Glu Val Cys Ser Phe Ala Glu His Ser Thr Ala Gln Ile Val Tyr Ile

45

50

55

ctc ccg ccg gaa cag gct ttt att gac ctt ttt tct gat ccg acc ggc 725

Leu Pro Pro Glu Gln Ala Phe Ile Asp Leu Phe Ser Asp Pro Thr Gly

60

65

70

cgt ttt gtc ttt cac ccc cgt tca tat ccg gga cgc tgc cct tcc ccc 773  
 Arg Phe Val Phe His Pro Arg Ser Tyr Pro Gly Arg Cys Pro Ser Pro  
 75 80 85

tct ccc gga tcg gcc ttc tcg aaa ttc agc gga ttt gct tat ttg atg 821  
 Ser Pro Gly Ser Ala Phe Ser Lys Phe Ser Gly Phe Ala Tyr Leu Met  
 90 95 100 105

cct atg gtc tct cgc tct cgt ccc tat gct gtt gtt tta cgt tac ttc 869  
 Pro Met Val Ser Arg Ser Arg Pro Tyr Ala Val Val Leu Arg Tyr Phe  
 110 115 120

aaa tgt ctg ccg ggc tct ccg cgt ccc acg cca cca aac aaa cgg ggt 917  
 Lys Cys Leu Pro Gly Ser Pro Arg Pro Thr Pro Pro Asn Lys Arg Gly  
 125 130 135

ctc ccc tgattttcgt cggctgcccg tctctgcttt ttgattaccc cccttctctt 973  
 Leu Pro

attgaagccc gcctcggctg gtttccatcg tccgctacgc gccgcaaag ttatgctttt 1033

ctttatctaa aggctctacc cttagtatct aactaacacc tgcattgcaca gaaatcggag 1093

tggctttgtg catgcaccga catcggagtg ggtctgtgca tgcaccgata tcggagagac 1153

tctgtgcatg caccgatatc ggagtggctc tgtgcatgca ccgatatcgg agtggctctg 1213

tgcattgcacc gatattcggag tggctctgtg catgcaccga tatcggagtg gctctcatgc 1273

acgtgttgat gaatgcggcc catgtacgtg ttgatgaatg cggcccatgt acgtgttgat 1333

gaatgcggcc catgtacgtg ttgatgaatg cggccattct tatcagggga cccaacggg 1393

attcttatca ggggaccca acgggattct tat 1426

<210> 142

<211> 139

<212> PRT

<213> Bacillus licheniformis

<400> 142

Val Ile Val Lys Thr Asp Arg Phe Ile Phe Thr Ser His Ser Lys Ser  
 1 5 10 15

Ile Ile Phe Pro Ile Ala Ser Phe Ser Phe Ile Leu Ala Lys Leu Ser  
 20 25 30

Thr Asp Val His Thr Cys Ala Leu Leu Glu Val Cys Ser Phe Ala Glu  
 35 40 45

His Ser Thr Ala Gln Ile Val Tyr Ile Leu Pro Pro Glu Gln Ala Phe  
 50 55 60

Ile Asp Leu Phe Ser Asp Pro Thr Gly Arg Phe Val Phe His Pro Arg  
 65 70 75 80

Ser Tyr Pro Gly Arg Cys Pro Ser Pro Ser Pro Gly Ser Ala Phe Ser  
 85 90 95

Lys Phe Ser Gly Phe Ala Tyr Leu Met Pro Met Val Ser Arg Ser Arg  
 100 105 110

Pro Tyr Ala Val Val Leu Arg Tyr Phe Lys Cys Leu Pro Gly Ser Pro  
 115 120 125

Arg Pro Thr Pro Pro Asn Lys Arg Gly Leu Pro  
 130 135

<210> 143  
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 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (496)..(1035)

<400> 143  
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 atattctttt tgatcgtgct gttgggagggc attattggca tgaagatggt tacaaaagag 120  
 aacaatgccc agtcaggagg tgatgaatga tgccatggat gtttttagtg atttccggaa 180  
 tcgaagaggt tattgccgcc atcgctatga aatatgtaga cggcacaaga aaaaaatggc 240  
 cgattatcgt catggtggtg gggtttggct tgtctttttt ctgcctttca aaagcaatgc 300  
 agatgctatc agccggtggt gcatatgccg tatggaccgg aatcggcagc atcggcatta 360  
 cggcagtcag tttatttttg tttaaggagc gtattcgtgc tccgcagctc atctcgcttg 420  
 gctttattat aatcgggggtg atcggcctgc gccttacatc atcttaaatt ttaatttgca 480  
 ttggaggttg ctgat atg att aat cag ctt aaa ttg cgt ccg ctt gaa aga 531  
 Met Ile Asn Gln Leu Lys Leu Arg Pro Leu Glu Arg  
 1 5 10  
 gaa gac ctt ccg ttt gtc cac cgt ctt aac aac gat gcg aaa att atg 579  
 Glu Asp Leu Pro Phe Val His Arg Leu Asn Asn Asp Ala Lys Ile Met



15	20	25	
tca tat tgg ttt gaa gaa ccg tac gag act ttt gtt gag ctg cag gat			627
Ser Tyr Trp Phe Glu Glu Pro Tyr Glu Thr Phe Val Glu Leu Gln Asp			
30	35	40	
tta ttt gac aaa cac att cac gac caa agc gag cgg cgc ttt atc ata			675
Leu Phe Asp Lys His Ile His Asp Gln Ser Glu Arg Arg Phe Ile Ile			
45	50	55	60
gag aaa gag act gag atg atc gga ttg gta gag ctg gtc gaa att gat			723
Glu Lys Glu Thr Glu Met Ile Gly Leu Val Glu Leu Val Glu Ile Asp			
	65	70	75
tat att cac agg cgg gcg gag ttt caa atc ata att gat ccc gag cat			771
Tyr Ile His Arg Arg Ala Glu Phe Gln Ile Ile Ile Asp Pro Glu His			
	80	85	90
caa ggg aac ggt tat tcg tca agc gca aca tat ttg gca atg aac tac			819
Gln Gly Asn Gly Tyr Ser Ser Ser Ala Thr Tyr Leu Ala Met Asn Tyr			
	95	100	105
gca ttt tcc gtc ttg aac ttg cac aaa ttg tat ttg atc gtc gac gaa			867
Ala Phe Ser Val Leu Asn Leu His Lys Leu Tyr Leu Ile Val Asp Glu			
	110	115	120
gat aat gca aaa gcg att cac ttg tat aaa aag gca ggg ttc act atc			915
Asp Asn Ala Lys Ala Ile His Leu Tyr Lys Lys Ala Gly Phe Thr Ile			
	125	130	135
gag agc gag ctg cag gat gaa ttt ttc gtc gac ggc tat tat cgt aac			963
Glu Ser Glu Leu Gln Asp Glu Phe Phe Val Asp Gly Tyr Tyr Arg Asn			
	145	150	155
gcc att aga atg tgc att ttt cag gat gag ttt tta tca ctt aaa aaa			1011
Ala Ile Arg Met Cys Ile Phe Gln Asp Glu Phe Leu Ser Leu Lys Lys			
	160	165	170
agc aaa gag gaa ggc atg cag gga taaataaaaag agatggcggc gccatctcct			1065
Ser Lys Glu Glu Gly Met Gln Gly			
	175	180	
gcatgctttt ttaatttttc acacctaatt gctctttggc tttggcggga atatcgtctt			1125
tgtcaacctc ttcccatgac ttcacgcctt tgttttcaga atagaaaagc ctcaaaaacg			1185
cgcttatgcg aagggttttta tcagctgtga attccattgt tttttcttga ccgtcttcat			1245
caaaaccggc cagttcatat ttgaagacgg agtattcctc gccgtcgtca aatttcgacg			1305
tgtcttcctc cccgtttcca gtaatgtgaa cataatattc gtccgtcccc acacggttta			1365
agttacatcc gcttaaaaaat gcggcaaata tgatcatcag gctgatccat ggaatatggg			1425
tttttcactt tttctectca tttatggttt ctgtgtaaat gataagattc attgtctgat			1485
aaaaaaattg aataacgtga catgaaca			1513

<210> 144  
 <211> 180  
 <212> PRT  
 <213> Bacillus licheniformis  
  
 <400> 144  
  
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 1 5 10 15  
  
 Phe Val His Arg Leu Asn Asn Asp Ala Lys Ile Met Ser Tyr Trp Phe  
 20 25 30  
  
 Glu Glu Pro Tyr Glu Thr Phe Val Glu Leu Gln Asp Leu Phe Asp Lys  
 35 40 45  
  
 His Ile His Asp Gln Ser Glu Arg Arg Phe Ile Ile Glu Lys Glu Thr  
 50 55 60  
  
 Glu Met Ile Gly Leu Val Glu Leu Val Glu Ile Asp Tyr Ile His Arg  
 65 70 75 80  
  
 Arg Ala Glu Phe Gln Ile Ile Ile Asp Pro Glu His Gln Gly Asn Gly  
 85 90 95  
  
 Tyr Ser Ser Ser Ala Thr Tyr Leu Ala Met Asn Tyr Ala Phe Ser Val  
 100 105 110  
  
 Leu Asn Leu His Lys Leu Tyr Leu Ile Val Asp Glu Asp Asn Ala Lys  
 115 120 125  
  
 Ala Ile His Leu Tyr Lys Lys Ala Gly Phe Thr Ile Glu Ser Glu Leu  
 130 135 140  
  
 Gln Asp Glu Phe Phe Val Asp Gly Tyr Tyr Arg Asn Ala Ile Arg Met  
 145 150 155 160  
  
 Cys Ile Phe Gln Asp Glu Phe Leu Ser Leu Lys Lys Ser Lys Glu Glu  
 165 170 175  
  
 Gly Met Gln Gly  
 180

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<220>
<221> CDS
<222> (503) .. (1264)
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279

110	115	120	
tat tcg caa atg aag aaa agc gag atc aaa aaa gac tta gca aaa gca			916
Tyr Ser Gln Met Lys Lys Ser Glu Ile Lys Lys Asp Leu Ala Lys Ala			
125	130	135	
cga cac tcc ttt caa aaa ctc ggg ctt gac gac ctt acg ctt tta aga			964
Arg His Ser Phe Gln Lys Leu Gly Leu Asp Asp Leu Thr Leu Leu Arg			
140	145	150	
ccg ccg acc ggc cag ttt aat aaa gac gta ctc gat gtt gct aaa cag			1012
Pro Pro Thr Gly Gln Phe Asn Lys Asp Val Leu Asp Val Ala Lys Gln			
155	160	165	170
tac ggc tac acc gtt gtt cat tat agt att aac tcg gat gac tgg acg			1060
Tyr Gly Tyr Thr Val Val His Tyr Ser Ile Asn Ser Asp Asp Trp Thr			
175	180	185	
aac ccg ggg gtt caa aag atc gtc caa aac gta aat gga acg gta aac			1108
Asn Pro Gly Val Gln Lys Ile Val Gln Asn Val Asn Gly Thr Val Asn			
190	195	200	
gcc ggt gac atc gtg ctc ttt cac gct tca gat tcc gcc aaa caa aca			1156
Ala Gly Asp Ile Val Leu Phe His Ala Ser Asp Ser Ala Lys Gln Thr			
205	210	215	
aaa gaa gcc ctg cca gag atc gtg cac cat ctc aga agc aag ggg ctc			1204
Lys Glu Ala Leu Pro Glu Ile Val His His Leu Arg Ser Lys Gly Leu			
220	225	230	
aaa aac gta aca gtc agc gaa tta atc gca aat acg gat gca aaa tct			1252
Lys Asn Val Thr Val Ser Glu Leu Ile Ala Asn Thr Asp Ala Lys Ser			
235	240	245	250
tca gaa gta aag tagcagccgg tctaagcgcg tgcctgaaat tttggcagca			1304
Ser Glu Val Lys			
ttaaaagctg aaaagcgttg caggctaata aaggaagcag cattaaatag agccagtcct			1364
cttcattgac ccttaacgcc gggaaccact ccatcacagt aaaaacaaac attagaaata			1424
atgcggaaac gaacgttttt ttagaggact gtttttgctt tgcataagcg gccgcaatgc			1484
ctaccgcaa aataaagagc ggcagccaaa tgtacggaat gatggagcct ccatcttttt			1544
caaaaaacag aaagcgcaag taaaccaagt caaacgcgac aaatataatc aaaaacagct			1604
gaatcgaatt ccacaaagaa tgagatctga aaatttccag tgcaaagcgg tgaatcgta			1664
agaaaatcac aaatcccatt tgagcaatca cgctaaagat catgcccaacc ccgataaacc			1724
agaaaagaac agacagaatc tccaatacct cgaaggaaa			1763
<210> 146			
<211> 254			

<212> PRT

<213> Bacillus licheniformis

<400> 146

Val Asn His Phe Tyr Val Trp His Ile Lys Arg Ile Lys Gln Leu Ile  
1 5 10 15

Ile Ile Met Ile Ala Ala Phe Ala Thr Ala Ser Phe Phe Tyr Val Gln  
20 25 30

Asn Leu Leu Pro Leu Pro Val Phe Ser Thr Glu Gly Gly Ala Lys Ala  
35 40 45

Val Tyr Arg Gly Asp Ser Asp Thr Asn Glu Val Ala Leu Thr Phe Asn  
50 55 60

Ile Ser Trp Gly Asp Gln Lys Ala Met Pro Ile Leu Asp Thr Leu Lys  
65 70 75 80

Ala Asn Gly Ile Lys Asp Ala Thr Phe Phe Leu Ser Ala Ser Trp Ala  
85 90 95

Glu Arg His Pro Asp Val Val Glu Arg Ile Arg Lys Asp Gly His Gln  
100 105 110

Ile Gly Ser Met Gly Tyr Ala Tyr Lys Asn Tyr Ser Gln Met Lys Lys  
115 120 125

Ser Glu Ile Lys Lys Asp Leu Ala Lys Ala Arg His Ser Phe Gln Lys  
130 135 140

Leu Gly Leu Asp Asp Leu Thr Leu Leu Arg Pro Pro Thr Gly Gln Phe  
145 150 155 160

Asn Lys Asp Val Leu Asp Val Ala Lys Gln Tyr Gly Tyr Thr Val Val  
165 170 175

His Tyr Ser Ile Asn Ser Asp Asp Trp Thr Asn Pro Gly Val Gln Lys  
180 185 190

Ile Val Gln Asn Val Asn Gly Thr Val Asn Ala Gly Asp Ile Val Leu  
195 200 205

Phe His Ala Ser Asp Ser Ala Lys Gln Thr Lys Glu Ala Leu Pro Glu  
 210 215 220

Ile Val His His Leu Arg Ser Lys Gly Leu Lys Asn Val Thr Val Ser  
 225 230 235 240

Glu Leu Ile Ala Asn Thr Asp Ala Lys Ser Ser Glu Val Lys  
 245 250

<210> 147  
 <211> 1855  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (480)..(1346)

<400> 147  
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 aaatagggag attataacat agagaagatg cagatcagtg atggggaggg cgaagataac 120  
 acacgaggaa gacgcggaat aaggaggaac atagtgacgc aggggtgaacg gtagggaggg 180  
 tggcaaatag tagtatgata tttgaaagac ggggtcccgta cgaaatcggg gaaaaacaaa 240  
 ggcggaaaaa cgaagtacaa gccgtatgtt tcaaaagcgc tttatgatgc caataagaag 300  
 ctggaccgcg ataaagacaa aattgcctgt gagcgctgat atatccaaaa aaagatctct 360  
 gccaaaggat ctttttttgt ttatcaggaa atttatgaaa attaaagact gctgaaacat 420  
 aatcttaaca gtgcgaacct atactttggc aagagaagag caaaagggga gtggatgat 479  
 gtg tca gct tta ttc aaa aaa ttg atg tta tct tca ttg atc ggg gtt 527  
 Val Ser Ala Leu Phe Lys Lys Leu Met Leu Ser Ser Leu Ile Gly Val  
 1 5 10 15  
 tcc atc ggg tca gcg ctg ttt gca ccg aat gcg ggt gca caa gag ccg 575  
 Ser Ile Gly Ser Ala Leu Phe Ala Pro Asn Ala Gly Ala Gln Glu Pro  
 20 25 30  
 gcg gtg aag cct aaa aaa gtg gat gtc att gca cac aga ggc gct tcg 623  
 Ala Val Lys Pro Lys Lys Val Asp Val Ile Ala His Arg Gly Ala Ser  
 35 40 45  
 gga tat gcg ccg gaa aac acg atg gct gct ttt gat aaa gcg ctt cag 671  
 Gly Tyr Ala Pro Glu Asn Thr Met Ala Ala Phe Asp Lys Ala Leu Gln  
 50 55 60  
 atg aaa gca gat tat atc gag ctg gat gtt caa atg tcc aaa gac ggg 719  
 Met Lys Ala Asp Tyr Ile Glu Leu Asp Val Gln Met Ser Lys Asp Gly

65	70	75	80	
gag ctt gtc atc att cac gat acg acc gta aac cgt acg aca gat att				767
Glu Leu Val Ile Ile His Asp Thr Thr Val Asn Arg Thr Thr Asp Ile				
	85	90	95	
gac tca gtg ctg ccg gtt gcc gta aag gat ttg acg ctt gcc gag ctg				815
Asp Ser Val Leu Pro Val Ala Val Lys Asp Leu Thr Leu Ala Glu Leu				
	100	105	110	
cgc aag ctt gat gcc ggc agc ttc ttc ggt ccg cag ttc gca gga gag				863
Arg Lys Leu Asp Ala Gly Ser Phe Phe Gly Pro Gln Phe Ala Gly Glu				
	115	120	125	
cgc att ccg aca ttt gaa gaa gtg ctt gac cgg tat aaa ggg aag gtc				911
Arg Ile Pro Thr Phe Glu Glu Val Leu Asp Arg Tyr Lys Gly Lys Val				
	130	135	140	
gga atg ctg atc gaa ttg aaa gag cct gca cgc tat ccg gga atc gaa				959
Gly Met Leu Ile Glu Leu Lys Glu Pro Ala Arg Tyr Pro Gly Ile Glu				
	145	150	155	160
gga aaa gtg tca gca gca ttg aaa gag cgg aga atg gat aag cct aaa				1007
Gly Lys Val Ser Ala Ala Leu Lys Glu Arg Arg Met Asp Lys Pro Lys				
	165	170	175	
aac gga aaa atc att gta caa tcg ttt gat ttt aac tct gtc tat aaa				1055
Asn Gly Lys Ile Ile Val Gln Ser Phe Asp Phe Asn Ser Val Tyr Lys				
	180	185	190	
att cat cag ctg ctt cca tcg atg ccg aca ggt gtc ttg acg tca aaa				1103
Ile His Gln Leu Leu Pro Ser Met Pro Thr Gly Val Leu Thr Ser Lys				
	195	200	205	
gcg gcg gac tta aca gat gca aag ctt aag gaa ttt tcc ggc tat gcc				1151
Ala Ala Asp Leu Thr Asp Ala Lys Leu Lys Glu Phe Ser Gly Tyr Ala				
	210	215	220	
aaa tac gtg aac gcc aac ttg aaa aat gtg gcc gct gat cct acg ctt				1199
Lys Tyr Val Asn Ala Asn Leu Lys Asn Val Ala Ala Asp Pro Thr Leu				
	225	230	235	240
gtg ccg aga att cat gcg ctc ggc atg aag ata cgc cct tgg acc gtc				1247
Val Pro Arg Ile His Ala Leu Gly Met Lys Ile Arg Pro Trp Thr Val				
	245	250	255	
cgc tcc cgc gat gaa gtg cct ccg cta ttt agg ccc gcg tgg aac ggg				1295
Arg Ser Arg Asp Glu Val Pro Pro Leu Phe Arg Pro Ala Trp Asn Gly				
	260	265	270	
att gtg aca aac ttt ccc gac tat tgt tcc aaa aaa gta cgg gag ccc				1343
Ile Val Thr Asn Phe Pro Asp Tyr Cys Ser Lys Lys Val Arg Glu Pro				
	275	280	285	
caa taaaaaaccc tgaagtttgc tttgaagggc tttttaattt aaaaataaaa				1396
Gln				

atggggctta aaacaaaaaa ggttaacgtt aacgggttta tcgttcccc cgattttttt 1456  
 tgggacacct gggaaaaacg ggtataaacc tttgggggcc ctttttgggg gccttaaaaa 1516  
 ttttgaaatt tgccccgggg gccctccttg tggccggagg ggggaaaatt ttttttttat 1576  
 tccggggttt ttataggggg gcaaaatttt aaacccctt ttctctcaaa aaaaaaacc 1636  
 cgggggtttt tttttttggg tactgccgcc gatgacctta catatgggct gaactgcaaa 1696  
 aacaatggaa gaggaaaacc tgcaggcccg catcgtctca ttcagcgttg atcccgaaaa 1756  
 tgatacgctt gaaaaattga agaaatttgc ggccaactac ccgctcagtt ttcaaaattg 1816  
 ggacttttta accggatact cgcaggaaga aatcgaaaa 1855

<210> 148  
 <211> 289  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 148

Val Ser Ala Leu Phe Lys Lys Leu Met Leu Ser Ser Leu Ile Gly Val  
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Ser Ile Gly Ser Ala Leu Phe Ala Pro Asn Ala Gly Ala Gln Glu Pro  
 20 25 30

Ala Val Lys Pro Lys Lys Val Asp Val Ile Ala His Arg Gly Ala Ser  
 35 40 45

Gly Tyr Ala Pro Glu Asn Thr Met Ala Ala Phe Asp Lys Ala Leu Gln  
 50 55 60

Met Lys Ala Asp Tyr Ile Glu Leu Asp Val Gln Met Ser Lys Asp Gly  
 65 70 75 80

Glu Leu Val Ile Ile His Asp Thr Thr Val Asn Arg Thr Thr Asp Ile  
 85 90 95

Asp Ser Val Leu Pro Val Ala Val Lys Asp Leu Thr Leu Ala Glu Leu  
 100 105 110

Arg Lys Leu Asp Ala Gly Ser Phe Phe Gly Pro Gln Phe Ala Gly Glu  
 115 120 125



Arg Ile Pro Thr Phe Glu Glu Val Leu Asp Arg Tyr Lys Gly Lys Val  
 130 135 140

Gly Met Leu Ile Glu Leu Lys Glu Pro Ala Arg Tyr Pro Gly Ile Glu  
 145 150 155 160

Gly Lys Val Ser Ala Ala Leu Lys Glu Arg Arg Met Asp Lys Pro Lys  
 165 170 175

Asn Gly Lys Ile Ile Val Gln Ser Phe Asp Phe Asn Ser Val Tyr Lys  
 180 185 190

Ile His Gln Leu Leu Pro Ser Met Pro Thr Gly Val Leu Thr Ser Lys  
 195 200 205

Ala Ala Asp Leu Thr Asp Ala Lys Leu Lys Glu Phe Ser Gly Tyr Ala  
 210 215 220

Lys Tyr Val Asn Ala Asn Leu Lys Asn Val Ala Ala Asp Pro Thr Leu  
 225 230 235 240

Val Pro Arg Ile His Ala Leu Gly Met Lys Ile Arg Pro Trp Thr Val  
 245 250 255

Arg Ser Arg Asp Glu Val Pro Pro Leu Phe Arg Pro Ala Trp Asn Gly  
 260 265 270

Ile Val Thr Asn Phe Pro Asp Tyr Cys Ser Lys Lys Val Arg Glu Pro  
 275 280 285

Gln

<210> 149  
 <211> 2200  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501) .. (1697)

<400> 149  
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gaagggatgc tccctcttga cgaatggttc aattttgcag gcggtaatga aaactaccgg 180  
gtatgggcggtg ctttagagga cggcaagcct gtcggcggtg tcatggttga agttgaggag 240  
gacttgaccg ggaacattgc ccttttagtc gatccgtttt tgcgcggagg gggatatgga 300  
aaagcgctca tcaaaaggac gatggcattg ccggaaatga gccggatcaa caaatggttc 360  
gccggaattg aagaggataa caagaggtgc ttagcgtgct tccgatccgt cgggtattca 420  
ttggaacacg aacagccgga cgaagactgc tactactctc ttattttattt cccggaatct 480  
taaataagga gcataagaag atg aac ttg atc aaa tgg att ttg ttt tcc gtt 533  
Met Asn Leu Ile Lys Trp Ile Leu Phe Ser Val  
1 5 10  
att tca ttc gcc ttt ttt cag ccg gca cca gcc gct cta tta aaa gaa 581  
Ile Ser Phe Ala Phe Phe Gln Pro Ala Pro Ala Ala Leu Leu Lys Glu  
15 20 25  
aag gac gac tat act att ctt gtt tat atg att ggt tct gac atg gaa 629  
Lys Asp Asp Tyr Thr Ile Leu Val Tyr Met Ile Gly Ser Asp Met Glu  
30 35 40  
agc gat ttt cat atg gca agc gat gac att cag gaa atg atg gat gcg 677  
Ser Asp Phe His Met Ala Ser Asp Asp Ile Gln Glu Met Met Asp Ala  
45 50 55  
ggg tca tct tca aac gtc aat gtc gtt ctt cag aca gga gga gca aaa 725  
Gly Ser Ser Ser Asn Val Asn Val Val Leu Gln Thr Gly Gly Ala Lys  
60 65 70 75  
aaa tgg gcg aac ccg tcg atc agt cac aag gtg aat cag agg tgg aaa 773  
Lys Trp Ala Asn Pro Ser Ile Ser His Lys Val Asn Gln Arg Trp Lys  
80 85 90  
gtt gaa cat cag aag ctg gtg ccc ctc gaa aat gtc ggg aag aaa aat 821  
Val Glu His Gln Lys Leu Val Pro Leu Glu Asn Val Gly Lys Lys Asn  
95 100 105  
atg gac agt ccc ggc tcc gtc aca gat ttt atc aca tgg gga gtc aaa 869  
Met Asp Ser Pro Gly Ser Val Thr Asp Phe Ile Thr Trp Gly Val Lys  
110 115 120  
aca tat ccg gct aaa aaa tat gta ttg atc ttt tgg ggg cat ggg ctt 917  
Thr Tyr Pro Ala Lys Lys Tyr Val Leu Ile Phe Trp Gly His Gly Leu  
125 130 135  
ggc tca gtt gac ggc tac ggg gga gac gaa aac ttc ggc aat aag aaa 965  
Gly Ser Val Asp Gly Tyr Gly Gly Asp Glu Asn Phe Gly Asn Lys Lys  
140 145 150 155  
atg aaa ata agc gag ctg cag tcg gga atc aaa acg gcc tat gaa cat 1013  
Met Lys Ile Ser Glu Leu Gln Ser Gly Ile Lys Thr Ala Tyr Glu His  
160 165 170

acg aag caa aag ttt gat tta atc ggt ttt gac aac tgc aaa atg gcc	1061
Thr Lys Gln Lys Phe Asp Leu Ile Gly Phe Asp Asn Cys Lys Met Ala	
175 180 185	
ggg att gaa acg gca tat gcc ttg agg gat tat ggt aag tac atg ctg	1109
Gly Ile Glu Thr Ala Tyr Ala Leu Arg Asp Tyr Gly Lys Tyr Met Leu	
190 195 200	
gct tca gtc gac tat acg aat caa aac ggc tgg gat tat aaa agg gcg	1157
Ala Ser Val Asp Tyr Thr Asn Gln Asn Gly Trp Asp Tyr Lys Arg Ala	
205 210 215	
ctg cag tct gta caa gac gac cct tca atc gat ccg aaa gag ctt ggc	1205
Leu Gln Ser Val Gln Asp Asp Pro Ser Ile Asp Pro Lys Glu Leu Gly	
220 225 230 235	
agg gaa atc gct gca ggc tac gta cag cag tca aaa gaa aac ggt gaa	1253
Arg Glu Ile Ala Ala Gly Tyr Val Gln Gln Ser Lys Glu Asn Gly Glu	
240 245 250	
aca gaa gac ctg cag cag tct tta att caa ttg aac cgt gtc aaa gac	1301
Thr Glu Asp Leu Gln Gln Ser Leu Ile Gln Leu Asn Arg Val Lys Asp	
255 260 265	
gct gtc gat gcc ctc gac aga ttg agc gta aac atg aac ctg gca ttg	1349
Ala Val Asp Ala Leu Asp Arg Leu Ser Val Asn Met Asn Leu Ala Leu	
270 275 280	
aaa gag cct gac gga aag cgc ctg ctc cac tac gcg cgt ctc gct gct	1397
Lys Glu Pro Asp Gly Lys Arg Leu Leu His Tyr Ala Arg Leu Ala Ala	
285 290 295	
gaa gat tat gca gat gaa tcg gat atg gtt gat ttg gcg gat ttg tca	1445
Glu Asp Tyr Ala Asp Glu Ser Asp Met Val Asp Leu Ala Asp Leu Ser	
300 305 310 315	
agc ttg atc ggt cag cag atc gga gcc gag aaa gaa gca aaa gag gtc	1493
Ser Leu Ile Gly Gln Gln Ile Gly Ala Glu Lys Glu Ala Lys Glu Val	
320 325 330	
gta aaa tcc gtc aag aag gct gtc atc atg aac atc aaa tct ccg gag	1541
Val Lys Ser Val Lys Lys Ala Val Ile Met Asn Ile Lys Ser Pro Glu	
335 340 345	
cat cca aga gga agc ggc atg tcc gtt tat tat ccg gcc aga gac aac	1589
His Pro Arg Gly Ser Gly Met Ser Val Tyr Tyr Pro Ala Arg Asp Asn	
350 355 360	
cat aag cgg ttt gcg gaa aaa tcg aaa ata tac cgc ctg ctt gac ttc	1637
His Lys Arg Phe Ala Glu Lys Ser Lys Ile Tyr Arg Leu Leu Asp Phe	
365 370 375	
agc agc cgg tat caa aca ttc atc aaa gat tac tcg cat tca aca ttt	1685
Ser Ser Arg Tyr Gln Thr Phe Ile Lys Asp Tyr Ser His Ser Thr Phe	
380 385 390 395	

aac ttt gat cta tagttgcgtt taacagcaaa aaagcgccgg cggaataacc 1737  
Asn Phe Asp Leu

ggcacttttt ttatcggctc atgtgcttcc ggatcaatgg aagtcgtag atgatgaaag 1797  
cggcgacatg ggcgatgaca acgttgagaa taaagagtgc gatcatgaga gagtgcctg 1857  
taggagaaag gctgctggtc atatagaaaa agaagaatac ccacattaaa atgatgggcg 1917  
gaatagaaga aattgcgacc tttttgttgt ccagccataa aaataaagga gtggcgcttg 1977  
caatcagcaa gtaagcgaaa aacatatcca tgcgttttca gcccctttcg ataatgatag 2037  
cgctgtcaaa aaaagcggaa tgaaacatca attgtgtcta attggagaat attttgtgaa 2097  
cattctgtta cttttattat accacgttct tcgaaaaatg atacatactg gaaagcattt 2157  
tccgtccaa ctatcggctc aattttcacg gtgattcagt tag 2200

<210> 150  
<211> 399  
<212> PRT  
<213> Bacillus licheniformis

<400> 150

Met Asn Leu Ile Lys Trp Ile Leu Phe Ser Val Ile Ser Phe Ala Phe  
1 5 10 15

Phe Gln Pro Ala Pro Ala Ala Leu Leu Lys Glu Lys Asp Asp Tyr Thr  
20 25 30

Ile Leu Val Tyr Met Ile Gly Ser Asp Met Glu Ser Asp Phe His Met  
35 40 45

Ala Ser Asp Asp Ile Gln Glu Met Met Asp Ala Gly Ser Ser Ser Asn  
50 55 60

Val Asn Val Val Leu Gln Thr Gly Gly Ala Lys Lys Trp Ala Asn Pro  
65 70 75 80

Ser Ile Ser His Lys Val Asn Gln Arg Trp Lys Val Glu His Gln Lys  
85 90 95

Leu Val Pro Leu Glu Asn Val Gly Lys Lys Asn Met Asp Ser Pro Gly  
100 105 110

Ser Val Thr Asp Phe Ile Thr Trp Gly Val Lys Thr Tyr Pro Ala Lys

115		120		125
Lys Tyr Val Leu Ile Phe Trp Gly His Gly Leu Gly Ser Val Asp Gly				
130		135		140
Tyr Gly Gly Asp Glu Asn Phe Gly Asn Lys Lys Met Lys Ile Ser Glu				
145		150		155 160
Leu Gln Ser Gly Ile Lys Thr Ala Tyr Glu His Thr Lys Gln Lys Phe				
	165		170	175
Asp Leu Ile Gly Phe Asp Asn Cys Lys Met Ala Gly Ile Glu Thr Ala				
	180		185	190
Tyr Ala Leu Arg Asp Tyr Gly Lys Tyr Met Leu Ala Ser Val Asp Tyr				
	195		200	205
Thr Asn Gln Asn Gly Trp Asp Tyr Lys Arg Ala Leu Gln Ser Val Gln				
	210		215	220
Asp Asp Pro Ser Ile Asp Pro Lys Glu Leu Gly Arg Glu Ile Ala Ala				
225		230		235 240
Gly Tyr Val Gln Gln Ser Lys Glu Asn Gly Glu Thr Glu Asp Leu Gln				
	245		250	255
Gln Ser Leu Ile Gln Leu Asn Arg Val Lys Asp Ala Val Asp Ala Leu				
	260		265	270
Asp Arg Leu Ser Val Asn Met Asn Leu Ala Leu Lys Glu Pro Asp Gly				
	275		280	285
Lys Arg Leu Leu His Tyr Ala Arg Leu Ala Ala Glu Asp Tyr Ala Asp				
	290		295	300
Glu Ser Asp Met Val Asp Leu Ala Asp Leu Ser Ser Leu Ile Gly Gln				
305		310		315 320
Gln Ile Gly Ala Glu Lys Glu Ala Lys Glu Val Val Lys Ser Val Lys				
	325		330	335
Lys Ala Val Ile Met Asn Ile Lys Ser Pro Glu His Pro Arg Gly Ser				
	340		345	350

Gly Met Ser Val Tyr Tyr Pro Ala Arg Asp Asn His Lys Arg Phe Ala  
 355 360 365

Glu Lys Ser Lys Ile Tyr Arg Leu Leu Asp Phe Ser Ser Arg Tyr Gln  
 370 375 380

Thr Phe Ile Lys Asp Tyr Ser His Ser Thr Phe Asn Phe Asp Leu  
 385 390 395

<210> 151  
 <211> 1170  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(674)

<400> 151  
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 tttaatgcaa aggatttctt aatctcccat aaaaaagag acttgccgaa gcccaaacta 120  
 acgcctgaaa aagcgaaagc aagcctgaat cccaacgtaa agttcagga gacgcgctt 180  
 gctttagtca cgaacgagct ttcgcaagaa gtgctctgct acgaaattct cggcacgatt 240  
 gaaaacgata cattccgcat gttcatcaat gccaatgacg gcacggaaga gaagggttcag 300  
 aaaatgaaaa ggcgagaacc gatatacaac gacttgtaaa aacgatagat caaagggaaa 360  
 aggcgataac atgccttttc ctttttagca ttcggaataa ttcgccctaa acatttccat 420  
 actgaacata tgggcggaac gtccgccggt aaattgaaaa tgcccggggc cataaatttt 480  
 ccgggcagcg gaggaataat atg aaa aca atc gaa cgg tta tta ttt aag ata 533  
 Met Lys Thr Ile Glu Arg Leu Leu Phe Lys Ile  
 1 5 10  
 ctc gtc gta cag acg gtc att tta atc agc gtg cag ctt ctt ttt cat 581  
 Leu Val Val Gln Thr Val Ile Leu Ile Ser Val Gln Leu Leu Phe His  
 15 20 25  
 ttc tcc aag gct gag cct tat ctg tca aag gtc gtg cag tat gaa ggc 629  
 Phe Ser Lys Ala Glu Pro Tyr Leu Ser Lys Val Val Gln Tyr Glu Gly  
 30 35 40  
 gtg aac aac atg aaa atc ggc gaa tgg atc gag aca ttt aag ccg 674  
 Val Asn Asn Met Lys Ile Gly Glu Trp Ile Glu Thr Phe Lys Pro  
 45 50 55

taattcacgc taaaatctcc cctttttcgc ctaatacatg atacaatcct ataaggagta 734  
 ccagatagca aggagaggaa ttatggaaaa gaaattatgc attgcaatag acggccctgc 794  
 ggcagccgga aaaagcaccg tggcgaaaaat cgtggccaga aaaaagtcgt atatttatat 854  
 tgatacgggt gccatgtaca gggcgattac gtatctagcg ctggaaaagg gcgttgattt 914  
 aaacgacgaa gcggcgctga cggccttggt aaaagaatct gccatcgatc tcacggtttc 974  
 gcctgaagga gagcagaagg tttatatcgc aggcgaagat gtaacagagg cgatccgcac 1034  
 ggatagcgtg agcaaccaag tctccatcgt cgccaaatac gccgggatcc gcgaagaaat 1094  
 gacgaaaagg cagcagcagc tggctgaaaa aggcggagtc gtcatggacg gccgcgacat 1154  
 cggaaccac gttctc 1170

<210> 152  
 <211> 58  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 152

Met Lys Thr Ile Glu Arg Leu Leu Phe Lys Ile Leu Val Val Gln Thr  
 1 5 10 15

Val Ile Leu Ile Ser Val Gln Leu Leu Phe His Phe Ser Lys Ala Glu  
 20 25 30

Pro Tyr Leu Ser Lys Val Val Gln Tyr Glu Gly Val Asn Asn Met Lys  
 35 40 45

Ile Gly Glu Trp Ile Glu Thr Phe Lys Pro  
 50 55

<210> 153  
 <211> 1435  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(932)

<400> 153  
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 tcaaaaacgc gcctatgcga aggtttttat cagctgtgaa ttccattggt ttttcttgac 120

cgtcttcacac aaaaccggcc agttcatatt tgaagacgga gtattcctcg ccgtcgtcaa 180  
atctcgacgt gtcttctctcc ccgtttccag taatgtgaac ataattctcg tccgtcccca 240  
cacggtttaa gttacatccg cttaaaaatg cggcaaatat gatcatcagg ctgatccatg 300  
gaatatgggt ttttcacttt ttctcctcat ttatggtttc tgtgtaaag ataagattca 360  
ttgtctgata aaaaaattga ataacgtgac atgaacatta cacttttgta agggatcggt 420  
ttagcacacg caggcaaatt aaatttcaat atccttttta ttcaataaag tttataatat 480  
ggaaaaaagg aggggcgcca atg aaa aaa atc gta tgt ttg atg gtg ttt tca 533  
Met Lys Lys Ile Val Cys Leu Met Val Phe Ser  
1 5 10  
atc atg acg gcc ttc ggt att cac atc cag cct gct gaa gct gcg gtt 581  
Ile Met Thr Ala Phe Gly Ile His Ile Gln Pro Ala Glu Ala Ala Val  
15 20 25  
ata aaa gat gag aaa aag atg acc atg aca atg act gaa gat cat gtg 629  
Ile Lys Asp Glu Lys Lys Met Thr Met Thr Met Thr Glu Asp His Val  
30 35 40  
gga ttt ttt atg gcg gac agc acc aat gta aat tac tac ccg aca tgg 677  
Gly Phe Phe Met Ala Asp Ser Thr Asn Val Asn Tyr Tyr Pro Thr Trp  
45 50 55  
ctg tat tac aag ctt acg att ttt aac gcg gaa ggc tgc aca ctc aac 725  
Leu Tyr Tyr Lys Leu Thr Ile Phe Asn Ala Glu Gly Cys Thr Leu Asn  
60 65 70 75  
atc aag ctg cag aga atc acg tta aca gga cat gcg gtc act tta agc 773  
Ile Lys Leu Gln Arg Ile Thr Leu Thr Gly His Ala Val Thr Leu Ser  
80 85 90  
gag aaa gag tat acg gga aat cat ctt cat tta agt gct gca gat aaa 821  
Glu Lys Glu Tyr Thr Gly Asn His Leu His Leu Ser Ala Ala Asp Lys  
95 100 105  
gtg agc ggg tcg ccg cac cga aat cat ttc ttg gat atc aca aaa gtg 869  
Val Ser Gly Ser Pro His Arg Asn His Phe Leu Asp Ile Thr Lys Val  
110 115 120  
tcg ggg tgc ggg gat gtt gga atc aca ggt ttt tac ggc ttt gag cac 917  
Ser Gly Cys Gly Asp Val Gly Ile Thr Gly Phe Tyr Gly Phe Glu His  
125 130 135  
caa atg ccg ggc tac taattgatat agaaagcgcg ggaggggact tttccagagt 972  
Gln Met Pro Gly Tyr  
140  
ccttttttca tatcatcgca aaaaatgcta aatatcagga gaaaaaaca acgctgcttt 1032  
tattgagagg cgccatcctc ttgctgctat gttctgcggc tggttatgct ctttatcagc 1092  
atgttgccgg aggccggaat gaacaggcag gcgccgtcct tcatcagcag gcattacatt 1152



ttaaattatc gacttttagag ggcggtgaca tcgaactgaa aaaatgacgg ggaaaggcgg 1212  
 tgcttgtcaa cttttggggg gctttttgta caccgtgcaa agaggagatg cccgtcatgc 1272  
 aaaaagctta tgaccgtttt aaaggagacg gttttgaaat catcgctgtc aatgtgcgtg 1332  
 aatcgaaagg tgcggtaaag agctttgtcg accgccatgg cttaactttt ccggtcgctt 1392  
 tggatcaatc ggctgaagtt taccgttctt gggaaatgta tta 1435

<210> 154  
 <211> 144  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 154

Met Lys Lys Ile Val Cys Leu Met Val Phe Ser Ile Met Thr Ala Phe  
 1 5 10 15

Gly Ile His Ile Gln Pro Ala Glu Ala Ala Val Ile Lys Asp Glu Lys  
 20 25 30

Lys Met Thr Met Thr Met Thr Glu Asp His Val Gly Phe Phe Met Ala  
 35 40 45

Asp Ser Thr Asn Val Asn Tyr Tyr Pro Thr Trp Leu Tyr Tyr Lys Leu  
 50 55 60

Thr Ile Phe Asn Ala Glu Gly Cys Thr Leu Asn Ile Lys Leu Gln Arg  
 65 70 75 80

Ile Thr Leu Thr Gly His Ala Val Thr Leu Ser Glu Lys Glu Tyr Thr  
 85 90 95

Gly Asn His Leu His Leu Ser Ala Ala Asp Lys Val Ser Gly Ser Pro  
 100 105 110

His Arg Asn His Phe Leu Asp Ile Thr Lys Val Ser Gly Cys Gly Asp  
 115 120 125

Val Gly Ile Thr Gly Phe Tyr Gly Phe Glu His Gln Met Pro Gly Tyr  
 130 135 140

<210> 155  
 <211> 1768

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(1265)

<400> 155

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aacgatcaat tgatggacaa attggagcca tatccatatg atcagctgaa agatttttaa      120
acggcctatt tggcaggcta catcgctgaa aaatataatt acgatgatga agagcttttt      180
ccgcggggcga aaagcaaaat cagcggctac atcgagtcac atatcgattc caccctgtcc      240
gggtacagct cagtcgatgt gaaaacgaaa cacgtcgata cacaaaaagt gaaaagcttg      300
tatgtgcttt tgcctgtctg gatggccaat tacaactaca aacaaaagga ttacatcttt      360
gccatgaacg gacaaacggg aaaagtcgtc ggcaagccgc cgatcagctc atttaaagaa      420
aaaatgtggt tcagcgggct ggccgtctcc atatttgcac tctggaaaat cattgctgct      480
gtaatgggag gcggggcggtg atg aga agt tta ttg aga agc gcg atg atc tta      533
                        Met Arg Ser Leu Leu Arg Ser Ala Met Ile Leu
                        1           5           10

tgt atg att ttc ctt gtc ttc atc cct ata gcc tcc ggt gcg gca gcc      581
Cys Met Ile Phe Leu Val Phe Ile Pro Ile Ala Ser Gly Ala Ala Ala
                        15           20           25

tct gaa cag aag cgg ttt gtt tat gat gaa gcc ggg ctt ctg acc aaa      629
Ser Glu Gln Lys Arg Phe Val Tyr Asp Glu Ala Gly Leu Leu Thr Lys
                        30           35           40

cag gaa atc gag aag ctg gaa acg ctg gca gcc aaa ttg ggc gcc gaa      677
Gln Glu Ile Glu Lys Leu Glu Thr Leu Ala Ala Lys Leu Gly Ala Glu
                        45           50           55

cgg gag acc gac ttt atc att gtg acg acc aat gat aca aac ggc cgc      725
Arg Glu Thr Asp Phe Ile Ile Val Thr Thr Asn Asp Thr Asn Gly Arg
60           65           70           75

gat gta aag aaa tat gcg gag gac ttc tat gac gaa aaa gcg ccc ggc      773
Asp Val Lys Lys Tyr Ala Glu Asp Phe Tyr Asp Glu Lys Ala Pro Gly
                        80           85           90

tac cag aag aag cac gga aat gca gcc gta tta acg gta gat atg gag      821
Tyr Gln Lys Lys His Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu
                        95           100          105

cat aga gaa gtc tat ctt gcc ggc ttt aaa aag gct gaa gaa tat ttg      869
His Arg Glu Val Tyr Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu
110           115          120
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aat gac gcc agg ctg gac aaa att aga gaa aaa atc acg ccg gat ata	917
Asn Asp Ala Arg Leu Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile	
125 130 135	
tcc gac aag cat tat gag gcc gca ttc gaa atg ttt atg aag gcg gcg	965
Ser Asp Lys His Tyr Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala	
140 145 150 155	
cat gat gat atg gag aag aaa ccg tgg gcg gac agc atc ttt ttt aag	1013
His Asp Asp Met Glu Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys	
160 165 170	
acg tgg ttt caa ttg ctt gtt tcg gca gtc atc gcg gga att gcc gtc	1061
Thr Trp Phe Gln Leu Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val	
175 180 185	
gcc att atg aaa tac aat tca ggc ggc aaa gtg aca gta agt gca agc	1109
Ala Ile Met Lys Tyr Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser	
190 195 200	
act tat atg aac ggt gat acg tcc gga gtg atc aga aat aat gac gaa	1157
Thr Tyr Met Asn Gly Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu	
205 210 215	
tac atc aga acg acc gtc aca aaa cag aga aaa ccg tcc aat aat aaa	1205
Tyr Ile Arg Thr Thr Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys	
220 225 230 235	
agc tca ggc ggc gga acg acg agc gga ggc cat tcg cac agc ggc agc	1253
Ser Ser Gly Gly Gly Thr Thr Ser Gly Gly His Ser His Ser Gly Ser	
240 245 250	
cgg gga agc ttt tagaaaggggaa aaggaagagc ttaaattggtg ttttttagaa	1305
Arg Gly Ser Phe	
255	
atcaattttgc aaatgtagta gagtgggatg aatttcgcga tgatatgatt ttctataaat	1365
ggaacaaccg cgaaatcaaaa aaggggagcc ggctgatcat tcgccccggt caggatgccg	1425
tcttttttaaa caacggaaaa attgaaggca ttttccagga tgagggcgac tatgatattg	1485
aatccgaaat tattcctttt ttatccactt taaaagggtt taaatttggc tttaacagcg	1545
ggatgcgcgc cgaagtcctg tttgtcaaca cgaaggaatt taccgtcaag tgggggacga	1605
agaatgccat caatatcccg gctgcaggac ttccgggcgg catgccgatc agggcgaacg	1665
gaagatttaa ctttaaggtg aatgattatg tcgcattaat cgataaaaatt gccggtgtga	1725
aagatcagta tgttgtggaa gatatacaaaa tacggatcac atc	1768
<210> 156	
<211> 255	
<212> PRT	
<213> Bacillus licheniformis	

<400> 156

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1 5 10 15

Val Phe Ile Pro Ile Ala Ser Gly Ala Ala Ala Ser Glu Gln Lys Arg  
20 25 30

Phe Val Tyr Asp Glu Ala Gly Leu Leu Thr Lys Gln Glu Ile Glu Lys  
35 40 45

Leu Glu Thr Leu Ala Ala Lys Leu Gly Ala Glu Arg Glu Thr Asp Phe  
50 55 60

Ile Ile Val Thr Thr Asn Asp Thr Asn Gly Arg Asp Val Lys Lys Tyr  
65 70 75 80

Ala Glu Asp Phe Tyr Asp Glu Lys Ala Pro Gly Tyr Gln Lys Lys His  
85 90 95

Gly Asn Ala Ala Val Leu Thr Val Asp Met Glu His Arg Glu Val Tyr  
100 105 110

Leu Ala Gly Phe Lys Lys Ala Glu Glu Tyr Leu Asn Asp Ala Arg Leu  
115 120 125

Asp Lys Ile Arg Glu Lys Ile Thr Pro Asp Ile Ser Asp Lys His Tyr  
130 135 140

Glu Ala Ala Phe Glu Met Phe Met Lys Ala Ala His Asp Asp Met Glu  
145 150 155 160

Lys Lys Pro Trp Ala Asp Ser Ile Phe Phe Lys Thr Trp Phe Gln Leu  
165 170 175

Leu Val Ser Ala Val Ile Ala Gly Ile Ala Val Ala Ile Met Lys Tyr  
180 185 190

Asn Ser Gly Gly Lys Val Thr Val Ser Ala Ser Thr Tyr Met Asn Gly  
195 200 205

Asp Thr Ser Gly Val Ile Arg Asn Asn Asp Glu Tyr Ile Arg Thr Thr  
210 215 220

Val Thr Lys Gln Arg Lys Pro Ser Asn Asn Lys Ser Ser Gly Gly Gly  
 225 230 235 240

Thr Thr Ser Gly Gly His Ser His Ser Gly Ser Arg Gly Ser Phe  
 245 250 255

<210> 157  
 <211> 1688  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1652)

<400> 157  
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 gtctatcatc gatgcataga agaatttttt acaccgaaaa aagatacttg gtacgaagac 180  
 agcagagcgg cctacacggg aaaaaacgcc atttgctttc acgaaccagc gccggcctca 240  
 ttaaaaaatt tgatggcttc gcttgaaaca ggatatcaat cgatgagaga agaattggaa 300  
 tactatgcga ctgactatcg aatgaagatg gttcagccga gatcatagct taaatgaacc 360  
 gtgagccgga actccccctt tcatgaaagg ggggttttta tcttgcttta gattttttctc 420  
 gggaaatcat ccaattggtg ttcataacaa aaagacaagc gcataaactt gtacaaacaa 480  
 ccacaaggac gtgagaaaaa atg cgc ttt ttt cta aaa caa gcg gca gca gcc 533  
 Met Arg Phe Phe Leu Lys Gln Ala Ala Ala Ala  
 1 5 10  
 atc atg ata tgc tct ctt tta tgc tct tca tac gaa acc gct caa gca 581  
 Ile Met Ile Cys Ser Leu Leu Cys Ser Ser Tyr Glu Thr Ala Gln Ala  
 15 20 25  
 cag ccc tcc ctt cat atc agc gca aaa agc gcg att gtc atg gac ggg 629  
 Gln Pro Ser Leu His Ile Ser Ala Lys Ser Ala Ile Val Met Asp Gly  
 30 35 40  
 caa tcc gga cgg gtt ttg ttt gca aag gat gag cat gaa aaa cgg cgc 677  
 Gln Ser Gly Arg Val Leu Phe Ala Lys Asp Glu His Glu Lys Arg Arg  
 45 50 55  
 att gca agc att acg aag att atg aca gcc att ttg gcc gtg gaa tcg 725  
 Ile Ala Ser Ile Thr Lys Ile Met Thr Ala Ile Leu Ala Val Glu Ser  
 60 65 70 75

ggc aaa ttg gat gag acg gtc acg gtc agc gac aga gcg gtc agg aca	773
Gly Lys Leu Asp Glu Thr Val Thr Val Ser Asp Arg Ala Val Arg Thr	
80 85 90	
gag gga tca tcg atc tat tta aca agc ggg caa aag gtg aag ctg aag	821
Glu Gly Ser Ser Ile Tyr Leu Thr Ser Gly Gln Lys Val Lys Leu Lys	
95 100 105	
gac ctt gtt tac ggt ttg atg ctg aga tcg gga aat gat gca gcc gtt	869
Asp Leu Val Tyr Gly Leu Met Leu Arg Ser Gly Asn Asp Ala Ala Val	
110 115 120	
gcg att gcc gaa cat gtg ggc gga agc ctg gaa ggc ttt gtc tac atg	917
Ala Ile Ala Glu His Val Gly Gly Ser Leu Glu Gly Phe Val Tyr Met	
125 130 135	
atg aat caa aaa gcg gcc gag ctc ggc atg gaa aac acc ctg ttc cgc	965
Met Asn Gln Lys Ala Ala Glu Leu Gly Met Glu Asn Thr Leu Phe Arg	
140 145 150 155	
aat ccg cac gga ctt gat gac cac cct gat cac tat tcc tcg gcc tat	1013
Asn Pro His Gly Leu Asp Asp His Pro Asp His Tyr Ser Ser Ala Tyr	
160 165 170	
gat atg gcg ctt tta aca aaa tat gcg atg agc aat gaa acg tac aaa	1061
Asp Met Ala Leu Leu Thr Lys Tyr Ala Met Ser Asn Glu Thr Tyr Lys	
175 180 185	
aaa atc gcc gga acg aaa cgc tat aaa gca gaa acg atg caa ggc atc	1109
Lys Ile Ala Gly Thr Lys Arg Tyr Lys Ala Glu Thr Met Gln Gly Ile	
190 195 200	
tgg gag aat aaa aac aag ctt tta aca ggg ctt tac aaa tac agt aca	1157
Trp Glu Asn Lys Asn Lys Leu Leu Thr Gly Leu Tyr Lys Tyr Ser Thr	
205 210 215	
ggc ggg aag acg gga tat aca agg ctt gca aag cgg acg ctc gtc tcc	1205
Gly Gly Lys Thr Gly Tyr Thr Arg Leu Ala Lys Arg Thr Leu Val Ser	
220 225 230 235	
att tca tcg aaa gac gga acc gat ttg atc gcc gtc aca atc aat gcc	1253
Ile Ser Ser Lys Asp Gly Thr Asp Leu Ile Ala Val Thr Ile Asn Ala	
240 245 250	
cct gac gac tgg aat gat cat atg aac atg ttc aac tat gta ttc ggc	1301
Pro Asp Asp Trp Asn Asp His Met Asn Met Phe Asn Tyr Val Phe Gly	
255 260 265	
cag tac aaa aca tat atc atc gcc aaa aaa ggc gag att ccg aaa tta	1349
Gln Tyr Lys Thr Tyr Ile Ile Ala Lys Lys Gly Glu Ile Pro Lys Leu	
270 275 280	
aaa gac tct ttt tac gga cat aca gct ttt att aaa cgg gat gtc aca	1397
Lys Asp Ser Phe Tyr Gly His Thr Ala Phe Ile Lys Arg Asp Val Thr	
285 290 295	
tat ctt tta aac gaa gag gaa aaa gaa gat gtg aag gtt gat atc gag	1445

Tyr Leu Leu Asn Glu Glu Glu Lys Glu Asp Val Lys Val Asp Ile Glu  
 300 305 310 315  
 ctt ctt gaa ccg aaa aaa tca tgg cgt aaa aac aaa aaa gaa atc ccg 1493  
 Leu Leu Glu Pro Lys Lys Ser Trp Arg Lys Asn Lys Lys Glu Ile Pro  
 320 325 330  
 gac atc atc gga gaa atg aac gtc atg ttc gac gga aaa acg att gca 1541  
 Asp Ile Ile Gly Glu Met Asn Val Met Phe Asp Gly Lys Thr Ile Ala  
 335 340 345  
 agc gta ccg atc tat tat gaa aac gag cga aac aaa aat ccg aaa aaa 1589  
 Ser Val Pro Ile Tyr Tyr Glu Asn Glu Arg Asn Lys Asn Pro Lys Lys  
 350 355 360  
 tcg ttt ttc gag acc ttt caa tcc gta ttc caa aaa gcg gcg ggc ggt 1637  
 Ser Phe Phe Glu Thr Phe Gln Ser Val Phe Gln Lys Ala Ala Gly Gly  
 365 370 375  
 tca tca tgg tca ata taatctgggt cggcttaacg gtgatcggta tgggtgt 1688  
 Ser Ser Trp Ser Ile  
 380

<210> 158  
 <211> 384  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 158

Met Arg Phe Phe Leu Lys Gln Ala Ala Ala Ala Ile Met Ile Cys Ser  
 1 5 10 15

Leu Leu Cys Ser Ser Tyr Glu Thr Ala Gln Ala Gln Pro Ser Leu His  
 20 25 30

Ile Ser Ala Lys Ser Ala Ile Val Met Asp Gly Gln Ser Gly Arg Val  
 35 40 45

Leu Phe Ala Lys Asp Glu His Glu Lys Arg Arg Ile Ala Ser Ile Thr  
 50 55 60

Lys Ile Met Thr Ala Ile Leu Ala Val Glu Ser Gly Lys Leu Asp Glu  
 65 70 75 80

Thr Val Thr Val Ser Asp Arg Ala Val Arg Thr Glu Gly Ser Ser Ile  
 85 90 95

Tyr Leu Thr Ser Gly Gln Lys Val Lys Leu Lys Asp Leu Val Tyr Gly  
 100 105 110

Leu Met Leu Arg Ser Gly Asn Asp Ala Ala Val Ala Ile Ala Glu His  
 115 120 125

Val Gly Gly Ser Leu Glu Gly Phe Val Tyr Met Met Asn Gln Lys Ala  
 130 135 140

Ala Glu Leu Gly Met Glu Asn Thr Leu Phe Arg Asn Pro His Gly Leu  
 145 150 155 160

Asp Asp His Pro Asp His Tyr Ser Ser Ala Tyr Asp Met Ala Leu Leu  
 165 170 175

Thr Lys Tyr Ala Met Ser Asn Glu Thr Tyr Lys Lys Ile Ala Gly Thr  
 180 185 190

Lys Arg Tyr Lys Ala Glu Thr Met Gln Gly Ile Trp Glu Asn Lys Asn  
 195 200 205

Lys Leu Leu Thr Gly Leu Tyr Lys Tyr Ser Thr Gly Gly Lys Thr Gly  
 210 215 220

Tyr Thr Arg Leu Ala Lys Arg Thr Leu Val Ser Ile Ser Ser Lys Asp  
 225 230 235 240

Gly Thr Asp Leu Ile Ala Val Thr Ile Asn Ala Pro Asp Asp Trp Asn  
 245 250 255

Asp His Met Asn Met Phe Asn Tyr Val Phe Gly Gln Tyr Lys Thr Tyr  
 260 265 270

Ile Ile Ala Lys Lys Gly Glu Ile Pro Lys Leu Lys Asp Ser Phe Tyr  
 275 280 285

Gly His Thr Ala Phe Ile Lys Arg Asp Val Thr Tyr Leu Leu Asn Glu  
 290 295 300

Glu Glu Lys Glu Asp Val Lys Val Asp Ile Glu Leu Leu Glu Pro Lys  
 305 310 315 320

Lys Ser Trp Arg Lys Asn Lys Lys Glu Ile Pro Asp Ile Ile Gly Glu  
 325 330 335



Met Asn Val Met Phe Asp Gly Lys Thr Ile Ala Ser Val Pro Ile Tyr  
 340 345 350

Tyr Glu Asn Glu Arg Asn Lys Asn Pro Lys Lys Ser Phe Phe Glu Thr  
 355 360 365

Phe Gln Ser Val Phe Gln Lys Ala Ala Gly Gly Ser Ser Trp Ser Ile  
 370 375 380

<210> 159  
 <211> 1617  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1118)

<400> 159  
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 cctgctgctg cggttgctt tacagccccg ggtattaaag ataaggtacg ggggtgaaaa 120  
 aattcagcgg gtgaggtggt cgacatgagg aaaggagtca tccttgttct gttcgctatg 180  
 ctgttattgg caggctgcgg cacaacgcag cataatgggc aaagcgggtga tgagagccga 240  
 aaaggaacag gcgaggaaaac gctcgtgaaa gaaggcacct ttgtcggttt ggcggaccag 300  
 cataccgtcg ccgtcaatat tgacggcaaa gaaacgatgt ttcaggtccc tcccgaaaaa 360  
 cgggacaaat ataaagggat cgaggatgat acaaagggtg aagtggagta cacgaaagca 420  
 gaggacggaa cattacagct tgaagatatg aaaaagaaaag aatgatcgtt tgcaaaaagg 480  
 gattgtagga ggaacaaatc gtg aaa ctg tta ata aag agt ttt gtt ttg ctg 533  
 Val Lys Leu Leu Ile Lys Ser Phe Val Leu Leu  
 1 5 10  
 ctg ttt tcg ttt atg gcg gct ttt cca gct gct ttt gcg gct gag ccg 581  
 Leu Phe Ser Phe Met Ala Ala Phe Pro Ala Ala Phe Ala Ala Glu Pro  
 15 20 25  
 ctt tcc ggg aag acg gta tat gtt gac gca ggt cac ggg ggt gaa gac 629  
 Leu Ser Gly Lys Thr Val Tyr Val Asp Ala Gly His Gly Gly Glu Asp  
 30 35 40  
 agc ggt gct gtc gga aac ggg ctg ctt gag aaa gat gtc aac ctt gaa 677  
 Ser Gly Ala Val Gly Asn Gly Leu Leu Glu Lys Asp Val Asn Leu Glu  
 45 50 55  
 gtg gca atg ctg att gat gaa aag ctg aaa gaa gaa gga gcc gac aca 725

Val	Ala	Met	Leu	Ile	Asp	Glu	Lys	Leu	Lys	Glu	Glu	Gly	Ala	Asp	Thr	
60					65					70					75	
gtc	gcc	tca	aga	acg	gat	gat	acg	ttt	ttg	acg	ctg	gaa	gac	cgg	gtg	773
Val	Ala	Ser	Arg	Thr	Asp	Asp	Thr	Phe	Leu	Thr	Leu	Glu	Asp	Arg	Val	
				80					85					90		
gcc	aag	gcg	agc	aaa	aat	gct	tca	gac	ttg	ttt	atc	agc	att	cat	gca	821
Ala	Lys	Ala	Ser	Lys	Asn	Ala	Ser	Asp	Leu	Phe	Ile	Ser	Ile	His	Ala	
				95				100					105			
aac	tcg	gcc	gtc	cct	gaa	gcg	tcc	ggg	aca	gaa	aca	tat	ttc	gat	tcc	869
Asn	Ser	Ala	Val	Pro	Glu	Ala	Ser	Gly	Thr	Glu	Thr	Tyr	Phe	Asp	Ser	
				110				115					120			
acg	tat	caa	gcc	gct	gac	agc	gaa	cgg	ctg	gca	tct	gac	att	caa	gag	917
Thr	Tyr	Gln	Ala	Ala	Asp	Ser	Glu	Arg	Leu	Ala	Ser	Asp	Ile	Gln	Glu	
				125				130					135			
cgg	ctt	ccg	gat	gcg	ctg	ggc	act	cgg	gac	aga	ggg	gta	aaa	gaa	tca	965
Arg	Leu	Pro	Asp	Ala	Leu	Gly	Thr	Arg	Asp	Arg	Gly	Val	Lys	Glu	Ser	
				140			145			150				155		
ggg	ttt	tat	gtc	atc	aaa	aat	tct	caa	atg	ccg	agt	gtt	tta	gtc	gaa	1013
Gly	Phe	Tyr	Val	Ile	Lys	Asn	Ser	Gln	Met	Pro	Ser	Val	Leu	Val	Glu	
				160					165					170		
ctg	ggc	ttt	atc	aca	aac	aaa	act	gat	gca	gat	aaa	ctc	gaa	agt	ccg	1061
Leu	Gly	Phe	Ile	Thr	Asn	Lys	Thr	Asp	Ala	Asp	Lys	Leu	Glu	Ser	Pro	
				175				180					185			
gaa	tat	cag	gaa	aaa	gct	gca	gac	gcg	att	gct	gac	gct	gtc	gta	tct	1109
Glu	Tyr	Gln	Glu	Lys	Ala	Ala	Asp	Ala	Ile	Ala	Asp	Ala	Val	Val	Ser	
				190				195					200			
tat	tat	gaa	taatagaagg	gccctgggtat	atgaccggggg	ttcttgtgtt										1158
Tyr	Tyr	Glu														
				205												
atgtttatgt	taaaaaaggc	cttatgtgtg	gaaagaaaac	agtaagacct	tcataatggg											1218
ttataaactt	gcaattcttg	tagagggtgaa	ccagaaatga	cgaaaatatt	tgcacacaga											1278
ggggcttcag	gcacttttcc	cgaaaataca	atggcggcgt	ttaagcatgc	ggcggccatt											1338
gggtccgacg	gcatcgaatt	ggatgttcaa	atggcaaaaag	acggacgtct	tgttgtcatt											1398
catgatgaaa	agcttgacag	gacgacttca	ctgaaagggt	atgtgaaaga	tcttacatat											1458
gaggaaataa	aacatggaga	cgcaagccac	cgttttgccg	aaaaaacggg	ttctgtccct											1518
gtgccgaccc	ttgaagaagt	gtttgagtgg	gcggcagatg	ctgaatttct	tcttaatggt											1578
gaattgaaaa	acagcattat	ccgctatgaa	gggatggaa													1617

<210> 160

<211> 206  
<212> PRT  
<213> Bacillus licheniformis

<400> 160

Val Lys Leu Leu Ile Lys Ser Phe Val Leu Leu Leu Phe Ser Phe Met  
1 5 10 15

Ala Ala Phe Pro Ala Ala Phe Ala Ala Glu Pro Leu Ser Gly Lys Thr  
20 25 30

Val Tyr Val Asp Ala Gly His Gly Gly Glu Asp Ser Gly Ala Val Gly  
35 40 45

Asn Gly Leu Leu Glu Lys Asp Val Asn Leu Glu Val Ala Met Leu Ile  
50 55 60

Asp Glu Lys Leu Lys Glu Glu Gly Ala Asp Thr Val Ala Ser Arg Thr  
65 70 75 80

Asp Asp Thr Phe Leu Thr Leu Glu Asp Arg Val Ala Lys Ala Ser Lys  
85 90 95

Asn Ala Ser Asp Leu Phe Ile Ser Ile His Ala Asn Ser Ala Val Pro  
100 105 110

Glu Ala Ser Gly Thr Glu Thr Tyr Phe Asp Ser Thr Tyr Gln Ala Ala  
115 120 125

Asp Ser Glu Arg Leu Ala Ser Asp Ile Gln Glu Arg Leu Pro Asp Ala  
130 135 140

Leu Gly Thr Arg Asp Arg Gly Val Lys Glu Ser Gly Phe Tyr Val Ile  
145 150 155 160

Lys Asn Ser Gln Met Pro Ser Val Leu Val Glu Leu Gly Phe Ile Thr  
165 170 175

Asn Lys Thr Asp Ala Asp Lys Leu Glu Ser Pro Glu Tyr Gln Glu Lys  
180 185 190

Ala Ala Asp Ala Ile Ala Asp Ala Val Val Ser Tyr Tyr Glu  
195 200 205

<210> 161  
 <211> 1803  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (165)..(1487)

<400> 161  
 atacagttca tagccttcat gaacatgcgg cgcgttcac tcggtaaatc cttttctctg 60  
 catatatattga atcgaaaaag aatgctcggc tatgaaatat ttaggatgga gcatgtcggg 120  
 cattcctcct tgagagcgtt ttcttaacaa acgggaggga tcgt atg aaa aag tta 176  
 Met Lys Lys Leu  
 1  
 tgt tgc ctg atc ttg gtc ttg gtt ttt tcc gcg ggc tgt act cag caa 224  
 Cys Cys Leu Ile Leu Val Leu Val Phe Ser Ala Gly Cys Thr Gln Gln  
 5 10 15 20  
 aag gca tca acg gaa gag gac ggg gcg ctt gaa atc aat tgg ctc gta 272  
 Lys Ala Ser Thr Glu Glu Asp Gly Ala Leu Glu Ile Asn Trp Leu Val  
 25 30 35  
 ccg ctc cac aca ccg cag cct ccg aaa gag aag gcg ctt gac atc att 320  
 Pro Leu His Thr Pro Gln Pro Pro Lys Glu Lys Ala Leu Asp Ile Ile  
 40 45 50  
 gaa gac aaa acg aat aca aag ctg aag ctc atc tgg gtt ccg gat tca 368  
 Glu Asp Lys Thr Asn Thr Lys Leu Lys Leu Ile Trp Val Pro Asp Ser  
 55 60 65  
 aca aaa gaa gag cgg atc aat aca acc ctt gca agc gga aac atg cct 416  
 Thr Lys Glu Glu Arg Ile Asn Thr Thr Leu Ala Ser Gly Asn Met Pro  
 70 75 80  
 aaa gta atg aca ttg cct gat ctt gaa gat tca gcg gtt gtc agc gcg 464  
 Lys Val Met Thr Leu Pro Asp Leu Glu Asp Ser Ala Val Val Ser Ala  
 85 90 95 100  
 ctg cgc tcg gga atg ttc tgg gaa atc gga ccg tat ttc aaa gac tat 512  
 Leu Arg Ser Gly Met Phe Trp Glu Ile Gly Pro Tyr Phe Lys Asp Tyr  
 105 110 115  
 ccg aat tta aga aaa ctt gat aaa act ata ttg aaa aat att tcg gtt 560  
 Pro Asn Leu Arg Lys Leu Asp Lys Thr Ile Leu Lys Asn Ile Ser Val  
 120 125 130  
 gat ggc aaa gtt tac ggg att tat aga gaa agg ccg atg gcc agg cag 608  
 Asp Gly Lys Val Tyr Gly Ile Tyr Arg Glu Arg Pro Met Ala Arg Gln  
 135 140 145  
 gga gtc gtg att cgg aaa gac tgg ctc gac aat ctc gga ttg gaa atg 656

Gly	Val	Val	Ile	Arg	Lys	Asp	Trp	Leu	Asp	Asn	Leu	Gly	Leu	Glu	Met	
150						155					160					
ccg	gaa	acc	gtt	gat	gac	ctt	tat	aaa	ata	gcg	aaa	gca	ttt	aca	gaa	704
Pro	Glu	Thr	Val	Asp	Asp	Leu	Tyr	Lys	Ile	Ala	Lys	Ala	Phe	Thr	Glu	
165					170				175						180	
cag	gac	ccc	gat	caa	aac	gga	aaa	gac	gac	acg	ttc	ggt	ctc	gcc	gac	752
Gln	Asp	Pro	Asp	Gln	Asn	Gly	Lys	Asp	Asp	Thr	Phe	Gly	Leu	Ala	Asp	
				185				190						195		
cgc	aat	gat	ctc	acc	ttc	gga	gcg	ttt	aaa	acc	ctg	gct	tcg	tac	ttt	800
Arg	Asn	Asp	Leu	Thr	Phe	Gly	Ala	Phe	Lys	Thr	Leu	Ala	Ser	Tyr	Phe	
			200					205					210			
ggc	gcg	ccg	aac	gaa	tgg	gga	acg	gac	gaa	gac	gga	aat	ctc	ttc	ccc	848
Gly	Ala	Pro	Asn	Glu	Trp	Gly	Thr	Asp	Glu	Asp	Gly	Asn	Leu	Phe	Pro	
		215					220					225				
tat	ttt	aag	cat	gag	gcc	tat	aaa	gac	gca	atg	gca	tac	atg	aaa	aag	896
Tyr	Phe	Lys	His	Glu	Ala	Tyr	Lys	Asp	Ala	Met	Ala	Tyr	Met	Lys	Lys	
	230					235					240					
ctt	tat	gaa	gaa	ggc	ctg	atg	aac	agg	gac	ttt	gcg	gtg	aca	agc	aaa	944
Leu	Tyr	Glu	Glu	Gly	Leu	Met	Asn	Arg	Asp	Phe	Ala	Val	Thr	Ser	Lys	
245					250				255						260	
acg	cag	cag	cag	gat	tta	gtg	att	cag	ggg	aaa	gcg	gga	atc	tat	atc	992
Thr	Gln	Gln	Gln	Asp	Leu	Val	Ile	Gln	Gly	Lys	Ala	Gly	Ile	Tyr	Ile	
				265				270						275		
ggc	gcg	atg	agc	gat	gcc	atg	aac	ttg	cgt	gat	cag	gga	ctc	gct	ttg	1040
Gly	Ala	Met	Ser	Asp	Ala	Met	Asn	Leu	Arg	Asp	Gln	Gly	Leu	Ala	Leu	
			280					285					290			
aac	ccc	ggc	ttt	cag	ctt	gat	atc	gca	aac	cgg	atc	aag	ggc	ccc	gac	1088
Asn	Pro	Gly	Phe	Gln	Leu	Asp	Ile	Ala	Asn	Arg	Ile	Lys	Gly	Pro	Asp	
		295					300					305				
ggc	aag	gag	cgc	aca	tgg	gcg	ctc	ggc	ggg	cat	ggc	ggg	atg	ttc	gcc	1136
Gly	Lys	Glu	Arg	Thr	Trp	Ala	Leu	Gly	Gly	His	Gly	Gly	Met	Phe	Ala	
	310					315					320					
att	tcg	aaa	tca	agc	gtc	aag	act	gaa	aaa	gag	gtc	aga	aaa	atc	ctc	1184
Ile	Ser	Lys	Ser	Ser	Val	Lys	Thr	Glu	Lys	Glu	Val	Arg	Lys	Ile	Leu	
325					330					335					340	
gca	ttt	ttt	gac	aga	atc	gct	gaa	gaa	gac	ctc	aac	aat	ttg	atg	ttg	1232
Ala	Phe	Phe	Asp	Arg	Ile	Ala	Glu	Glu	Asp	Leu	Asn	Asn	Leu	Met	Leu	
				345					350					355		
tat	gga	ata	gaa	ggc	gta	cac	tat	gaa	aag	aaa	ggg	ggg	agc	ggc	tat	1280
Tyr	Gly	Ile	Glu	Gly	Val	His	Tyr	Glu	Lys	Lys	Gly	Gly	Ser	Gly	Tyr	
			360					365					370			
ttt	cga	aag	cag	gaa	aac	tac	cat	ctg	tgg	gaa	gcg	gaa	att	cag	ccg	1328
Phe	Arg	Lys	Gln	Glu	Asn	Tyr	His	Leu	Trp	Glu	Ala	Glu	Ile	Gln	Pro	

375	380	385	
tta aac cag ctg att ggc gtc aat aaa caa gct tta aaa agc gct gaa			1376
Leu Asn Gln Leu Ile Gly Val Asn Lys Gln Ala Leu Lys Ser Ala Glu			
390	395	400	
gat ccg ctc cgc gcc aaa aat gaa aag ctt gag gag gac aac cgg gca			1424
Asp Pro Leu Arg Ala Lys Asn Glu Lys Leu Glu Glu Asp Asn Arg Ala			
405	410	415	420
atc gca gtc cag aat ccg gcc gaa ccg tgt att ctg ccg cac aga tgg			1472
Ile Ala Val Gln Asn Pro Ala Glu Pro Cys Ile Leu Pro His Arg Trp			
	425	430	435
aca ggg gaa cag aat tgaagaaaat cattgatgac gccacatttc aattttattct			1527
Thr Gly Glu Gln Asn			
440			
cggggaaatc aatgaaaaag ctttgaccag gcagtcctga aatgggagaa gcatggcggc			1587
ggaaagatca tgaaagaact gaatgaagat ctgaaaaaag caaactaaac agaaaaccct			1647
ttccattttt ttgaaaagga aagggttttt catcgtattc gctccaagtt cattttcttt			1707
aaattctgca aaataaacia tataattcca tcataggacg aaaaggagga agcgatatgc			1767
agactgccgt tatatatgca cacccaaadc caaaca			1803
<210>	162		
<211>	441		
<212>	PRT		
<213>	Bacillus licheniformis		
<400>	162		
Met Lys Lys Leu Cys Cys Leu Ile Leu Val Leu Val Phe Ser Ala Gly			
1	5	10	15
Cys Thr Gln Gln Lys Ala Ser Thr Glu Glu Asp Gly Ala Leu Glu Ile			
	20	25	30
Asn Trp Leu Val Pro Leu His Thr Pro Gln Pro Pro Lys Glu Lys Ala			
	35	40	45
Leu Asp Ile Ile Glu Asp Lys Thr Asn Thr Lys Leu Lys Leu Ile Trp			
	50	55	60
Val Pro Asp Ser Thr Lys Glu Glu Arg Ile Asn Thr Thr Leu Ala Ser			
	65	70	75
Gly Asn Met Pro Lys Val Met Thr Leu Pro Asp Leu Glu Asp Ser Ala			

85

90

95

Val Val Ser Ala Leu Arg Ser Gly Met Phe Trp Glu Ile Gly Pro Tyr  
 100 105 110

Phe Lys Asp Tyr Pro Asn Leu Arg Lys Leu Asp Lys Thr Ile Leu Lys  
 115 120 125

Asn Ile Ser Val Asp Gly Lys Val Tyr Gly Ile Tyr Arg Glu Arg Pro  
 130 135 140

Met Ala Arg Gln Gly Val Val Ile Arg Lys Asp Trp Leu Asp Asn Leu  
 145 150 155 160

Gly Leu Glu Met Pro Glu Thr Val Asp Asp Leu Tyr Lys Ile Ala Lys  
 165 170 175

Ala Phe Thr Glu Gln Asp Pro Asp Gln Asn Gly Lys Asp Asp Thr Phe  
 180 185 190

Gly Leu Ala Asp Arg Asn Asp Leu Thr Phe Gly Ala Phe Lys Thr Leu  
 195 200 205

Ala Ser Tyr Phe Gly Ala Pro Asn Glu Trp Gly Thr Asp Glu Asp Gly  
 210 215 220

Asn Leu Phe Pro Tyr Phe Lys His Glu Ala Tyr Lys Asp Ala Met Ala  
 225 230 235 240

Tyr Met Lys Lys Leu Tyr Glu Glu Gly Leu Met Asn Arg Asp Phe Ala  
 245 250 255

Val Thr Ser Lys Thr Gln Gln Gln Asp Leu Val Ile Gln Gly Lys Ala  
 260 265 270

Gly Ile Tyr Ile Gly Ala Met Ser Asp Ala Met Asn Leu Arg Asp Gln  
 275 280 285

Gly Leu Ala Leu Asn Pro Gly Phe Gln Leu Asp Ile Ala Asn Arg Ile  
 290 295 300

Lys Gly Pro Asp Gly Lys Glu Arg Thr Trp Ala Leu Gly Gly His Gly  
 305 310 315 320

Gly Met Phe Ala Ile Ser Lys Ser Ser Val Lys Thr Glu Lys Glu Val  
325 330 335

Arg Lys Ile Leu Ala Phe Phe Asp Arg Ile Ala Glu Glu Asp Leu Asn  
340 345 350

Asn Leu Met Leu Tyr Gly Ile Glu Gly Val His Tyr Glu Lys Lys Gly  
355 360 365

Gly Ser Gly Tyr Phe Arg Lys Gln Glu Asn Tyr His Leu Trp Glu Ala  
370 375 380

Glu Ile Gln Pro Leu Asn Gln Leu Ile Gly Val Asn Lys Gln Ala Leu  
385 390 395 400

Lys Ser Ala Glu Asp Pro Leu Arg Ala Lys Asn Glu Lys Leu Glu Glu  
405 410 415

Asp Asn Arg Ala Ile Ala Val Gln Asn Pro Ala Glu Pro Cys Ile Leu  
420 425 430

Pro His Arg Trp Thr Gly Glu Gln Asn  
435 440

<210> 163  
<211> 1400  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(983)

<400> 163  
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cgagcaagac taaattttctc attggttaatt ccccttttcc cctcagatta agaaactcac 120  
cttttacact gcaaaaaaaaa aaaactatgt aaaaaccata tagaattata tctaatttga 180  
tgtgaaatca caatattttct cgggaaaata acatacacta acgcctagaa tcgataatta 240  
gtaaaaactct ttaaagtatt aatatgttac aaaagcttta ttctccagcc ttaaactttg 300  
actaatgaaa cgcatttagg gtacgataaa aagtcgatgt gaggtgagat aaggtgtcaa 360



ggcgcttttg	aaattgaagc	atctgctgga	taaagtgggtg	caatagcatg	taagctgccg		420
gcataaaacc	ggcagcattt	tttaagcgtc	cgacgggaag	tctttttttg	attaaatttc		480
atgggttagcg	agtgaaaaaat	atg tca aca ata tta tgg ctt gtg agc ttc acg					533
		Met Ser Thr Ile Leu Trp Leu Val Ser Phe Thr					
		1	5		10		
ctc cac ggt ata ttg att tat ttc gtc atc att ttg aat acg agg ctc							581
Leu His Gly Ile Leu Ile Tyr Phe Val Ile Ile Leu Asn Thr Arg Leu							
	15		20		25		
agc gct ttc aag gca gcg gag aaa gag caa aaa cag ctt ttg gaa gaa							629
Ser Ala Phe Lys Ala Ala Glu Lys Glu Gln Lys Gln Leu Leu Glu Glu							
	30		35		40		
acc gag aat aca ttg acc gct ttt ttg atg gag tta aaa gac gaa aat							677
Thr Glu Asn Thr Leu Thr Ala Phe Leu Met Glu Leu Lys Asp Glu Asn							
	45		50		55		
gaa aaa ctc gtt caa gag att cgg gcg aat gcc gaa aaa gag ccg caa							725
Glu Lys Leu Val Gln Glu Ile Arg Ala Asn Ala Glu Lys Glu Pro Gln							
60		65		70		75	
aga ccg gaa aca cag cct gaa att ccc gct caa acc ccc gtc ctt ccg							773
Arg Pro Glu Thr Gln Pro Glu Ile Pro Ala Gln Thr Pro Val Leu Pro							
	80		85		90		
gaa gcg gac gaa tcg cgc gat ctg ccg ctt cac atc gaa gcg atg atc							821
Glu Ala Asp Glu Ser Arg Asp Leu Pro Leu His Ile Glu Ala Met Ile							
	95		100		105		
aat gag gtg gag cag gaa gag gat gag ctc aat caa aag gag cag gaa							869
Asn Glu Val Glu Gln Glu Glu Asp Glu Leu Asn Gln Lys Glu Gln Glu							
	110		115		120		
gca tcc ata tcc tat gaa gaa gaa gct ctc gca tta gaa aaa cat ggg							917
Ala Ser Ile Ser Tyr Glu Glu Glu Ala Leu Ala Leu Glu Lys His Gly							
	125		130		135		
gac tgg ggg aaa gaa ttt ttt cat aaa aca ggc ccc aaa atg ggg ggg							965
Asp Trp Gly Lys Glu Phe Phe His Lys Thr Gly Pro Lys Met Gly Gly							
140		145		150		155	
ggg ggt gtt cca gtc tct taaagaaaaa aaaaattcaa cctctcttct							1013
Gly Gly Val Pro Val Ser							
	160						
ttgggggaggg	gggggggggga	aaaaataagg	tggttggtaga	gggggggagga	attttttttt		1073
aaaggaaacc	ctcatgggga	gggagatgtg	ctttaaacga	gggaggggagc	gaggaaatgg		1133
cactggttcc	ataggatgaa	acgcgcggga	ttgtctccag	aaaacaggga	gaccccgga		1193
aaggagcggg	gcagccaatt	catcactttt	taagtttcaa	agcctcagca	aatttggggg		1253
ttaaaaatttc	acacggaatt	ggttggggagg	gaataaggag	agttttaaaaa	cccggccaatt		1313

tatcaagagg gagccgcagg gaggaata caatccacgg atcctaagtg gtgagatgtc 1373  
atgggggggat atggttttcgg actcgaa 1400

<210> 164  
<211> 161  
<212> PRT  
<213> Bacillus licheniformis  
<400> 164

Met Ser Thr Ile Leu Trp Leu Val Ser Phe Thr Leu His Gly Ile Leu  
1 5 10 15

Ile Tyr Phe Val Ile Ile Leu Asn Thr Arg Leu Ser Ala Phe Lys Ala  
20 25 30

Ala Glu Lys Glu Gln Lys Gln Leu Leu Glu Glu Thr Glu Asn Thr Leu  
35 40 45

Thr Ala Phe Leu Met Glu Leu Lys Asp Glu Asn Glu Lys Leu Val Gln  
50 55 60

Glu Ile Arg Ala Asn Ala Glu Lys Glu Pro Gln Arg Pro Glu Thr Gln  
65 70 75 80

Pro Glu Ile Pro Ala Gln Thr Pro Val Leu Pro Glu Ala Asp Glu Ser  
85 90 95

Arg Asp Leu Pro Leu His Ile Glu Ala Met Ile Asn Glu Val Glu Gln  
100 105 110

Glu Glu Asp Glu Leu Asn Gln Lys Glu Gln Glu Ala Ser Ile Ser Tyr  
115 120 125

Glu Glu Glu Ala Leu Ala Leu Glu Lys His Gly Asp Trp Gly Lys Glu  
130 135 140

Phe Phe His Lys Thr Gly Pro Lys Met Gly Gly Gly Gly Val Pro Val  
145 150 155 160

Ser

[illegible]

110	115	120	
ctg caa gga cag ata cat gga aat gag ccg gca gcg gga gaa tct gct			915
Leu Gln Gly Gln Ile His Gly Asn Glu Pro Ala Ala Gly Glu Ser Ala			
125	130	135	
ctg gcg ata gct gaa aaa ctg gcc gga ccg tat ggc gac aaa gtg ttg			963
Leu Ala Ile Ala Glu Lys Leu Ala Gly Pro Tyr Gly Asp Lys Val Leu			
140	145	150	
gac aag atc aat gtc atc gtt gtt ccg cgg gtc aat cct gac gga tca			1011
Asp Lys Ile Asn Val Ile Val Val Pro Arg Val Asn Pro Asp Gly Ser			
155	160	165	170
tat cag ttc aac aga cgg ctg gcg aac gga atc gac gga aac agg gat			1059
Tyr Gln Phe Asn Arg Arg Leu Ala Asn Gly Ile Asp Gly Asn Arg Asp			
175	180	185	
cat gtc aag ctc gag tct cca gaa gtg cgc gcc att cac caa gaa ttc			1107
His Val Lys Leu Glu Ser Pro Glu Val Arg Ala Ile His Gln Glu Phe			
190	195	200	
aat aag tat tcg cct gaa gtc gtt atc gat gcc cat gaa tac ggt gtc			1155
Asn Lys Tyr Ser Pro Glu Val Val Ile Asp Ala His Glu Tyr Gly Val			
205	210	215	
ggc caa aac gaa ttt cag agc ata ggc gaa aaa ggg tca tta aaa tac			1203
Gly Gln Asn Glu Phe Gln Ser Ile Gly Glu Lys Gly Ser Leu Lys Tyr			
220	225	230	
cat gat att tta att tta tca gga aaa aat tta aac att ccc aag tcg			1251
His Asp Ile Leu Ile Leu Ser Gly Lys Asn Leu Asn Ile Pro Lys Ser			
235	240	245	250
atc agg cat gcg tcc gac agc ctt tat gtg aac ggc gtc aga gct aaa			1299
Ile Arg His Ala Ser Asp Ser Leu Tyr Val Asn Gly Val Arg Ala Lys			
255	260	265	
ctt gat gaa aaa gga ttt tct aat gat gct tat tat acg aca gga aaa			1347
Leu Asp Glu Lys Gly Phe Ser Asn Asp Ala Tyr Tyr Thr Thr Gly Lys			
270	275	280	
agc aag gac gga aaa atc gaa atc tat gaa ggc ggt aca gaa gcg aga			1395
Ser Lys Asp Gly Lys Ile Glu Ile Tyr Glu Gly Gly Thr Glu Ala Arg			
285	290	295	
atc ggg cgt aat gca ttc gcc ctc cag cct gcc ctt tcc ttc ctg gtg			1443
Ile Gly Arg Asn Ala Phe Ala Leu Gln Pro Ala Leu Ser Phe Leu Val			
300	305	310	
gaa agc agg gga ata gac atc gga cgc gaa aat ttt gca aga aga gtc			1491
Glu Ser Arg Gly Ile Asp Ile Gly Arg Glu Asn Phe Ala Arg Arg Val			
315	320	325	330
gcg gct cag gtt gct aca cat gag acg atc atc gac acg aca gtg aag			1539
Ala Ala Gln Val Ala Thr His Glu Thr Ile Ile Asp Thr Thr Val Lys			
335	340	345	

cat gca gcc gag atc aag cgc ctt gtc tcc aaa gaa aaa tta aag ctg	1587
His Ala Ala Glu Ile Lys Arg Leu Val Ser Lys Glu Lys Leu Lys Leu	
350 355 360	
ata caa aac ggc gct aaa gtg agc gat aaa gac caa gtg gtc atc aac	1635
Ile Gln Asn Gly Ala Lys Val Ser Asp Lys Asp Gln Val Val Ile Asn	
365 370 375	
agt gag ttt gca ggc ccg ttt aaa gac acg ctt aaa gtc gct gat att	1683
Ser Glu Phe Ala Gly Pro Phe Lys Asp Thr Leu Lys Val Ala Asp Ile	
380 385 390	
gcc tca gga caa gca gtt gac gtt cct gtc caa tat tac agc gcc tca	1731
Ala Ser Gly Gln Ala Val Asp Val Pro Val Gln Tyr Tyr Ser Ala Ser	
395 400 405 410	
gag gcc gtt cct gtg ctg tca aga act cgg ccg acc gct tac ctt gtc	1779
Glu Ala Val Pro Val Leu Ser Arg Thr Arg Pro Thr Ala Tyr Leu Val	
415 420 425	
ctt ccg ggc cat caa gat atc gaa cag aag ctg aag gat cag gga tta	1827
Leu Pro Gly His Gln Asp Ile Glu Gln Lys Leu Lys Asp Gln Gly Leu	
430 435 440	
aag agc gtg aca ctg gct ttc aaa caa aaa ctc acc gct gaa gcg tat	1875
Lys Ser Val Thr Leu Ala Phe Lys Gln Lys Leu Thr Ala Glu Ala Tyr	
445 450 455	
gag gtt tta tcg aaa gaa aca gcg gga gaa tct gag ggc cgg cca gtg	1923
Glu Val Leu Ser Lys Glu Thr Ala Gly Glu Ser Glu Gly Arg Pro Val	
460 465 470	
atc aag gta gaa acg aag ctc aaa aaa cag aaa aaa gag ttt cct aaa	1971
Ile Lys Val Glu Thr Lys Leu Lys Lys Gln Lys Lys Glu Phe Pro Lys	
475 480 485 490	
gga aca aaa atc tat ttt aca gct cag cag caa agc aat ctg ctg tca	2019
Gly Thr Lys Ile Tyr Phe Thr Ala Gln Gln Gln Ser Asn Leu Leu Ser	
495 500 505	
atc gca ctt gag ccg gag tcg gtt gac agt tat gta agc aca ggt tac	2067
Ile Ala Leu Glu Pro Glu Ser Val Asp Ser Tyr Val Ser Thr Gly Tyr	
510 515 520	
att cct tct caa aaa ggc aaa gag ctg ccg gtt tac cgc ttc atg ctg	2115
Ile Pro Ser Gln Lys Gly Lys Glu Leu Pro Val Tyr Arg Phe Met Leu	
525 530 535	
aac acc aaa acg ctt aat ttt aag gaa taatcaccag gcatccgtct	2162
Asn Thr Lys Thr Leu Asn Phe Lys Glu	
540 545	
ttgacggatg ctttttagcg gttttttgtt ttttcataca taattgtttt aaactgagat	2222
cgaaacctat acaataaata tcagtctgaa atctggaagg agagaatccg gttggaatca	2282

catgaagaat tatggaggga agccaaggcc ttcacgcgagc tctgctacgg ggaactgtcg 2342  
aagtcggaag aagaaacaag gatgcgctta cataaaatag ataaagaaat cagagaaacc 2402  
ggaagctata cacatacatt agaagaaatc gaacatggag ccagaatggc gtggagaaac 2462  
agcagccgct gcatcggcag gctgttttgg cactctctta ctgtcatcga tcaaagaggc 2522  
gttcaaaccg aggagaggt gcgggatgcg cttttccacc atattcagct tgcaacaaac 2582  
ggagggaaaa tcagaccgtt cattacggtt ttcccccccg aacaaaacgg acacagcgaa 2642  
gt 2644

<210> 166  
<211> 547  
<212> PRT  
<213> Bacillus licheniformis

<400> 166

Met Lys Ile Gln Lys Arg Val Gln Ala Leu Leu Ala Thr Ser Ala Met  
1 5 10 15

Phe Ala Gly Leu Met Leu Ser Asp Ala Val Tyr Ala Ala Glu Thr Pro  
20 25 30

Tyr Tyr Gly Lys Asn Tyr Thr Gln Pro Glu Gln Val Ser Ser Leu Tyr  
35 40 45

Pro Glu Pro Glu Glu Thr Phe Ser Thr Pro Ala Phe Val Lys Glu Gly  
50 55 60

Glu Ala Phe Thr Thr Gln Glu Glu Met Met Lys Phe Ile Thr Ser Leu  
65 70 75 80

Thr Lys Lys Ser Pro Asn Val Lys Ile Gly Asn Ile Gly Phe Ser Ile  
85 90 95

Glu Lys Arg Asn Ile Pro Val Leu Tyr Phe Thr Lys Asp Lys Gln Ile  
100 105 110

Arg Ser Ile Ser Lys Lys Pro Thr Val Trp Leu Gln Gly Gln Ile His  
115 120 125

Gly Asn Glu Pro Ala Ala Gly Glu Ser Ala Leu Ala Ile Ala Glu Lys  
130 135 140

Leu Ala Gly Pro Tyr Gly Asp Lys Val Leu Asp Lys Ile Asn Val Ile  
 145 150 155 160

Val Val Pro Arg Val Asn Pro Asp Gly Ser Tyr Gln Phe Asn Arg Arg  
 165 170 175

Leu Ala Asn Gly Ile Asp Gly Asn Arg Asp His Val Lys Leu Glu Ser  
 180 185 190

Pro Glu Val Arg Ala Ile His Gln Glu Phe Asn Lys Tyr Ser Pro Glu  
 195 200 205

Val Val Ile Asp Ala His Glu Tyr Gly Val Gly Gln Asn Glu Phe Gln  
 210 215 220

Ser Ile Gly Glu Lys Gly Ser Leu Lys Tyr His Asp Ile Leu Ile Leu  
 225 230 235 240

Ser Gly Lys Asn Leu Asn Ile Pro Lys Ser Ile Arg His Ala Ser Asp  
 245 250 255

Ser Leu Tyr Val Asn Gly Val Arg Ala Lys Leu Asp Glu Lys Gly Phe  
 260 265 270

Ser Asn Asp Ala Tyr Tyr Thr Thr Gly Lys Ser Lys Asp Gly Lys Ile  
 275 280 285

Glu Ile Tyr Glu Gly Gly Thr Glu Ala Arg Ile Gly Arg Asn Ala Phe  
 290 295 300

Ala Leu Gln Pro Ala Leu Ser Phe Leu Val Glu Ser Arg Gly Ile Asp  
 305 310 315 320

Ile Gly Arg Glu Asn Phe Ala Arg Arg Val Ala Ala Gln Val Ala Thr  
 325 330 335

His Glu Thr Ile Ile Asp Thr Thr Val Lys His Ala Ala Glu Ile Lys  
 340 345 350

Arg Leu Val Ser Lys Glu Lys Leu Lys Leu Ile Gln Asn Gly Ala Lys  
 355 360 365

Val Ser Asp Lys Asp Gln Val Val Ile Asn Ser Glu Phe Ala Gly Pro  
 370 375 380

Phe Lys Asp Thr Leu Lys Val Ala Asp Ile Ala Ser Gly Gln Ala Val  
 385 390 395 400

Asp Val Pro Val Gln Tyr Tyr Ser Ala Ser Glu Ala Val Pro Val Leu  
 405 410 415

Ser Arg Thr Arg Pro Thr Ala Tyr Leu Val Leu Pro Gly His Gln Asp  
 420 425 430

Ile Glu Gln Lys Leu Lys Asp Gln Gly Leu Lys Ser Val Thr Leu Ala  
 435 440 445

Phe Lys Gln Lys Leu Thr Ala Glu Ala Tyr Glu Val Leu Ser Lys Glu  
 450 455 460

Thr Ala Gly Glu Ser Glu Gly Arg Pro Val Ile Lys Val Glu Thr Lys  
 465 470 475 480

Leu Lys Lys Gln Lys Lys Glu Phe Pro Lys Gly Thr Lys Ile Tyr Phe  
 485 490 495

Thr Ala Gln Gln Gln Ser Asn Leu Leu Ser Ile Ala Leu Glu Pro Glu  
 500 505 510

Ser Val Asp Ser Tyr Val Ser Thr Gly Tyr Ile Pro Ser Gln Lys Gly  
 515 520 525

Lys Glu Leu Pro Val Tyr Arg Phe Met Leu Asn Thr Lys Thr Leu Asn  
 530 535 540

Phe Lys Glu  
 545

<210> 167  
 <211> 2146  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1643)



<400> 167

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aagacaaaac taaagggaaa gatacaaaaag ataaagaaac gtctgcgagt gagcagaacg 120

gagaggttgt cacagaggaa tcacggttg atgaagattt attcacaaca taccgcatgg 180

aaatggacga tcagcgcagc agggagaggg aggaattaac cgaaatcgtc agaagcgata 240

aagcgacggc aaaagaaaaa agcgaagctt acgacaagat gacagagctc agcgaagctg 300

aaggaacgga aaagaccctt gaaaccctca tcaaaacaaa aggctattaa gacgccttgg 360

tcaacgccga cggcgataaa gtcaatatta cgggtgaaggc gaaggagcac tcgaaagccg 420

cctgcaccga gtttacattt cctcaaatga tagttttcat tgatttgcta gtataagtgt 480

tatcaaaagg aggttaatat atg aac ttt tac aaa acg ctc gcc tta tca act 533  
Met Asn Phe Tyr Lys Thr Leu Ala Leu Ser Thr  
1 5 10

ctt gcg gca tcc tta ttg tct ccc tca tgg agc att ctc ccc cgt gcc 581  
Leu Ala Ala Ser Leu Leu Ser Pro Ser Trp Ser Ile Leu Pro Arg Ala  
15 20 25

gaa gct tca gct tat aag gac ttc tcg gtg act gcc gat gca gag aca 629  
Glu Ala Ser Ala Tyr Lys Asp Phe Ser Val Thr Ala Asp Ala Glu Thr  
30 35 40

gag ccg gtg gat acc cct gac gac gcg gca gat gac ccg gcg att tgg 677  
Glu Pro Val Asp Thr Pro Asp Asp Ala Ala Asp Asp Pro Ala Ile Trp  
45 50 55

gtt cat ccg aag cag cct gaa aaa agc cgg ctg atc aca aca aat aaa 725  
Val His Pro Lys Gln Pro Glu Lys Ser Arg Leu Ile Thr Thr Asn Lys  
60 65 70 75

aaa tct ggc ttg atc gtt tac gat tta aac gga aaa cag ctg gca gcc 773  
Lys Ser Gly Leu Ile Val Tyr Asp Leu Asn Gly Lys Gln Leu Ala Ala  
80 85 90

tat ccg ttt ggc aaa tta aac aac gtc gat ctc cgc tac aat ttt ccg 821  
Tyr Pro Phe Gly Lys Leu Asn Asn Val Asp Leu Arg Tyr Asn Phe Pro  
95 100 105

ctc gat ggc aaa aaa att gat att gcc ggg gcc tca aac ccg tca gac 869  
Leu Asp Gly Lys Lys Ile Asp Ile Ala Gly Ala Ser Asn Arg Ser Asp  
110 115 120

ggc aaa aac acg gtt gaa ata tac gcc ttt gac ggc gaa aaa aac aag 917  
Gly Lys Asn Thr Val Glu Ile Tyr Ala Phe Asp Gly Glu Lys Asn Lys  
125 130 135

ctg aaa aac atc gtc aat cct caa aaa cct att caa acc gat att gag 965  
Leu Lys Asn Ile Val Asn Pro Gln Lys Pro Ile Gln Thr Asp Ile Glu  
140 145 150 155

gag gtg tat ggt ttc agc ctg tat cac agc cag aaa acc ggc aag ttc	1013
Glu Val Tyr Gly Phe Ser Leu Tyr His Ser Gln Lys Thr Gly Lys Phe	
160 165 170	
tac gcc atg gtg acc gga aag aac gga gaa ttc gag caa tac gaa ctg	1061
Tyr Ala Met Val Thr Gly Lys Asn Gly Glu Phe Glu Gln Tyr Glu Leu	
175 180 185	
ttt gac aac gga aaa gga caa gtc gaa ggc aaa aag gtc cgc tca ttc	1109
Phe Asp Asn Gly Lys Gly Gln Val Glu Gly Lys Lys Val Arg Ser Phe	
190 195 200	
aaa atg agc tct caa aca gaa ggg ctt gca gca gat gat gaa tac ggc	1157
Lys Met Ser Ser Gln Thr Glu Gly Leu Ala Ala Asp Asp Glu Tyr Gly	
205 210 215	
aaa atg tac atc gct gaa gaa gac gct gcg att tgg tct ttc agc gcc	1205
Lys Met Tyr Ile Ala Glu Glu Asp Ala Ala Ile Trp Ser Phe Ser Ala	
220 225 230 235	
gag cca aac ggc gga gat aaa gga aaa att gtc gat cgc gca ggc gga	1253
Glu Pro Asn Gly Gly Asp Lys Gly Lys Ile Val Asp Arg Ala Gly Gly	
240 245 250	
ccg cat tta acc gct gat att gaa ggg ctg acg att tac tac gga gaa	1301
Pro His Leu Thr Ala Asp Ile Glu Gly Leu Thr Ile Tyr Tyr Gly Glu	
255 260 265	
gac ggc gaa gga tat ttg atc gcg tcc agt cag ggc gat aac cgt tat	1349
Asp Gly Glu Gly Tyr Leu Ile Ala Ser Ser Gln Gly Asp Asn Arg Tyr	
270 275 280	
gcc atc tat gac cgg cgc ggg aaa aac gac tat gtc gcc gat ttt tca	1397
Ala Ile Tyr Asp Arg Arg Gly Lys Asn Asp Tyr Val Ala Asp Phe Ser	
285 290 295	
att gat gac ggt aaa gaa atc gac ggg aca agc gat acc gat gga atc	1445
Ile Asp Asp Gly Lys Glu Ile Asp Gly Thr Ser Asp Thr Asp Gly Ile	
300 305 310 315	
gac gtc atc ggc ttc ggc ctc ggc aaa aaa tat cca tac ggc atc ttt	1493
Asp Val Ile Gly Phe Gly Leu Gly Lys Lys Tyr Pro Tyr Gly Ile Phe	
320 325 330	
gtc gcc caa gac ggc gaa aat acg gaa aat gga cag cca gcc aat cag	1541
Val Ala Gln Asp Gly Glu Asn Thr Glu Asn Gly Gln Pro Ala Asn Gln	
335 340 345	
aac ttc aaa att gtc tcc tgg gaa aaa att gct gac gcg ctg gac gac	1589
Asn Phe Lys Ile Val Ser Trp Glu Lys Ile Ala Asp Ala Leu Asp Asp	
350 355 360	
aag cct gat atc gat gat cag gtc aat ccc cga aaa ctg aaa aaa cga	1637
Lys Pro Asp Ile Asp Asp Gln Val Asn Pro Arg Lys Leu Lys Lys Arg	
365 370 375	

gcc aaa taacgacgga tccgcgggaa atgcccgcgg atttttcaca ttcctttatg 1693  
 Ala Lys  
 380

ttaagataac tattaatgga gggatgggtat tgcgtttaaa tctctatgcc gtagtggttta 1753  
 tcatgttggc ggttttatca aatgtgggtgt ttctctgcgt ttttaatcaa ggtgtattgg 1813  
 cgtacacttc tgctgtcatc ttctgtcttg ctgctgcata ttgcacgaag cgtcggcctg 1873  
 aaaagtaagg cttcctatgc cttatggctt ctccgtaaaa tgctcgttcc gtaaggcggc 1933  
 agtttgagcg cgcctttttt ccggggttccc tttaaaacgt ccgtatttgt ttcctccgga 1993  
 agcgagacac ttctgttttc cgctgtaaaa ttcatacacg aaatataatc gtggcggccg 2053  
 tctgtgcgga gctgggcggg gacgccttcc gggagctctg tatcgagcac tttggcaatc 2113  
 ccgcactctt caatgagcct ggatataaac gcc 2146

<210> 168  
 <211> 381  
 <212> PRT  
 <213> Bacillus licheniformis  
 <400> 168

Met Asn Phe Tyr Lys Thr Leu Ala Leu Ser Thr Leu Ala Ala Ser Leu  
 1 5 10 15

Leu Ser Pro Ser Trp Ser Ile Leu Pro Arg Ala Glu Ala Ser Ala Tyr  
 20 25 30

Lys Asp Phe Ser Val Thr Ala Asp Ala Glu Thr Glu Pro Val Asp Thr  
 35 40 45

Pro Asp Asp Ala Ala Asp Asp Pro Ala Ile Trp Val His Pro Lys Gln  
 50 55 60

Pro Glu Lys Ser Arg Leu Ile Thr Thr Asn Lys Lys Ser Gly Leu Ile  
 65 70 75 80

Val Tyr Asp Leu Asn Gly Lys Gln Leu Ala Ala Tyr Pro Phe Gly Lys  
 85 90 95

Leu Asn Asn Val Asp Leu Arg Tyr Asn Phe Pro Leu Asp Gly Lys Lys  
 100 105 110

Ile Asp Ile Ala Gly Ala Ser Asn Arg Ser Asp Gly Lys Asn Thr Val

115

120

125

Glu Ile Tyr Ala Phe Asp Gly Glu Lys Asn Lys Leu Lys Asn Ile Val  
 130 135 140

Asn Pro Gln Lys Pro Ile Gln Thr Asp Ile Glu Glu Val Tyr Gly Phe  
 145 150 155 160

Ser Leu Tyr His Ser Gln Lys Thr Gly Lys Phe Tyr Ala Met Val Thr  
 165 170 175

Gly Lys Asn Gly Glu Phe Glu Gln Tyr Glu Leu Phe Asp Asn Gly Lys  
 180 185 190

Gly Gln Val Glu Gly Lys Lys Val Arg Ser Phe Lys Met Ser Ser Gln  
 195 200 205

Thr Glu Gly Leu Ala Ala Asp Asp Glu Tyr Gly Lys Met Tyr Ile Ala  
 210 215 220

Glu Glu Asp Ala Ala Ile Trp Ser Phe Ser Ala Glu Pro Asn Gly Gly  
 225 230 235 240

Asp Lys Gly Lys Ile Val Asp Arg Ala Gly Gly Pro His Leu Thr Ala  
 245 250 255

Asp Ile Glu Gly Leu Thr Ile Tyr Tyr Gly Glu Asp Gly Glu Gly Tyr  
 260 265 270

Leu Ile Ala Ser Ser Gln Gly Asp Asn Arg Tyr Ala Ile Tyr Asp Arg  
 275 280 285

Arg Gly Lys Asn Asp Tyr Val Ala Asp Phe Ser Ile Asp Asp Gly Lys  
 290 295 300

Glu Ile Asp Gly Thr Ser Asp Thr Asp Gly Ile Asp Val Ile Gly Phe  
 305 310 315 320

Gly Leu Gly Lys Lys Tyr Pro Tyr Gly Ile Phe Val Ala Gln Asp Gly  
 325 330 335

Glu Asn Thr Glu Asn Gly Gln Pro Ala Asn Gln Asn Phe Lys Ile Val  
 340 345 350

Ser Trp Glu Lys Ile Ala Asp Ala Leu Asp Asp Lys Pro Asp Ile Asp  
 355 360 365

Asp Gln Val Asn Pro Arg Lys Leu Lys Lys Arg Ala Lys  
 370 375 380

<210> 169  
 <211> 1301  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(803)

<400> 169  
 gaactgtcct tggcccttga aaccacggt tagcgaggcc tcattatacc gtattctcaa 60  
 taaactctct aatggttgaa tcagaataga ttttcgtctg cattcatcac ttatcgatcat 120  
 ctgttcgcgt gtactgcgtt ccctaatacga cgtggaacca cgtgctgaac agtggactat 180  
 ctctcgctct ctccataacc tggcttatcc ttcgcgcgcg gtcttaaaac atgctctcct 240  
 ataagcagct ttgggtaatg tctgcttatt ccatcaccct cgcaaccgtg ttttttgcaa 300  
 ttatggacgc gctggaggcg gtgggttccaa gtcagttcct cctgaactgg tttgtgaact 360  
 ttatcatgct gtttctcgcc attaaagaaa cgccggcttc taaagcagcg aggtaaagcg 420  
 ggcaggagca aatttgttgt catgttggaa gagggacaag cgtaacataa taaaaaatgc 480  
 acgaaatggg gacaaatcag atg aaa cgt gtc att gtg ctg ttt tcg att ttg 533  
 Met Lys Arg Val Ile Val Leu Phe Ser Ile Leu  
 1 5 10  
 ctc gcc ctg ttc att gtt tat tat gac ttg aaa tca ggc acc atc cct 581  
 Leu Ala Leu Phe Ile Val Tyr Tyr Asp Leu Lys Ser Gly Thr Ile Pro  
 15 20 25  
 caa aac gcc tta ccg gct tca acc atg gca gcg gaa gct ccg gct gca 629  
 Gln Asn Ala Leu Pro Ala Ser Thr Met Ala Ala Glu Ala Pro Ala Ala  
 30 35 40  
 agc ctg caa tat aag tcc gtt acg gta aag ccc gga caa acg gta ttt 677  
 Ser Leu Gln Tyr Lys Ser Val Thr Val Lys Pro Gly Gln Thr Val Phe  
 45 50 55  
 tca atc atc ggg aac agc gcc gtt ccg gct gac aaa ata gcc gaa gat 725  
 Ser Ile Ile Gly Asn Ser Ala Val Pro Ala Asp Lys Ile Ala Glu Asp  
 60 65 70 75

ttt gaa gag ttg aat ccg aat gtt gag gcg ggc cgc att caa gca ggt 773  
Phe Glu Glu Leu Asn Pro Asn Val Glu Ala Gly Arg Ile Gln Ala Gly  
80 85 90

gtc acc tac aag ttt ccc gtt tat cct gat taagcgttaa tttcttgtca 823  
Val Thr Tyr Lys Phe Pro Val Tyr Pro Asp  
95 100

gtttcatgaa cgggctgtta caataagact tgtaaacgat ttggtataag aaaaggagca 883

accgcctccg aattatactt aaggagcgaa ttcaagttag tgaaatcaca catcgtacaa 943

aaacgcgtcc cgttaaagtg ggacctttta caataggcgg caataacgaa gtcgtcattc 1003

aaagcatgac aacaacgaaa acacatgacg ttgaagcaac cgtcgccgaa atcaacagac 1063

tcgcggaagc aggatgtcaa atcgtccgcg tcgcctgtcc tgatgaacgg gctgcccagc 1123

ccattccaga gatcaaaaag cggatatcca tccctcttgt cgtggatatt catttcaact 1183

ataaattggc attaaaagcg atcgaaggcg gagccgataa aatccgcatc aatccgggta 1243

acatcggccg ccgcgaaaag gttgaagcgg tcgtcaacgc agcgaaggaa aagggcat 1301

<210> 170

<211> 101

<212> PRT

<213> Bacillus licheniformis

<400> 170

Met Lys Arg Val Ile Val Leu Phe Ser Ile Leu Leu Ala Leu Phe Ile  
1 5 10 15

Val Tyr Tyr Asp Leu Lys Ser Gly Thr Ile Pro Gln Asn Ala Leu Pro  
20 25 30

Ala Ser Thr Met Ala Ala Glu Ala Pro Ala Ala Ser Leu Gln Tyr Lys  
35 40 45

Ser Val Thr Val Lys Pro Gly Gln Thr Val Phe Ser Ile Ile Gly Asn  
50 55 60

Ser Ala Val Pro Ala Asp Lys Ile Ala Glu Asp Phe Glu Glu Leu Asn  
65 70 75 80

Pro Asn Val Glu Ala Gly Arg Ile Gln Ala Gly Val Thr Tyr Lys Phe  
85 90 95

Pro Val Tyr Pro Asp

<210> 171  
 <211> 1627  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1124)

<400> 171  
 cggggttcac agcttgtcac atcgctaaag aaaacggctc agtcagacga tgaatttctc 60  
 ttcaatctcg gaaaagaact gacagattgc agctttagaa tttacatgtg cgatgaagac 120  
 ggtattcagc tgacgaaaaa cgtgtttaag catgacggag catggatatt tcagcctgag 180  
 tacatcggca aaaattggag ctggcgccct tattttctcg agaatatcat gaggatgaga 240  
 acgatgagaa aagggttttt cagcgatttg tacagcgata tcgaaacggg ggaaatgac 300  
 agaacgtttt cctatccgat ggatgaagaa ttgtatctgt tcattgacct gtcctactca 360  
 tatttatacg aacaagacgg attaatttaa gcggcggcct ttcgccgctt tttctttttg 420  
 aaaaaatgaa tcccagagagg tttgtttcgc gtatataaag gaaaatgtga aaatataaat 480  
 gctaaaaagg ggtggatcat atg aag aac gtt tgg tca tcc tta ctg tgc gcg 533  
                                   Met Lys Asn Val Trp Ser Ser Leu Leu Cys Ala  
                                   1                                  5                                  10  
 ctt ctg gct gcg gct ctt gta ttc ttc tgc gcg gat ttt gcc aaa gcc 581  
 Leu Leu Ala Ala Ala Leu Val Phe Phe Cys Ala Asp Phe Ala Lys Ala  
                                   15                                  20                                  25  
 gga gaa aaa ccg aca aga gca tcg tta ttt gag acc ctt caa tcc gta 629  
 Gly Glu Lys Pro Thr Arg Ala Ser Leu Phe Glu Thr Leu Gln Ser Val  
                                   30                                  35                                  40  
 tcg gac gtc cat ttt cag ctg acc gaa aag gaa aga acg aaa aca gac 677  
 Ser Asp Val His Phe Gln Leu Thr Glu Lys Glu Arg Thr Lys Thr Asp  
                                   45                                  50                                  55  
 atg ata tcc ctc ttg gaa cct tat atg gag cac gcc atg gca gtg aag 725  
 Met Ile Ser Leu Leu Glu Pro Tyr Met Glu His Ala Met Ala Val Lys  
                                   60                                  65                                  70                                  75  
 tat gta gag gcg aac gcc ttt cct gaa caa gcg ggg tgg att ttt tac 773  
 Tyr Val Glu Ala Asn Ala Phe Pro Glu Gln Ala Gly Trp Ile Phe Tyr  
                                   80                                  85                                  90  
 ggg aca gac gcg cct gaa gtt gca atc cct ttc ttc agc tat ggc gga 821  
 Gly Thr Asp Ala Pro Glu Val Ala Ile Pro Phe Phe Ser Tyr Gly Gly  
                                   95                                  100                                  105

gac aca aaa gtg gcg ggg aaa gac gga agc tat acc gta tat gaa ttt 869  
 Asp Thr Lys Val Ala Gly Lys Asp Gly Ser Tyr Thr Val Tyr Glu Phe  
 110 115 120

gtt gga gat caa aac gac ggc cct gtt tca tat caa aaa aat tat cag 917  
 Val Gly Asp Gln Asn Asp Gly Pro Val Ser Tyr Gln Lys Asn Tyr Gln  
 125 130 135

acg gtg acg ctg aag aat acc ggc ggc agc ttc aaa gta acg gat atc 965  
 Thr Val Thr Leu Lys Asn Thr Gly Gly Ser Phe Lys Val Thr Asp Ile  
 140 145 150 155

ggc caa tct gat aca aaa ccg gct gga gaa gaa ata atg tcc aaa caa 1013  
 Gly Gln Ser Asp Thr Lys Pro Ala Gly Glu Glu Ile Met Ser Lys Gln  
 160 165 170

ccg gat gaa aaa gaa aca agc tcg aat ttt gcg gat aaa ggg gaa gga 1061  
 Pro Asp Glu Lys Glu Thr Ser Ser Asn Phe Ala Asp Lys Gly Glu Gly  
 175 180 185

gac cag gct gca ttt ccg ctt ttt gcc acc gat gtt aac tgg aca ttg 1109  
 Asp Gln Ala Ala Phe Pro Leu Phe Ala Thr Asp Val Asn Trp Thr Leu  
 190 195 200

gcc gga att ttc agc tagcaaaaga atttaaagaa aatcattgac aatgatactg 1164  
 Ala Gly Ile Phe Ser  
 205

ataatcatta tcatttaatt atagagagat gaacctctct gttccccaac ccctctatca 1224

gatcaagatt taaaaaactt ggcgctgccc ccgccaagtt ttttatttgc atggaatccc 1284

gcacttcaaaa tagctgcggg atttttgggc attaggcgcg cgcaggaata agacaatcct 1344

ttgctccata aatctaaatt ggtggttcaa atagactcct ctgcagtcaa aaaaatattt 1404

ttcatgtatg acatgaaaaa agaaaactca aactatgaaa aagcggtttt tctttttcat 1464

gatcaaaaag gaaaaatgtc atcggctgat actttgtggt atgatgcttt gtagaacttg 1524

tattataatt aatacttggt gatcctgaag ttgttttttt gaaaggagtc ttttttagaa 1584

tgtcacaatt aatgggtatc atcacgagac tgcagagcct gca 1627

<210> 172

<211> 208

<212> PRT

<213> Bacillus licheniformis

<400> 172

Met Lys Asn Val Trp Ser Ser Leu Leu Cys Ala Leu Leu Ala Ala Ala  
 1 5 10 15



Leu Val Phe Phe Cys Ala Asp Phe Ala Lys Ala Gly Glu Lys Pro Thr  
 20 25 30

Arg Ala Ser Leu Phe Glu Thr Leu Gln Ser Val Ser Asp Val His Phe  
 35 40 45

Gln Leu Thr Glu Lys Glu Arg Thr Lys Thr Asp Met Ile Ser Leu Leu  
 50 55 60

Glu Pro Tyr Met Glu His Ala Met Ala Val Lys Tyr Val Glu Ala Asn  
 65 70 75 80

Ala Phe Pro Glu Gln Ala Gly Trp Ile Phe Tyr Gly Thr Asp Ala Pro  
 85 90 95

Glu Val Ala Ile Pro Phe Phe Ser Tyr Gly Gly Asp Thr Lys Val Ala  
 100 105 110

Gly Lys Asp Gly Ser Tyr Thr Val Tyr Glu Phe Val Gly Asp Gln Asn  
 115 120 125

Asp Gly Pro Val Ser Tyr Gln Lys Asn Tyr Gln Thr Val Thr Leu Lys  
 130 135 140

Asn Thr Gly Gly Ser Phe Lys Val Thr Asp Ile Gly Gln Ser Asp Thr  
 145 150 155 160

Lys Pro Ala Gly Glu Glu Ile Met Ser Lys Gln Pro Asp Glu Lys Glu  
 165 170 175

Thr Ser Ser Asn Phe Ala Asp Lys Gly Glu Gly Asp Gln Ala Ala Phe  
 180 185 190

Pro Leu Phe Ala Thr Asp Val Asn Trp Thr Leu Ala Gly Ile Phe Ser  
 195 200 205

<210> 173  
 <211> 2297  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1802)

<400> 173

gacatcgccg ccaagatgcg ggatgggatt gagaaattga tggaatcgct gatcctttct	60
ggcctagtca tgctggttct cgaccattca aggccggcctt ccggcggcga gcaccatctt	120
tcccactacc ttgaaatgaa agcgctggag aacaataagc ggcaagtgcct ccacggtgct	180
aaagtcggct gcagcgcgat tatgctgact gacatttacc gatctcttat cggtgcaagc	240
ctgggtgatc aacacgctga gcaagcgatt cgctccgttt atgaaaagct ccctgacggt	300
aagaaaatgg cagagtggat gaggcgtatc ggcgggcctg tatcattcaa agaactcgat	360
gttgaagaag agctggtgag agaagcgctc gcatacgccc atcagctcag agaccggtat	420
acgggactga aaatcatcaa tcaatacggc cttttgccgg ggcttttagg caaaggacca	480
ggcgtgaaaag ggggttaaaat gtg aaa agg ttc ctt tca tct atc ttt atg gtc	533
Val Lys Arg Phe Leu Ser Ser Ile Phe Met Val	
1 5 10	
acg gtc gct gta tgt ttg ctt tta tcg ggg tgc aag gcg agt cct gcc	581
Thr Val Ala Val Cys Leu Leu Leu Ser Gly Cys Lys Ala Ser Pro Ala	
15 20 25	
tcc gat caa gcg gac ggc acc gaa ctg aca ttt tgg aca ttc aac ggc	629
Ser Asp Gln Ala Asp Gly Thr Glu Leu Thr Phe Trp Thr Phe Asn Gly	
30 35 40	
ctt cat gaa cag ttt tat gct gag atg gtg aaa gaa tgg aac aaa aag	677
Leu His Glu Gln Phe Tyr Ala Glu Met Val Lys Glu Trp Asn Lys Lys	
45 50 55	
tat ccc gag cga aaa atc aaa tta aat aca gtg gtg tat ccg tat gga	725
Tyr Pro Glu Arg Lys Ile Lys Leu Asn Thr Val Val Tyr Pro Tyr Gly	
60 65 70 75	
cag atg cat gac aat tta tct atc tcg ctt tta gcc ggg aaa ggg gtt	773
Gln Met His Asp Asn Leu Ser Ile Ser Leu Leu Ala Gly Lys Gly Val	
80 85 90	
cca gat att gcc gat gtt gag ctg ggg cgc tat tcg aac ttt ttg aag	821
Pro Asp Ile Ala Asp Val Glu Leu Gly Arg Tyr Ser Asn Phe Leu Lys	
95 100 105	
ggc tct gac att cct ctt acc gat tta acg ccg ctt gtg gag gac gaa	869
Gly Ser Asp Ile Pro Leu Thr Asp Leu Thr Pro Leu Val Glu Asp Glu	
110 115 120	
cgc gac aag ttt gtt gaa gcg agg ctg acg ctc tac agc aag aac ggc	917
Arg Asp Lys Phe Val Glu Ala Arg Leu Thr Leu Tyr Ser Lys Asn Gly	
125 130 135	
aag ctt tac gga ctt gac aca cat gtc gga act acc gtg atg tat tac	965
Lys Leu Tyr Gly Leu Asp Thr His Val Gly Thr Thr Val Met Tyr Tyr	
140 145 150 155	

aac atg gaa atg atg aat aaa gca ggc gtt gat ccg gac gac atc aaa	1013
Asn Met Glu Met Met Asn Lys Ala Gly Val Asp Pro Asp Asp Ile Lys	
160 165 170	
aca tgg gaa gat tac agg gaa gcg ggc aaa aag gtc gtc aaa gct ctc	1061
Thr Trp Glu Asp Tyr Arg Glu Ala Gly Lys Lys Val Val Lys Ala Leu	
175 180 185	
gga aag ccg atg acg acg att gaa acg acc gac ccg aat tca ttt ctg	1109
Gly Lys Pro Met Thr Thr Ile Glu Thr Thr Asp Pro Asn Ser Phe Leu	
190 195 200	
ccg ctg gtt tcc cag cag gga tcc ggt tac ttt gat gag cag ggg ccg	1157
Pro Leu Val Ser Gln Gln Gly Ser Gly Tyr Phe Asp Glu Gln Gly Arg	
205 210 215	
ttg aca tta aac aat gag aca aac gtg aaa acg ctc gaa ttt tta aag	1205
Leu Thr Leu Asn Asn Glu Thr Asn Val Lys Thr Leu Glu Phe Leu Lys	
220 225 230 235	
act tta att gag aaa gac aaa att gcc gtc aca acg ccc gga ggc aat	1253
Thr Leu Ile Glu Lys Asp Lys Ile Ala Val Thr Thr Pro Gly Gly Asn	
240 245 250	
cat cac agt gaa gag tat tac gga ttt atg aac caa ggc ggc gcg gcg	1301
His His Ser Glu Glu Tyr Tyr Gly Phe Met Asn Gln Gly Gly Ala Ala	
255 260 265	
tct gtc tta atg ccg atc tgg tat atg ggc cgt ttt ttg gat tat atg	1349
Ser Val Leu Met Pro Ile Trp Tyr Met Gly Arg Phe Leu Asp Tyr Met	
270 275 280	
cct gac ttg aaa ggg aaa atc gcg atc aga ccg ctg ccg gca tgg gaa	1397
Pro Asp Leu Lys Gly Lys Ile Ala Ile Arg Pro Leu Pro Ala Trp Glu	
285 290 295	
gaa ggg gga gac cgc tca gcg gga atg ggc gga acg gcc acc gtg att	1445
Glu Gly Gly Asp Arg Ser Ala Gly Met Gly Gly Thr Ala Thr Val Ile	
300 305 310 315	
cca aaa cag gcg aaa cag gtc gat ctg gcc aag gat ttc ttg aaa ttt	1493
Pro Lys Gln Ala Lys Gln Val Asp Leu Ala Lys Asp Phe Leu Lys Phe	
320 325 330	
gcc aaa gcg tca aaa gaa ggc aac atc aag ctg tgg acc gtg ctc ggg	1541
Ala Lys Ala Ser Lys Glu Gly Asn Ile Lys Leu Trp Thr Val Leu Gly	
335 340 345	
ttc gat ccg ctc aga tgg gat gtg tgg gac tcg gac gaa ttg aaa aaa	1589
Phe Asp Pro Leu Arg Trp Asp Val Trp Asp Ser Asp Glu Leu Lys Lys	
350 355 360	
cca aat caa tat aca gaa tac ttt caa aac gga caa cac atc ttt tcc	1637
Pro Asn Gln Tyr Thr Glu Tyr Phe Gln Asn Gly Gln His Ile Phe Ser	
365 370 375	

gtg	ctt	ctt	gac	ata	aag	gat	gag	atc	aat	ccg	ctt	tac	ctt	act	gag	1685
Val	Leu	Leu	Asp	Ile	Lys	Asp	Glu	Ile	Asn	Pro	Leu	Tyr	Leu	Thr	Glu	
380					385				390						395	

gat	tat	gcg	aag	act	tcc	gat	ctc	gtc	aac	aga	aac	ata	ctg	tac	gaa	1733
Asp	Tyr	Ala	Lys	Thr	Ser	Asp	Leu	Val	Asn	Arg	Asn	Ile	Leu	Tyr	Glu	
			400					405					410			

gcg	ctc	aaa	acg	aag	agc	aaa	aca	ccg	aaa	gaa	gca	ttg	gac	aaa	gca	1781
Ala	Leu	Lys	Thr	Lys	Ser	Lys	Thr	Pro	Lys	Glu	Ala	Leu	Asp	Lys	Ala	
			415					420					425			

gca	gct	gaa	gtg	aaa	ggg	caa	tagtctttca	ttactgtaaa	gcgaggcgat	1832
Ala	Ala	Glu	Val	Lys	Gly	Gln				
			430							

aacttgaaga	ctgttaaaac	agatacagt	g	cattcgtttc	cgccggtgag	cagaaaaaga	1892
------------	------------	-----------	---	------------	------------	------------	------

aagatcagac	gtttattata	ttcagcaaaa	gccgcaccct	acattttttac	agcacctttt	1952
------------	------------	------------	------------	-------------	------------	------

gtactctcct	tttgcataatt	ttttctttat	ccgcttatca	gcgtcgtcat	catgagtttt	2012
------------	-------------	------------	------------	------------	------------	------

caaagcattc	tccccgggga	agtccgcttc	atcgggacgg	agaactataa	agcattaaac	2072
------------	------------	------------	------------	------------	------------	------

aatcctacat	tttataccgc	actattcaac	accgtaaaat	acaccttttg	gacattgctg	2132
------------	------------	------------	------------	------------	------------	------

attttaatac	ctgttcctct	tattctggca	gtcttttttag	attctaaact	cgtaaagt	2192
------------	------------	------------	-------------	------------	----------	------

aaaaacgtgt	tcaaatcggc	tttattcatc	ccggctctga	cttcaaccat	tgtggcgggg	2252
------------	------------	------------	------------	------------	------------	------

attattttca	ggctgatttt	tggagaaatg	gatacatccc	tggcg	2297
------------	------------	------------	------------	-------	------

<210> 174

<211> 434

<212> PRT

<213> Bacillus licheniformis

<400> 174

Val	Lys	Arg	Phe	Leu	Ser	Ser	Ile	Phe	Met	Val	Thr	Val	Ala	Val	Cys
1				5					10					15	

Leu	Leu	Leu	Ser	Gly	Cys	Lys	Ala	Ser	Pro	Ala	Ser	Asp	Gln	Ala	Asp
			20					25					30		

Gly	Thr	Glu	Leu	Thr	Phe	Trp	Thr	Phe	Asn	Gly	Leu	His	Glu	Gln	Phe
		35					40					45			

Tyr	Ala	Glu	Met	Val	Lys	Glu	Trp	Asn	Lys	Lys	Tyr	Pro	Glu	Arg	Lys
	50					55					60				

Ile	Lys	Leu	Asn	Thr	Val	Val	Tyr	Pro	Tyr	Gly	Gln	Met	His	Asp	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65

70

75

80

Leu Ser Ile Ser Leu Leu Ala Gly Lys Gly Val Pro Asp Ile Ala Asp  
                     85                    90                    95

Val Glu Leu Gly Arg Tyr Ser Asn Phe Leu Lys Gly Ser Asp Ile Pro  
                     100                    105                    110

Leu Thr Asp Leu Thr Pro Leu Val Glu Asp Glu Arg Asp Lys Phe Val  
                     115                    120                    125

Glu Ala Arg Leu Thr Leu Tyr Ser Lys Asn Gly Lys Leu Tyr Gly Leu  
                     130                    135                    140

Asp Thr His Val Gly Thr Thr Val Met Tyr Tyr Asn Met Glu Met Met  
                     145                    150                    155                    160

Asn Lys Ala Gly Val Asp Pro Asp Asp Ile Lys Thr Trp Glu Asp Tyr  
                     165                    170                    175

Arg Glu Ala Gly Lys Lys Val Val Lys Ala Leu Gly Lys Pro Met Thr  
                     180                    185                    190

Thr Ile Glu Thr Thr Asp Pro Asn Ser Phe Leu Pro Leu Val Ser Gln  
                     195                    200                    205

Gln Gly Ser Gly Tyr Phe Asp Glu Gln Gly Arg Leu Thr Leu Asn Asn  
                     210                    215                    220

Glu Thr Asn Val Lys Thr Leu Glu Phe Leu Lys Thr Leu Ile Glu Lys  
                     225                    230                    235                    240

Asp Lys Ile Ala Val Thr Thr Pro Gly Gly Asn His His Ser Glu Glu  
                     245                    250                    255

Tyr Tyr Gly Phe Met Asn Gln Gly Gly Ala Ala Ser Val Leu Met Pro  
                     260                    265                    270

Ile Trp Tyr Met Gly Arg Phe Leu Asp Tyr Met Pro Asp Leu Lys Gly  
                     275                    280                    285

Lys Ile Ala Ile Arg Pro Leu Pro Ala Trp Glu Glu Gly Gly Asp Arg  
                     290                    295                    300

Ser Ala Gly Met Gly Gly Thr Ala Thr Val Ile Pro Lys Gln Ala Lys  
 305 310 315 320

Gln Val Asp Leu Ala Lys Asp Phe Leu Lys Phe Ala Lys Ala Ser Lys  
 325 330 335

Glu Gly Asn Ile Lys Leu Trp Thr Val Leu Gly Phe Asp Pro Leu Arg  
 340 345 350

Trp Asp Val Trp Asp Ser Asp Glu Leu Lys Lys Pro Asn Gln Tyr Thr  
 355 360 365

Glu Tyr Phe Gln Asn Gly Gln His Ile Phe Ser Val Leu Leu Asp Ile  
 370 375 380

Lys Asp Glu Ile Asn Pro Leu Tyr Leu Thr Glu Asp Tyr Ala Lys Thr  
 385 390 395 400

Ser Asp Leu Val Asn Arg Asn Ile Leu Tyr Glu Ala Leu Lys Thr Lys  
 405 410 415

Ser Lys Thr Pro Lys Glu Ala Leu Asp Lys Ala Ala Ala Glu Val Lys  
 420 425 430

Gly Gln

<210> 175  
 <211> 1864  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (533)..(991)

<400> 175  
 tatgctgctgc gagcactgcg ccgtcgggta tacgctccag acgaaggacc cggacgcgct 60  
 gccagtcagc cttctgttga aacggcttga tgagattccc cgccttcggt ctttaagcat 120  
 tacgggcggc gagccgatgc tctcattaaa atctgttaaag gaatatgtcg ttcctttatt 180  
 aaaatacgct catgaacgcg gcgtgcggac gcagatcaac tcaaacttga cgctcgatat 240



cgtgtaaatt tcccagtttt ttcggctgca ctttataaat ctgatcgcgt tttgtaccgg 1261  
 agccgaccac tgtttcaaag gcgagcggca gctttgtttt ttccatggct ttgagcatca 1321  
 tcatatTTTT gacatcttcc gcctttggaa ctttcgctgt taagccgcct ttgattttgc 1381  
 tcgtctgttc ctgggaatac gtgagttctg caggtgcttt cccgccccgg ttgtcaaagc 1441  
 ggtttgtgtt gatTTTgcgg tattcccagt tcgcaacggg ttcatcagag gtgtaaccta 1501  
 gcgcccattc gcccaaataa atcgtcgcgc gatagccgat tgccagcggg gtgccggaaa 1561  
 tgcttgactc attcagcatt ttaatcagat gcggattttc aatcgcaata tcggttgttt 1621  
 tcagcagctc ttcggctaata tcgctcggct gcagcctcgg ctgatcctga gaggcgtag 1681  
 ggtatgtgtt ctctttggaa atattcgtga cagagcttgg aatcttgatc ggcttggctg 1741  
 cgtcagcttc ctgtacagcg aaaaaactaa aggataaaaa cgcagtcagc gtaaaacaca 1801  
 aaagcttttt catactatca ctctttctgt ttctttttcc ttattgtttt ccggatgctc 1861  
 tct 1864

<210> 176  
 <211> 153  
 <212> PRT  
 <213> *Bacillus licheniformis*

<400> 176

Met Tyr Pro Ser Asp Phe Ala Ser Ala Leu Glu Ser Leu Ser Leu Lys  
 1 5 10 15

Asp Met Arg Lys Ala Ile His Arg Leu Leu Asp Ile Arg Asp Glu Asn  
 20 25 30

Thr Trp Met Leu Phe Gly Thr Leu Pro Phe Tyr Ala Cys Ser Pro Asp  
 35 40 45

Pro Glu Asp His Ala Leu Leu Gln Arg Leu Arg Glu Ala Lys Asn Val  
 50 55 60

Thr Val Arg Asn Asp Pro Asp Gly Arg Ser Arg Leu Asn Val Asn Ile  
 65 70 75 80

Phe Asp Gly Asn Ile Ile Val Thr Asp Phe Gly Asp Thr Pro Pro Leu  
 85 90 95



Gly Asn Ile Gln Thr Asp Ser Leu Pro Ser Ala Tyr Ala Lys Trp Arg  
 100 105 110

Lys Thr Glu Leu Ala Lys Glu Leu Asn Cys His Cys Pro His Val Arg  
 115 120 125

Cys Leu Gly Pro Asn Val Leu Val Lys Asn Ser Tyr Tyr Gln Asp Val  
 130 135 140

Asp Phe Thr Ser Arg Thr Ala Arg Val  
 145 150

<210> 177  
 <211> 1763  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (503) .. (1264)

<400> 177  
 gccgctgacc taagggagca agctcccgctc ggtccgctcg acttgcatgt attaggcacg 60  
 ccgccagcgt tcgtcctgag ccaggatcaa actctccatg aaataatgga gcgcagatta 120  
 agttcgtcac atcctgtgac aacatctgca tgacctgcat cgtgcaggcc cctgactacg 180  
 cacactcaaa tgtgcgattt ataaaaatga attaacagggt acgtttttgtc ttgttttagtt 240  
 ttcaaagatc atttccgctt cgttcagcgg cttaataat ataacatcaa gctcacatat 300  
 ttgtcaataa ctttttctcaa aattattttt tggagctttt tcatgtcagc tgtttatcag 360  
 cgacgaataa caatataaca tgtttatatta attccggtca accctctttt taattttttt 420  
 cttaagatga attattgtta tgttctatatt taaacaagca taggatgaaa acaaagcagc 480  
 atggacaagg aggagttttt ct gtg aac cat ttt tat gtg tgg cat atc aaa 532  
 Val Asn His Phe Tyr Val Trp His Ile Lys  
 1 5 10  
 cgg att aag cag cta atc att att atg ata gcc gct ttt gcg aca gca 580  
 Arg Ile Lys Gln Leu Ile Ile Ile Met Ile Ala Ala Phe Ala Thr Ala  
 15 20 25  
 agt ttt ttt tat gtg caa aac ctg ctc cct ctt cct gtg ttt tct aca 628  
 Ser Phe Phe Tyr Val Gln Asn Leu Leu Pro Leu Pro Val Phe Ser Thr  
 30 35 40  
 gaa ggc gga gca aaa gcg gta tat aga gga gat tca gat aca aat gaa 676  
 Glu Gly Gly Ala Lys Ala Val Tyr Arg Gly Asp Ser Asp Thr Asn Glu

45	50	55		
gta gcc ctt aca ttt aat atc agc tgg gga gat	caa aag gca atg ccc	724		
Val Ala Leu Thr Phe Asn Ile Ser Trp Gly Asp	Gln Lys Ala Met Pro			
60	65	70		
att tta gac aca tta aaa gca aac ggt att aaa gac gcg acc ttt ttt	772			
Ile Leu Asp Thr Leu Lys Ala Asn Gly Ile Lys Asp Ala Thr Phe Phe				
75	80	85	90	
cta tca gct tca tgg gca gag cgc cac ccg gat gtc gta gaa aga atc	820			
Leu Ser Ala Ser Trp Ala Glu Arg His Pro Asp Val Val Glu Arg Ile				
	95	100	105	
cgt aaa gat ggt cac cag atc ggg agt atg ggc tat gct tat aaa aac	868			
Arg Lys Asp Gly His Gln Ile Gly Ser Met Gly Tyr Ala Tyr Lys Asn				
	110	115	120	
tat tcg caa atg aag aaa agc gag atc aaa aaa gac tta gca aaa gca	916			
Tyr Ser Gln Met Lys Lys Ser Glu Ile Lys Lys Asp Leu Ala Lys Ala				
	125	130	135	
cga cac tcc ttt caa aaa ctc ggg ctt gac gac ctt acg ctt tta aga	964			
Arg His Ser Phe Gln Lys Leu Gly Leu Asp Asp Leu Thr Leu Leu Arg				
	140	145	150	
ccg ccg acc ggc cag ttt aat aaa gac gta ctc gat gtt gct aaa cag	1012			
Pro Pro Thr Gly Gln Phe Asn Lys Asp Val Leu Asp Val Ala Lys Gln				
	155	160	165	170
tac ggc tac acc gtt gtt cat tat agt att aac tcg gat gac tgg acg	1060			
Tyr Gly Tyr Thr Val Val His Tyr Ser Ile Asn Ser Asp Asp Trp Thr				
	175	180	185	
aac ccg ggg gtt caa aag atc gtc caa aac gta aat gga acg gta aac	1108			
Asn Pro Gly Val Gln Lys Ile Val Gln Asn Val Asn Gly Thr Val Asn				
	190	195	200	
gcc ggt gac atc gtg ctc ttt cac gct tca gat tcc gcc aaa caa aca	1156			
Ala Gly Asp Ile Val Leu Phe His Ala Ser Asp Ser Ala Lys Gln Thr				
	205	210	215	
aaa gaa gcc ctg cca gag atc gtg cac cat ctc aga agc aag ggg ctc	1204			
Lys Glu Ala Leu Pro Glu Ile Val His His Leu Arg Ser Lys Gly Leu				
	220	225	230	
aaa aac gta aca gtc agc gaa tta atc gca aat acg gat gca aaa tct	1252			
Lys Asn Val Thr Val Ser Glu Leu Ile Ala Asn Thr Asp Ala Lys Ser				
	235	240	245	250
tca gaa gta aag tagcagccgg tctaagcgcg tgcctgaaat tttggcagca	1304			
Ser Glu Val Lys				
ttaaaagctg aaaagcggttg caggctaata aaggaagcag cattaaatag agccagtcct	1364			
cttcattgac ccttaacgcc gggaaccact ccatcacagt aaaaacaaac attagaaata	1424			

atgcggaac gaacgttttt ttagaggact gtttttgctt tgcataagcg gccgcaatgc 1484  
 ctaccgcaa aataaagagc ggagccaaa tgtacggaat gatggagcct ccattttttt 1544  
 caaaaaacag aaagcgcaag taaaccaagt caaacgagc aaatataatc aaaaacagct 1604  
 gaatcgaatt ccacaaagaa tgagatctga aaatttccag tgcaaagcgg tgaatcgta 1664  
 agaaaatcac aaatcccatt tgagcaatca cgctaaagat catgccaacc ccgataaacc 1724  
 agaaaagaac agacagaatc tccaatacct cgaaggaaa 1763

<210> 178  
 <211> 254  
 <212> PRT  
 <213> *Bacillus licheniformis*

<400> 178

Val Asn His Phe Tyr Val Trp His Ile Lys Arg Ile Lys Gln Leu Ile  
 1 5 10 15

Ile Ile Met Ile Ala Ala Phe Ala Thr Ala Ser Phe Phe Tyr Val Gln  
 20 25 30

Asn Leu Leu Pro Leu Pro Val Phe Ser Thr Glu Gly Gly Ala Lys Ala  
 35 40 45

Val Tyr Arg Gly Asp Ser Asp Thr Asn Glu Val Ala Leu Thr Phe Asn  
 50 55 60

Ile Ser Trp Gly Asp Gln Lys Ala Met Pro Ile Leu Asp Thr Leu Lys  
 65 70 75 80

Ala Asn Gly Ile Lys Asp Ala Thr Phe Phe Leu Ser Ala Ser Trp Ala  
 85 90 95

Glu Arg His Pro Asp Val Val Glu Arg Ile Arg Lys Asp Gly His Gln  
 100 105 110

Ile Gly Ser Met Gly Tyr Ala Tyr Lys Asn Tyr Ser Gln Met Lys Lys  
 115 120 125

Ser Glu Ile Lys Lys Asp Leu Ala Lys Ala Arg His Ser Phe Gln Lys  
 130 135 140

Leu Gly Leu Asp Asp Leu Thr Leu Leu Arg Pro Pro Thr Gly Gln Phe  
 145 150 155 160

Asn Lys Asp Val Leu Asp Val Ala Lys Gln Tyr Gly Tyr Thr Val Val  
 165 170 175

His Tyr Ser Ile Asn Ser Asp Asp Trp Thr Asn Pro Gly Val Gln Lys  
 180 185 190

Ile Val Gln Asn Val Asn Gly Thr Val Asn Ala Gly Asp Ile Val Leu  
 195 200 205

Phe His Ala Ser Asp Ser Ala Lys Gln Thr Lys Glu Ala Leu Pro Glu  
 210 215 220

Ile Val His His Leu Arg Ser Lys Gly Leu Lys Asn Val Thr Val Ser  
 225 230 235 240

Glu Leu Ile Ala Asn Thr Asp Ala Lys Ser Ser Glu Val Lys  
 245 250

<210> 179  
 <211> 1610  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1304)

<400> 179  
 agaaaaaatg caaacaaatc aaatcgtaa agatgacgaa ttgtttgaac ggttaagggc 60  
 gctgcgcaga aagcttgctc aggaacaagg cgtgcctcct tttgttgat tctctgacga 120  
 aacgctgcgg gaaatgagcg ggaaagtccc tctgacagac gaagagcttt tgtcagtcaa 180  
 aggagtggga gaacaaaaaa gagtaaaata cggagctgta tttctacagg agcttcaagc 240  
 ctataaaact gagaaagaag cataaaaacc caaaatttat atatgtaaaa ttttttttag 300  
 taaatctcct atttcagttg aaaaacgatt ggaacccttg atacatctga atttcggccg 360  
 atttttagggc ggctgaaatt cctcctcgta aaacaactgt aatcaaaaac aaattgtttt 420  
 gttattgatt tgacattttc atatgttacg attgctcctg ttagccggac aataaaaagc 480  
 taacaagggga ggatttactt atg aag aag acg ttt atg tcc ttt gtt gca gtt 533  
 Met Lys Lys Thr Phe Met Ser Phe Val Ala Val

	1	5	10	
gca gca tta tct tca act gca ttc gga gcg agt gcc tct gca aaa gaa				581
Ala Ala Leu Ser Ser Thr Ala Phe Gly Ala Ser Ala Ser Ala Lys Glu				
	15	20	25	
gta aca gtc caa aaa ggt gac acc ctt tgg gga atc tcg caa aaa caa				629
Val Thr Val Gln Lys Gly Asp Thr Leu Trp Gly Ile Ser Gln Lys Gln				
	30	35	40	
ggg gta aat ctg cag gac tta aaa gaa tgg aat cag ctt tcc tct gac				677
Gly Val Asn Leu Gln Asp Leu Lys Glu Trp Asn Gln Leu Ser Ser Asp				
	45	50	55	
ttg att att ccg gga caa aag ctg aac gtt tct gaa aaa cag aca gaa				725
Leu Ile Ile Pro Gly Gln Lys Leu Asn Val Ser Glu Lys Gln Thr Glu				
	60	65	70	75
gaa aag aaa caa tat acc att aaa aag gga gac act ctc tgg aaa atc				773
Glu Lys Lys Gln Tyr Thr Ile Lys Lys Gly Asp Thr Leu Trp Lys Ile				
	80	85	90	
gcc caa aaa ttc ggc gtt tca gtg aat gac ctt aaa aat tgg aac aac				821
Ala Gln Lys Phe Gly Val Ser Val Asn Asp Leu Lys Asn Trp Asn Asn				
	95	100	105	
ata aaa tca gat atc att tac ccg aat aca tcc ata act gtt gac gga				869
Ile Lys Ser Asp Ile Ile Tyr Pro Asn Thr Ser Ile Thr Val Asp Gly				
	110	115	120	
cag gcg acg gtc cag gct gct gcg gcg caa cct gcg gaa aca aag cct				917
Gln Ala Thr Val Gln Ala Ala Ala Gln Pro Ala Glu Thr Lys Pro				
	125	130	135	
gcc gta caa aaa gaa gcg aaa gtc gag aag gct gcg cct gcc cct gca				965
Ala Val Gln Lys Glu Ala Lys Val Glu Lys Ala Ala Pro Ala Pro Ala				
	140	145	150	155
cct aag cag gaa aaa gaa ccg gct tcc cgt tca aac gta tct caa agc				1013
Pro Lys Gln Glu Lys Glu Pro Ala Ser Arg Ser Asn Val Ser Gln Ser				
	160	165	170	
act gcc aaa gaa ctg acg gtt aca gca acg gca tac act gcc aat gac				1061
Thr Ala Lys Glu Leu Thr Val Thr Ala Thr Ala Tyr Thr Ala Asn Asp				
	175	180	185	
ggc ggt atg aca ggc gtg aca gcc acg ggt atc gat ctg aag gcc aat				1109
Gly Gly Met Thr Gly Val Thr Ala Thr Gly Ile Asp Leu Lys Ala Asn				
	190	195	200	
aaa aac gcc aag gtt att gcg gtg gat cca aac gta atc ccg ctt gga				1157
Lys Asn Ala Lys Val Ile Ala Val Asp Pro Asn Val Ile Pro Leu Gly				
	205	210	215	
tcc aag gtg tat gtg gaa ggc tac gga gaa gcg acc gct gcc gat acc				1205
Ser Lys Val Tyr Val Glu Gly Tyr Gly Glu Ala Thr Ala Ala Asp Thr				
	220	225	230	235

ggc ggt gcg atc aag ggg aac aaa atc gac gta ttt gtt cca agc aaa 1253  
 Gly Gly Ala Ile Lys Gly Asn Lys Ile Asp Val Phe Val Pro Ser Lys  
                   240                  245                  250

tcc gca gca aaa aac tgg ggc gtt aaa acg gtt aaa gtt aaa gtt tta 1301  
 Ser Ala Ala Lys Asn Trp Gly Val Lys Thr Val Lys Val Lys Val Leu  
                   255                  260                  265

aaa taatagggtt accattgatg gacactgacc atgaagatga tcagtgtctt 1354  
 Lys

ttttctgttt tctgcatctt tttttctatt ttgatgtttt ttttagattgg caaatgggta 1414

gttcaataga taaatacata tcagctgatc taaaaaggag ttgcagaagt attgggtgtgg 1474

attatcatga cattttttatt gattaatgca ggaattttta ttttttctta tttgaggaca 1534

aaagatattg atttaaaaaac gtcagacggc tatttttctcg gcggg'gcag tctcactgcc 1594

ctctatatcg gaagtt 1610

<210> 180

<211> 268

<212> PRT

<213> Bacillus licheniformis

<400> 180

Met Lys Lys Thr Phe Met Ser Phe Val Ala Val Ala Ala Leu Ser Ser  
 1                  5                  10                  15

Thr Ala Phe Gly Ala Ser Ala Ser Ala Lys Glu Val Thr Val Gln Lys  
                   20                  25                  30

Gly Asp Thr Leu Trp Gly Ile Ser Gln Lys Gln Gly Val Asn Leu Gln  
                   35                  40                  45

Asp Leu Lys Glu Trp Asn Gln Leu Ser Ser Asp Leu Ile Ile Pro Gly  
                   50                  55                  60

Gln Lys Leu Asn Val Ser Glu Lys Gln Thr Glu Glu Lys Lys Gln Tyr  
                   65                  70                  75                  80

Thr Ile Lys Lys Gly Asp Thr Leu Trp Lys Ile Ala Gln Lys Phe Gly  
                   85                  90                  95

Val Ser Val Asn Asp Leu Lys Asn Trp Asn Asn Ile Lys Ser Asp Ile  
                   100                  105                  110

Ile Tyr Pro Asn Thr Ser Ile Thr Val Asp Gly Gln Ala Thr Val Gln  
 115 120 125

Ala Ala Ala Ala Gln Pro Ala Glu Thr Lys Pro Ala Val Gln Lys Glu  
 130 135 140

Ala Lys Val Glu Lys Ala Ala Pro Ala Pro Ala Pro Lys Gln Glu Lys  
 145 150 155 160

Glu Pro Ala Ser Arg Ser Asn Val Ser Gln Ser Thr Ala Lys Glu Leu  
 165 170 175

Thr Val Thr Ala Thr Ala Tyr Thr Ala Asn Asp Gly Gly Met Thr Gly  
 180 185 190

Val Thr Ala Thr Gly Ile Asp Leu Lys Ala Asn Lys Asn Ala Lys Val  
 195 200 205

Ile Ala Val Asp Pro Asn Val Ile Pro Leu Gly Ser Lys Val Tyr Val  
 210 215 220

Glu Gly Tyr Gly Glu Ala Thr Ala Ala Asp Thr Gly Gly Ala Ile Lys  
 225 230 235 240

Gly Asn Lys Ile Asp Val Phe Val Pro Ser Lys Ser Ala Ala Lys Asn  
 245 250 255

Trp Gly Val Lys Thr Val Lys Val Lys Val Leu Lys  
 260 265

<210> 181  
 <211> 1547  
 <212> DNA  
 <213> *Bacillus licheniformis*

<220>  
 <221> CDS  
 <222> (501)..(1046)

<400> 181  
 gccgtatatt tttcaacggg cagacagtcg atgcagccta aaaaatcttg cagcagattg 60  
 tctggcgcgt tttcattcat agacaatttt tgatattcat aaattaattg atccagctcc 120

tggtcccgcc tgatcgtttc atccccctgta tatccataga tttcagcggc ttcaaccatc	180
at ttgcccgt tcttgctgat ggaaacgagc aatgcttctt tttcaatata cctttgcacc	240
cgctccccggg aggtcccaaa aaaatttttt tgcaaaaaaa aattttttccc cataaggctc	300
tagtgttatg agaaaaaaat ccgggaacgg aatcaaggac cataaaaaatt ttttctggcc	360
aacccaaaaac cccggtgctg ttaagtcgtc ataaataaga aaccagcggg ggaaaaattt	420
ttctcgcaac cctcttgtaa tctatctgac gttattgtaa catttgtaat ataagagata	480
tatttaagga gagaggacca ttg aaa aag tta atc gtt tgt tta tta gct gtt	533
Leu Lys Lys Leu Ile Val Cys Leu Leu Ala Val	
1 5 10	
tta ctg atc ttg cct gcc gga gcg tcc ctc gca gcg aaa aat caa aca	581
Leu Leu Ile Leu Pro Ala Gly Ala Ser Leu Ala Ala Lys Asn Gln Thr	
15 20 25	
tca ggg aat tta aca aat aag caa gtc atg caa tta acc ttg cag gca	629
Ser Gly Asn Leu Thr Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala	
30 35 40	
cgg gag cac ttt tgg aat acg atg agc ggc cac aat cca aaa gcg aaa	677
Arg Glu His Phe Trp Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys	
45 50 55	
aac tca act tgc cca tcc aaa aca ttt gaa tac cgc ggt ctt cca tat	725
Asn Ser Thr Cys Pro Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr	
60 65 70 75	
acg tat atg tgc agt gaa ttc agc aca aaa gca aaa tta aca gac tac	773
Thr Tyr Met Cys Ser Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr	
80 85 90	
ttg acg ccg gtt ttc aca aaa gac gcc att aaa aaa ggc ttg gaa aaa	821
Leu Thr Pro Val Phe Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys	
95 100 105	
tac aac atc att tct tat aaa gga aaa atg gcc gtg cct gtc ggc gat	869
Tyr Asn Ile Ile Ser Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp	
110 115 120	
ggg gac aac ctc tta gga tgg gac aag gca aaa atc aaa ctg atc tct	917
Gly Asp Asn Leu Leu Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser	
125 130 135	
caa aaa aac aat acc cgc act tat gaa ttt tcc gta ccg gca ttg gat	965
Gln Lys Asn Asn Thr Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp	
140 145 150 155	
gga tcg gtg act gcg aaa aga aag atc acg ttt gtg aaa gaa aac aac	1013
Gly Ser Val Thr Ala Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn	
160 165 170	
aaa tgg aaa atc aat cag ctc gat gct gcc atc taaacgaaaa agctaattgtc	1066



Lys Trp Lys Ile Asn Gln Leu Asp Ala Ala Ile  
 175 180

taaaaacgga cattagcttt tttccgtcaa acggtcagtt caacgatggt gccgtcagga 1126  
 tccagaatga ctctttcata ataccgtct cccgtgacgc gcggctttcc ggcaacctgg 1186  
 tacccttcct tttcaaagcg gctcgtcatc tcgtcaacct cttgccgcga ccctaaggaa 1246  
 aacgccatat gtgcatagcc ggaagcggtc tcctctcctt ttgcaaggtc ggggcgtctc 1306  
 atcagctcaa gccgtgttcc cgattcaaac tggatgaaat atgattcgaa atgctttttc 1366  
 ggattgacat atttttcatt cgtctttccg tgaaaaaac gggatatagaa atctttcatt 1426  
 tcctctaaat tgttcgtcca tatggcgatg tgttcgattt tcataaatct ccctcccatt 1486  
 tcatattacc atatagatcc tctgcctttt ttacacttt tttaaattga taagtattca 1546  
 t 1547

<210> 182  
 <211> 182  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 182

Leu Lys Lys Leu Ile Val Cys Leu Leu Ala Val Leu Leu Ile Leu Pro  
 1 5 10 15

Ala Gly Ala Ser Leu Ala Ala Lys Asn Gln Thr Ser Gly Asn Leu Thr  
 20 25 30

Asn Lys Gln Val Met Gln Leu Thr Leu Gln Ala Arg Glu His Phe Trp  
 35 40 45

Asn Thr Met Ser Gly His Asn Pro Lys Ala Lys Asn Ser Thr Cys Pro  
 50 55 60

Ser Lys Thr Phe Glu Tyr Arg Gly Leu Pro Tyr Thr Tyr Met Cys Ser  
 65 70 75 80

Glu Phe Ser Thr Lys Ala Lys Leu Thr Asp Tyr Leu Thr Pro Val Phe  
 85 90 95

Thr Lys Asp Ala Ile Lys Lys Gly Leu Glu Lys Tyr Asn Ile Ile Ser  
 100 105 110

Tyr Lys Gly Lys Met Ala Val Pro Val Gly Asp Gly Asp Asn Leu Leu  
 115 120 125

Gly Trp Asp Lys Ala Lys Ile Lys Leu Ile Ser Gln Lys Asn Asn Thr  
 130 135 140

Arg Thr Tyr Glu Phe Ser Val Pro Ala Leu Asp Gly Ser Val Thr Ala  
 145 150 155 160

Lys Arg Lys Ile Thr Phe Val Lys Glu Asn Asn Lys Trp Lys Ile Asn  
 165 170 175

Gln Leu Asp Ala Ala Ile  
 180

<210> 183  
 <211> 1317  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(818)

<400> 183  
 agcttcaaat cgctcccgct ccactgcttc tcattcttgag gaaaagttga ggccgctttc 60  
 attgtcatgc tgtatgtttc cacatcatga aatgatgcgt ttgtatgctg tgacagctga 120  
 ctccccaatc caattaacag gtatatgatc agcagcggtt gaaaaacgat aatgtttttt 180  
 ccggctcttt ttcggcatct cctagttcga gataatcgga acatgactac cctcctagcg 240  
 agtatgtaat ggcttttgggt tccgttcggt ttaaagaact ttatagttag agtataaaga 300  
 acaagtgtgc cgtttgaaaa ctgtcaaaaa agtcgattaa gttcgttcta aagaacattt 360  
 tcgtttaatt cctcaaaaaa cctctcaaatt tctcatcttt ttgaaaagtt ttagtttctt 420  
 tatagtgtac acaatttctt cttaattttt gtataaacac tgttgacaag gaaaaaatag 480  
 gatagaaagg atgatgaccc gtg ctg aaa aat gtc ata tta tgt tct ttt tta 533  
 Val Leu Lys Asn Val Ile Leu Cys Ser Phe Leu  
 1 5 10  
 ctg ctt tct agc att ggg cgg ctc aat gcc cat gcg gca gct tac gaa 581  
 Leu Leu Ser Ser Ile Gly Pro Leu Asn Ala His Ala Ala Ala Tyr Glu  
 15 20 25  
 aca gcc cgc atg tct aag tgg gaa gaa aaa gcg gtt gag gaa gca aaa 629  
 Thr Ala Arg Met Ser Lys Trp Glu Glu Lys Ala Val Glu Glu Ala Lys

30	35	40	
aag aga tat ccg gaa gca gaa gtg cgc ctc acg aaa aaa gta tgg gat			677
Lys Arg Tyr Pro Glu Ala Glu Val Arg Leu Thr Lys Lys Val Trp Asp			
45	50	55	
cga aag cgg gcc gat gaa gcg gtc aaa caa tac cat gtc aca ttg agt			725
Arg Lys Arg Ala Asp Glu Ala Val Lys Gln Tyr His Val Thr Leu Ser			
60	65	70	75
gaa gga aat aaa aat ttc gga gtg ttt gtc aca att tca ttt gaa cct			773
Glu Gly Asn Lys Asn Phe Gly Val Phe Val Thr Ile Ser Phe Glu Pro			
	80	85	90
gcg aca cac aaa att aac aaa gtc gtc gtt gtg gaa gaa tat aaa			818
Ala Thr His Lys Ile Asn Lys Val Val Val Val Glu Glu Tyr Lys			
	95	100	105
taagccgcat tgcagtgcaa agcggcttgt ctttatttat gctttttaaa aaacatgata			878
cagccaaggg gaagaatgcc gaaccattga tatatcctgg acggcggctt taattcttta			938
cgtttttctt tcatttcttt tctttcctgc ttaggcgtgt ccatatattt tacgagctgt			998
tccgtcatat atttaacata atcgttcggt ttcacgcgat cacctcttgg ggagttctgt			1058
cagttgaagt gttgtcatcc gaatcttttt ttatacatc ttcattgattt ggacacacaa			1118
tttttaatat tccttccact gcgtgatttt ttgatttctt aaatcatatt gaaattgagc			1178
gcttgtttct gtgccggaag ctgtcggttac ctgaatctgg actcgtgtga gctgctgatg			1238
agccgggctg acagaatacg atatcaagcc atgctgtttt tgaacttttt cttttgtctc			1298
ttcgtgaata tgggacaag			1317
<210>	184		
<211>	106		
<212>	PRT		
<213>	Bacillus licheniformis		
<400>	184		
Val Leu Lys Asn Val Ile Leu Cys Ser Phe Leu Leu Leu Ser Ser Ile			
1	5	10	15
Gly Pro Leu Asn Ala His Ala Ala Tyr Glu Thr Ala Arg Met Ser			
	20	25	30
Lys Trp Glu Glu Lys Ala Val Glu Glu Ala Lys Lys Arg Tyr Pro Glu			
	35	40	45
Ala Glu Val Arg Leu Thr Lys Lys Val Trp Asp Arg Lys Arg Ala Asp			

50

55

60

Glu Ala Val Lys Gln Tyr His Val Thr Leu Ser Glu Gly Asn Lys Asn  
65 70 75 80

Phe Gly Val Phe Val Thr Ile Ser Phe Glu Pro Ala Thr His Lys Ile  
85 90 95

Asn Lys Val Val Val Val Glu Glu Tyr Lys  
100 105

<210> 185

<211> 2347

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (518)..(1906)

<400> 185

acagggttca aattggtggc ggccggcggt cgggtcagc ggcgtcatcg gccgggcgga 60

aatgctcgat gcggcggtac cgggtgaact cgggggcacc tacgccggaa gtccgcttgg 120

atgcgtagcc gctttggcag tgctcgatat tatcgaatcg gaacagctca acaagcgctc 180

tgaagaaatc ggcaaagcca tcgaagagcg ggcgcttgaa tggaagatga aatatccgca 240

gattggggaa gtccgccgac ttggcgcaat ggctgcgatt gaaattgtcc gggacgaaaa 300

gacgcggggag ccggacaaaag cagctgcggc caagattgcc aagtacgcca atgaacacgg 360

tctgctcttg ttgacggcag ggatcaacgg caacattatc cgttttctgt ctccgctcgt 420

cattactgat gaattacttg aggaagggtt cggcatcatt gaagaagcgc tggaacagct 480

ctagtttgac atcttctaaa agaaggagcg gattttg atg ggt aaa cag caa atg 535

Met Gly Lys Gln Gln Met  
1 5

aaa aaa acg atg tcg cag acg gat gtg cta ttt tta gcg atc gga gct 583

Lys Lys Thr Met Ser Gln Thr Asp Val Leu Phe Leu Ala Ile Gly Ala  
10 15 20

atg ctc ggc tgg ggc tgg gtc gtc ctt tcc ggc gac tgg att tcg aca 631

Met Leu Gly Trp Gly Trp Val Val Leu Ser Gly Asp Trp Ile Ser Thr  
25 30 35

gcc ggc ttt ttg ggc agc acg atc gcg ttt atc atc ggc ggc ata ctc 679

Ala Gly Phe Leu Gly Ser Thr Ile Ala Phe Ile Ile Gly Gly Ile Leu  
40 45 50

gtc atc tta atc ggg tta acg tac gcg gag ctg tct tct gcc atc cct	727
Val Ile Leu Ile Gly Leu Thr Tyr Ala Glu Leu Ser Ser Ala Ile Pro	
55 60 65 70	
gaa acg ggt ggc ggc ttg att ttc gtc tac agg gcg ttc gga cga aaa	775
Glu Thr Gly Gly Gly Leu Ile Phe Val Tyr Arg Ala Phe Gly Arg Lys	
75 80 85	
acg gct ttt gtc gcc gct tgg ggt gtg ctg ttc ggc tat gtt tcg gtg	823
Thr Ala Phe Val Ala Ala Trp Gly Val Leu Phe Gly Tyr Val Ser Val	
90 95 100	
att aca ttt gag gcg gtc gca ttg cct acc gtc atc gat tac gtc ctg	871
Ile Thr Phe Glu Ala Val Ala Leu Pro Thr Val Ile Asp Tyr Val Leu	
105 110 115	
cct gtc gaa cat cag ggg ttt ctc tgg tcg cta agc ggc tgg gac gtg	919
Pro Val Glu His Gln Gly Phe Leu Trp Ser Leu Ser Gly Trp Asp Val	
120 125 130	
tat gtc act tgg gtg ttg atc ggt tcg gga ggt gcg gtc gtc ctg aca	967
Tyr Val Thr Trp Val Leu Ile Gly Ser Gly Gly Ala Val Val Leu Thr	
135 140 145 150	
gcg ctc aat tac ttc ggc gtc aag ccg gcc gcg att ttt cag tcg gtc	1015
Ala Leu Asn Tyr Phe Gly Val Lys Pro Ala Ala Ile Phe Gln Ser Val	
155 160 165	
ttt acg att gcg att atc gcc acg ggc ttt ctc ctt ttg ggc ggc gcc	1063
Phe Thr Ile Ala Ile Ile Ala Thr Gly Phe Leu Leu Leu Gly Gly Ala	
170 175 180	
ttg gta aac ggt gat ttc gaa cat gta cag ccc ctt ttt aaa gac ggg	1111
Leu Val Asn Gly Asp Phe Glu His Val Gln Pro Leu Phe Lys Asp Gly	
185 190 195	
ttt tcc ggt atg atg tcc gtc ctt gtc atg att ccg ttt cta ttt gtc	1159
Phe Ser Gly Met Met Ser Val Leu Val Met Ile Pro Phe Leu Phe Val	
200 205 210	
gga ttt gac gtc atc cct cag gtt gcg gct gaa att aat gcc ccg aaa	1207
Gly Phe Asp Val Ile Pro Gln Val Ala Ala Glu Ile Asn Ala Pro Lys	
215 220 225 230	
aaa atc atc ggc aaa att ttg att att tcg att atc agt gcg gtc gtg	1255
Lys Ile Ile Gly Lys Ile Leu Ile Ile Ser Ile Ile Ser Ala Val Val	
235 240 245	
ttt tat ttg ctg att gta ttc ggc gta acg atg ggt ctg tca gaa agc	1303
Phe Tyr Leu Leu Ile Val Phe Gly Val Thr Met Gly Leu Ser Glu Ser	
250 255 260	
gag ctt gcg acg act tct ttg gca acc gcg gat gca atg gtc aat ctg	1351
Glu Leu Ala Thr Thr Ser Leu Ala Thr Ala Asp Ala Met Val Asn Leu	
265 270 275	

ctc ggg aac cag ctg ttc ggc acg gtg ctt gtc ctc ggc ggc gtc gcc Leu Gly Asn Gln Leu Phe Gly Thr Val Leu Val Leu Gly Gly Val Ala 280 285 290	1399
gga atc att acg agc tgg aac gca ttt atc atc ggc gcg agc cgg att Gly Ile Ile Thr Ser Trp Asn Ala Phe Ile Ile Gly Ala Ser Arg Ile 295 300 305 310	1447
ctg ttt gca atg tcg gaa aag ggc atg gtg ccg aaa tgg ttc ggc ttc Leu Phe Ala Met Ser Glu Lys Gly Met Val Pro Lys Trp Phe Gly Phe 315 320 325	1495
atc cat ccg aag tat aaa acg ccg act aat gca att tta ttt ctg ggt Ile His Pro Lys Tyr Lys Thr Pro Thr Asn Ala Ile Leu Phe Leu Gly 330 335 340	1543
gcg ctg gcg ttt ttt gcc ccg ctg ctc gga cgc cct gcc ctt gtt tgg Ala Leu Ala Phe Phe Ala Pro Leu Leu Gly Arg Pro Ala Leu Val Trp 345 350 355	1591
atc gtc aat gca ggg gga aca ggt att ata gtc gga tat ttg atc gtc Ile Val Asn Ala Gly Gly Thr Gly Ile Ile Val Gly Tyr Leu Ile Val 360 365 370	1639
tcg att gca ttc atg aag ctg aga aaa aca gag ccg gat tta cac agg Ser Ile Ala Phe Met Lys Leu Arg Lys Thr Glu Pro Asp Leu His Arg 375 380 385 390	1687
ccg tat aaa atc aat aag tgg aaa aca acg ggt ata tct gct atc ctc Pro Tyr Lys Ile Asn Lys Trp Lys Thr Thr Gly Ile Ser Ala Ile Leu 395 400 405	1735
tta agt gtt atc ttc ctt gcc ttt tat ttg cca ggc atg ccg gcc gcg Leu Ser Val Ile Phe Leu Ala Phe Tyr Leu Pro Gly Met Pro Ala Ala 410 415 420	1783
ctc aca tgg ccg tat gag tgg ctg atc ttg gcg gga tgg aca ttg atc Leu Thr Trp Pro Tyr Glu Trp Leu Ile Leu Ala Gly Trp Thr Leu Ile 425 430 435	1831
ggt ttt ctt tta tac aac agc agt tca aaa cgt aaa ggg gag gag att Gly Phe Leu Leu Tyr Asn Ser Ser Ser Lys Arg Lys Gly Glu Glu Ile 440 445 450	1879
caa cat gac cag cat gct aga agt ata taatcctgcg actggagaaa Gln His Asp Gln His Ala Arg Ser Ile 455 460	1926
aaatcaaadc ggttccccag caatccgcaa aggaagtcga agaagctgtc gtacgctcgc	1986
atgaggcatt tcaaaaatgg tcgaaaacat cggctgcaga acgagcgggc ttgctgaaaa	2046
aatggtttga tttaattgtg gagcagaagg acgagctggc aaaattgatt acgcttgaaa	2106
acggcaagcc gtacgctgaa gcgcagggcg aagtcttata tagcgcaggc tatatcgaat	2166
ggatatgcgga ggaagcgaag cgcattctacg gaagaacggt tcccgcctct gtgacgaaca	2226

agcgcacatcat cgtcacacgc cagggagtcg gacctgttgc ggcgattacc ccgtggaatt 2286  
 ttccggcggc gatgatcacg agaaaagcgg ggccggcttt ggcggcgggc tgtaccttta 2346  
 t 2347

<210> 186  
 <211> 463  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 186

Met Gly Lys Gln Gln Met Lys Lys Thr Met Ser Gln Thr Asp Val Leu  
 1 5 10 15

Phe Leu Ala Ile Gly Ala Met Leu Gly Trp Gly Trp Val Val Leu Ser  
 20 25 30

Gly Asp Trp Ile Ser Thr Ala Gly Phe Leu Gly Ser Thr Ile Ala Phe  
 35 40 45

Ile Ile Gly Gly Ile Leu Val Ile Leu Ile Gly Leu Thr Tyr Ala Glu  
 50 55 60

Leu Ser Ser Ala Ile Pro Glu Thr Gly Gly Gly Leu Ile Phe Val Tyr  
 65 70 75 80

Arg Ala Phe Gly Arg Lys Thr Ala Phe Val Ala Ala Trp Gly Val Leu  
 85 90 95

Phe Gly Tyr Val Ser Val Ile Thr Phe Glu Ala Val Ala Leu Pro Thr  
 100 105 110

Val Ile Asp Tyr Val Leu Pro Val Glu His Gln Gly Phe Leu Trp Ser  
 115 120 125

Leu Ser Gly Trp Asp Val Tyr Val Thr Trp Val Leu Ile Gly Ser Gly  
 130 135 140

Gly Ala Val Val Leu Thr Ala Leu Asn Tyr Phe Gly Val Lys Pro Ala  
 145 150 155 160

Ala Ile Phe Gln Ser Val Phe Thr Ile Ala Ile Ile Ala Thr Gly Phe  
 165 170 175

Leu Leu Leu Gly Gly Ala Leu Val Asn Gly Asp Phe Glu His Val Gln  
180 185 190

Pro Leu Phe Lys Asp Gly Phe Ser Gly Met Met Ser Val Leu Val Met  
195 200 205

Ile Pro Phe Leu Phe Val Gly Phe Asp Val Ile Pro Gln Val Ala Ala  
210 215 220

Glu Ile Asn Ala Pro Lys Lys Ile Ile Gly Lys Ile Leu Ile Ile Ser  
225 230 235 240

Ile Ile Ser Ala Val Val Phe Tyr Leu Leu Ile Val Phe Gly Val Thr  
245 250 255

Met Gly Leu Ser Glu Ser Glu Leu Ala Thr Thr Ser Leu Ala Thr Ala  
260 265 270

Asp Ala Met Val Asn Leu Leu Gly Asn Gln Leu Phe Gly Thr Val Leu  
275 280 285

Val Leu Gly Gly Val Ala Gly Ile Ile Thr Ser Trp Asn Ala Phe Ile  
290 295 300

Ile Gly Ala Ser Arg Ile Leu Phe Ala Met Ser Glu Lys Gly Met Val  
305 310 315 320

Pro Lys Trp Phe Gly Phe Ile His Pro Lys Tyr Lys Thr Pro Thr Asn  
325 330 335

Ala Ile Leu Phe Leu Gly Ala Leu Ala Phe Phe Ala Pro Leu Leu Gly  
340 345 350

Arg Pro Ala Leu Val Trp Ile Val Asn Ala Gly Gly Thr Gly Ile Ile  
355 360 365

Val Gly Tyr Leu Ile Val Ser Ile Ala Phe Met Lys Leu Arg Lys Thr  
370 375 380

Glu Pro Asp Leu His Arg Pro Tyr Lys Ile Asn Lys Trp Lys Thr Thr  
385 390 395 400



Gly Ile Ser Ala Ile Leu Leu Ser Val Ile Phe Leu Ala Phe Tyr Leu  
405 410 415

Pro Gly Met Pro Ala Ala Leu Thr Trp Pro Tyr Glu Trp Leu Ile Leu  
420 425 430

Ala Gly Trp Thr Leu Ile Gly Phe Leu Leu Tyr Asn Ser Ser Ser Lys  
435 440 445

Arg Lys Gly Glu Glu Ile Gln His Asp Gln His Ala Arg Ser Ile  
450 455 460

<210> 187  
<211> 2506  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501) .. (1985)

<400> 187  
ttattaccaa taaatattcct agtgcagaat ctattaagat tacgaaaatc tcaagcctga 60  
ccctgagcag cgcaaaaact gccggtcagc ggccgaaaac agcagaggtg aagtttttctt 120  
actttgttaa agaaaaatca aatggctatg ttctatcaaa cggaaaactt tcttaaaaaa 180  
cagcgattat ttccgtgacg acgactcaat taagatcgat gctgggcggc atgaatatga 240  
agagcacgta tgcttctgta tccagcaata cgaacgcttt tactctcagc ggtaaaggat 300  
tcggacacgg catcggcatg agtcagtacg gatcaaatgc cagagctgct gccgggcacg 360  
attacaagaa gattttaagt ttctactatc caaatacgac tctatcaagc tattaataga 420  
gtttgaacag gaagcagcag tgcctcctct gttcatgttc aggggaaaac ataacattta 480  
cattttttgga gggtattttt ttg aag gtc ttt ctt aaa gct gta cct atg ttg 533  
Leu Lys Val Phe Leu Lys Ala Val Pro Met Leu  
1 5 10  
tgg tta cgg ttc ttt ttg ttt gtg cct aat gta ttt gcg gcc aac tct 581  
Trp Leu Arg Phe Phe Leu Phe Val Pro Asn Val Phe Ala Ala Asn Ser  
15 20 25  
gtc aca aga ttg gac ggt gca aac cga tat gag gtt gcg gtg aac gtt 629  
Val Thr Arg Leu Asp Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val  
30 35 40  
tcc aag cag ggg tgg aca agt gca agc act gtg att gtt gca aat gga 677

Ser	Lys	Gln	Gly	Trp	Thr	Ser	Ala	Ser	Thr	Val	Ile	Val	Ala	Asn	Gly		
45						50					55						
aag	gca	tat	gca	gac	gtc	ctt	tca	gcg	act	cca	ttt	gcc	tat	cga	aac	725	
Lys	Ala	Tyr	Ala	Asp	Val	Leu	Ser	Ala	Thr	Pro	Phe	Ala	Tyr	Arg	Asn		
60					65				70					75			
aac	gcg	cct	gtt	cta	tta	acg	gaa	gcg	tct	aaa	ctg	cca	acg	gcc	act	773	
Asn	Ala	Pro	Val	Leu	Leu	Thr	Glu	Ala	Ser	Lys	Leu	Pro	Thr	Ala	Thr		
				80					85					90			
aaa	aac	cga	atc	agt	caa	tta	aaa	cct	agc	aaa	gtg	atc	gta	atc	ggc	821	
Lys	Asn	Arg	Ile	Ser	Gln	Leu	Lys	Pro	Ser	Lys	Val	Ile	Val	Ile	Gly		
			95					100					105				
gga	acc	gtc	agc	gtt	caa	aac	ggg	gtc	gta	agc	gag	atc	aaa	aag	ctt	869	
Gly	Thr	Val	Ser	Val	Gln	Asn	Gly	Val	Val	Ser	Glu	Ile	Lys	Lys	Leu		
		110					115					120					
ggg	gtg	tca	tct	gtc	gaa	cg	atc	ggc	gga	gcg	aat	cg	tac	gag	gtt	917	
Gly	Val	Ser	Ser	Val	Glu	Arg	Ile	Gly	Gly	Ala	Asn	Arg	Tyr	Glu	Val		
	125					130					135						
gcg	gcg	aat	att	gcg	aat	aag	ctg	ccg	agc	aat	tcg	aaa	gct	gtc	atc	965	
Ala	Ala	Asn	Ile	Ala	Asn	Lys	Leu	Pro	Ser	Asn	Ser	Lys	Ala	Val	Ile		
140					145					150				155			
gca	aac	ggg	acg	gcc	tat	gct	gac	agc	ctt	gcg	atc	ggc	gca	tat	gcc	1013	
Ala	Asn	Gly	Thr	Ala	Tyr	Ala	Asp	Ser	Leu	Ala	Ile	Gly	Ala	Tyr	Ala		
				160					165					170			
gcg	aga	aac	ggc	atc	ccg	att	ctt	tta	aca	tcg	tcg	aat	tcc	ata	ccg	1061	
Ala	Arg	Asn	Gly	Ile	Pro	Ile	Leu	Leu	Thr	Ser	Ser	Asn	Ser	Ile	Pro		
			175					180					185				
aca	gcg	aca	aaa	aat	gcg	atg	aag	agc	aaa	gga	aca	aca	tcg	acc	att	1109	
Thr	Ala	Thr	Lys	Asn	Ala	Met	Lys	Ser	Lys	Gly	Thr	Thr	Ser	Thr	Ile		
		190					195					200					
gtc	gta	ggc	ggg	gaa	gtc	agc	atc	tcc	agc	agc	gtt	tac	aaa	cag	ctt	1157	
Val	Val	Gly	Gly	Glu	Val	Ser	Ile	Ser	Ser	Ser	Val	Tyr	Lys	Gln	Leu		
	205					210					215						
gct	tct	ccg	acg	cg	atc	ggc	ggc	agc	aac	cg	tat	gaa	gtc	gcg	gcc	1205	
Ala	Ser	Pro	Thr	Arg	Ile	Gly	Gly	Ser	Asn	Arg	Tyr	Glu	Val	Ala	Ala		
220					225					230				235			
aat	gtc	gtc	aag	aaa	tat	tat	tct	tct	gcc	aag	aat	gca	atc	atc	agc	1253	
Asn	Val	Val	Lys	Lys	Tyr	Tyr	Ser	Ser	Ala	Lys	Asn	Ala	Ile	Ile	Ser		
				240					245					250			
aac	ggc	tat	gcg	tat	gcc	gac	gga	tta	aca	gga	tct	gtt	ctg	gcg	gct	1301	
Asn	Gly	Tyr	Ala	Tyr	Ala	Asp	Gly	Leu	Thr	Gly	Ser	Val	Leu	Ala	Ala		
			255					260					265				
aag	caa	aac	cgt	ccg	atg	atg	ttc	acg	aat	gca	tca	tct	ttg	ccg	aca	1349	
Lys	Gln	Asn	Arg	Pro	Met	Met	Phe	Thr	Asn	Ala	Ser	Ser	Leu	Pro	Thr		

270	275	280	
ccg aca aga gaa gtg atc ggt tcc aaa aac atg acg acg ttt act gtg Pro Thr Arg Glu Val Ile Gly Ser Lys Asn Met Thr Thr Phe Thr Val 285 290 295			1397
ctt ggc gga acg gtt tct ctt caa tcc aat gtc gtg tca cag ctg aag Leu Gly Gly Thr Val Ser Leu Gln Ser Asn Val Val Ser Gln Leu Lys 300 305 310 315			1445
aat ccg atc gtc ggc aaa aaa atc ttc att gat gca ggg cac gga ggt Asn Pro Ile Val Gly Lys Lys Ile Phe Ile Asp Ala Gly His Gly Gly 320 325 330			1493
aca gac agc ggt gcc ctc ggc aac ggt tta tat gag aaa agc gtg aac Thr Asp Ser Gly Ala Leu Gly Asn Gly Leu Tyr Glu Lys Ser Val Asn 335 340 345			1541
ctt gat gtt gca aaa tta att aat acg aaa cta tca aac ggc ggt gct Leu Asp Val Ala Lys Leu Ile Asn Thr Lys Leu Ser Asn Gly Gly Ala 350 355 360			1589
ctg cca att atg gcg aga acg aac gac act tac ctg acg ctc gca cag Leu Pro Ile Met Ala Arg Thr Asn Asp Thr Tyr Leu Thr Leu Ala Gln 365 370 375			1637
cgc gtg tca aaa gcg cag tca aat cat gcg gat ttg ttt gtc agc atc Arg Val Ser Lys Ala Gln Ser Asn His Ala Asp Leu Phe Val Ser Ile 380 385 390 395			1685
cat gca aac tcg gca acg cca gct gct tcc gga aca gaa acc tac tat His Ala Asn Ser Ala Thr Pro Ala Ala Ser Gly Thr Glu Thr Tyr Tyr 400 405 410			1733
tat aca aca tat gaa tct gcc aac agc aaa cgg ctg gca acc gag att Tyr Thr Thr Tyr Glu Ser Ala Asn Ser Lys Arg Leu Ala Thr Glu Ile 415 420 425			1781
caa aac cgt ctc tat gtt gca ttg aat aca aaa aac cgc ggt gta aag Gln Asn Arg Leu Tyr Val Ala Leu Asn Thr Lys Asn Arg Gly Val Lys 430 435 440			1829
atc ggc aac ttc cat gtc atc agg gaa tca aaa atg cca agc tgc ctt Ile Gly Asn Phe His Val Ile Arg Glu Ser Lys Met Pro Ser Cys Leu 445 450 455			1877
gtt gaa ctt gcg ttt atc agc aat gta agc gat gcg aca aaa ctc aaa Val Glu Leu Ala Phe Ile Ser Asn Val Ser Asp Ala Thr Lys Leu Lys 460 465 470 475			1925
agc tcg act tac aaa gaa aaa ggc gct aaa gcg att tac gac gga atc Ser Ser Thr Tyr Lys Glu Lys Gly Ala Lys Ala Ile Tyr Asp Gly Ile 480 485 490			1973
gtt gct tac tat taaaaatataa acagaaaact cgtttttcga aaaattgcct Val Ala Tyr Tyr 495			2025

atgctgcctt tgttttgtct ttattatata gtatgatatt tttggtgaaa ttaaagataa 2085  
 aacggaggcg gtgcattttt aacaaaaaat caacgaattt actaatttta ataactcctt 2145  
 tacattgtgt ttacgttcgt atgctacact gacgaataga tcaaacagta acatactaata 2205  
 cgaggtgtat gctagtgagt atcgacaaaa gtttaagaat gtacaatgaa tattcaagcc 2265  
 agcaaaactta ttcctgtgct ctatctaaaa aagcagtacg ttatttatat atgaaacgga 2325  
 taatggatat cgtcctttcc ttgattgggc tcgctcttac actgccgttt attctgctgt 2385  
 tttgtatatt aatctgtatc gaaacaccgg gttctccgtt ataccggcag gaacgcgtcg 2445  
 gaaaagacgg gaagcatttc aaggatgatca agctgcgttc tatgagaatt gacgcagaaa 2505  
 a 2506

<210> 188  
 <211> 495  
 <212> PRT  
 <213> Bacillus licheniformis  
 <400> 188

Leu Lys Val Phe Leu Lys Ala Val Pro Met Leu Trp Leu Arg Phe Phe  
 1 5 10 15

Leu Phe Val Pro Asn Val Phe Ala Ala Asn Ser Val Thr Arg Leu Asp  
 20 25 30

Gly Ala Asn Arg Tyr Glu Val Ala Val Asn Val Ser Lys Gln Gly Trp  
 35 40 45

Thr Ser Ala Ser Thr Val Ile Val Ala Asn Gly Lys Ala Tyr Ala Asp  
 50 55 60

Val Leu Ser Ala Thr Pro Phe Ala Tyr Arg Asn Asn Ala Pro Val Leu  
 65 70 75 80

Leu Thr Glu Ala Ser Lys Leu Pro Thr Ala Thr Lys Asn Arg Ile Ser  
 85 90 95

Gln Leu Lys Pro Ser Lys Val Ile Val Ile Gly Gly Thr Val Ser Val  
 100 105 110

Gln Asn Gly Val Val Ser Glu Ile Lys Lys Leu Gly Val Ser Ser Val  
 115 120 125

Glu Arg Ile Gly Gly Ala Asn Arg Tyr Glu Val Ala Ala Asn Ile Ala  
 130 135 140

Asn Lys Leu Pro Ser Asn Ser Lys Ala Val Ile Ala Asn Gly Thr Ala  
 145 150 155 160

Tyr Ala Asp Ser Leu Ala Ile Gly Ala Tyr Ala Ala Arg Asn Gly Ile  
 165 170 175

Pro Ile Leu Leu Thr Ser Ser Asn Ser Ile Pro Thr Ala Thr Lys Asn  
 180 185 190

Ala Met Lys Ser Lys Gly Thr Thr Ser Thr Ile Val Val Gly Gly Glu  
 195 200 205

Val Ser Ile Ser Ser Ser Val Tyr Lys Gln Leu Ala Ser Pro Thr Arg  
 210 215 220

Ile Gly Gly Ser Asn Arg Tyr Glu Val Ala Ala Asn Val Val Lys Lys  
 225 230 235 240

Tyr Tyr Ser Ser Ala Lys Asn Ala Ile Ile Ser Asn Gly Tyr Ala Tyr  
 245 250 255

Ala Asp Gly Leu Thr Gly Ser Val Leu Ala Ala Lys Gln Asn Arg Pro  
 260 265 270

Met Met Phe Thr Asn Ala Ser Ser Leu Pro Thr Pro Thr Arg Glu Val  
 275 280 285

Ile Gly Ser Lys Asn Met Thr Thr Phe Thr Val Leu Gly Gly Thr Val  
 290 295 300

Ser Leu Gln Ser Asn Val Val Ser Gln Leu Lys Asn Pro Ile Val Gly  
 305 310 315 320

Lys Lys Ile Phe Ile Asp Ala Gly His Gly Gly Thr Asp Ser Gly Ala  
 325 330 335

Leu Gly Asn Gly Leu Tyr Glu Lys Ser Val Asn Leu Asp Val Ala Lys  
 340 345 350

Leu Ile Asn Thr Lys Leu Ser Asn Gly Gly Ala Leu Pro Ile Met Ala  
 355 360 365

Arg Thr Asn Asp Thr Tyr Leu Thr Leu Ala Gln Arg Val Ser Lys Ala  
 370 375 380

Gln Ser Asn His Ala Asp Leu Phe Val Ser Ile His Ala Asn Ser Ala  
 385 390 395 400

Thr Pro Ala Ala Ser Gly Thr Glu Thr Tyr Tyr Tyr Thr Thr Tyr Glu  
 405 410 415

Ser Ala Asn Ser Lys Arg Leu Ala Thr Glu Ile Gln Asn Arg Leu Tyr  
 420 425 430

Val Ala Leu Asn Thr Lys Asn Arg Gly Val Lys Ile Gly Asn Phe His  
 435 440 445

Val Ile Arg Glu Ser Lys Met Pro Ser Cys Leu Val Glu Leu Ala Phe  
 450 455 460

Ile Ser Asn Val Ser Asp Ala Thr Lys Leu Lys Ser Ser Thr Tyr Lys  
 465 470 475 480

Glu Lys Gly Ala Lys Ala Ile Tyr Asp Gly Ile Val Ala Tyr Tyr  
 485 490 495

<210> 189  
 <211> 2110  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1607)

<400> 189  
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 aatcgatacg ctgattctcg gatgtacgca ttatccgatt ttaaaagagc cgattcagcg 120  
 ctatatggga gagcgcgtca acatcatttc ctccggagat gaaacggcca gggaagtcag 180  
 cacgatcttg tcatacaacg gtttattaag caaaacggcg gaaccgccgg aacacttggt 240  
 tttaacaact ggggagcgtg cccgcttcac aaaaattgca aacgattggt ttggatacga 300



190	195	200	
tca gaa gaa ctc agc cgc gag gac ggc att aac ctc gac acg gcg ggt Ser Glu Glu Leu Ser Arg Glu Asp Gly Ile Asn Leu Asp Thr Ala Gly 205 210 215			1157
gtg aca gat ata acg gcg aca cag ccg gtc acc gtc tat tat ttg gct Val Thr Asp Ile Thr Ala Thr Gln Pro Val Thr Val Tyr Tyr Leu Ala 220 225 230 235			1205
gaa tca gat aaa ggc aca tat tac gtt ccg gtg aca aag cgg acg tct Glu Ser Asp Lys Gly Thr Tyr Tyr Val Pro Val Thr Lys Arg Thr Ser 240 245 250			1253
gca aaa gaa aaa gat cag gtg acg gcg gcg att aaa gag ctg act gaa Ala Lys Glu Lys Asp Gln Val Thr Ala Ala Ile Lys Glu Leu Thr Glu 255 260 265			1301
gga ccg gac aat aaa agc ggc ctg ctc tcc gat ttc cag ggc gac gtc Gly Pro Asp Asn Lys Ser Gly Leu Leu Ser Asp Phe Gln Gly Asp Val 270 275 280			1349
aag ctt gaa aac aag ccg aag att gaa gac ggc cat gta acc ctc gac Lys Leu Glu Asn Lys Pro Lys Ile Glu Asp Gly His Val Thr Leu Asp 285 290 295			1397
ttt aac gaa gcg atc tac gga agt gcc gac ggc cag aaa aaa gtg ata Phe Asn Glu Ala Ile Tyr Gly Ser Ala Asp Gly Gln Lys Lys Val Ile 300 305 310 315			1445
tcg gat gaa gtg tta aac agt atc gtg ttg aca tta acc gaa ctg cct Ser Asp Glu Val Leu Asn Ser Ile Val Leu Thr Leu Thr Glu Leu Pro 320 325 330			1493
gat gtg aaa agt gtg tcg gtt acc gtg aac gga aaa tcc gag ctc gtg Asp Val Lys Ser Val Ser Val Thr Val Asn Gly Lys Ser Glu Leu Val 335 340 345			1541
aat gaa aaa gga gaa aag ctt tcc aag ccg gtt tca aga ccg agc aag Asn Glu Lys Gly Glu Lys Leu Ser Lys Pro Val Ser Arg Pro Ser Lys 350 355 360			1589
gtg aac aca ggt agt ttt taagccgaaa tttttgatata actatagaaa Val Asn Thr Gly Ser Phe 365			1637
aagaggtgag cgatcaaagc tgcctctttc tttattcagc tttttggaag agcggaatga			1697
ttgtgaaaagg tttatgtaca tacaatcgga ggtaaaaaat gagatacgat ggaagaaaaa			1757
acaatgaact gcgccctgtc acaatggacc tcgactttat tacgcatccg gaaggatcgg			1817
tcctgattac agtcggcggg acaaaggtga tatgcaacgc gtctgtggaa gaccgcgtac			1877
cgcccttttt gagaggagaa gggaagggct ggatcaccgc ggaatacagc atgctgccgc			1937
gggccacgaa ccaaaggacg atcaggggaat cgtcaaaaagg gaaaatctcc gggcggacga			1997



tggaatcca acggctgac ggacgagctc ttcgggcggt tggtgatttg gaaaagctcg 2057

gtgagcggac gatctggac gactgcgacg tcattcaggc ggacggaggt acg 2110

<210> 190

<211> 369

<212> PRT

<213> Bacillus licheniformis

<400> 190

Met Leu Lys Lys Gly Met Lys Gly Ile Ala Val Thr Val Thr Ala Ser  
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Ala Leu Leu Leu Ser Gly Cys Gly Ile Phe Gln Ser Asp Gln Ala Ser  
20 25 30

Glu Glu Ile Asp Pro Pro Gln Asp Ile Thr Tyr Val Lys Glu Glu Lys  
35 40 45

Glu Gln Asp Lys Thr Asp Lys Thr Lys Asp Lys Thr Glu Asp Lys Gly  
50 55 60

Ser Lys Thr Thr Ser Asp Asp Lys Ala Ala Gln Thr Gly Asp Thr Val  
65 70 75 80

Met Arg Glu Leu Tyr Leu Ile Asp Lys Asn Gly Tyr Val Thr Ala Gln  
85 90 95

Thr Leu Pro Leu Pro Lys Gln Glu Gly Thr Ala Lys Gln Ala Leu Glu  
100 105 110

Tyr Leu Val Glu Gly Gly Pro Val Ser Asn Ile Leu Pro Asn Gly Phe  
115 120 125

Arg Ala Val Leu Pro Ala Asp Thr Thr Val Asn Val Asp Ile Lys Glu  
130 135 140

Asp Gly Thr Ala Ile Ala Asp Phe Ser Asn Glu Phe Lys Asn Tyr Lys  
145 150 155 160

Ala Glu Asp Glu Gln Lys Ile Val Gln Ala Ile Thr Trp Thr Leu Thr  
165 170 175

Gln Phe Asn Ser Ile Asp Lys Val Lys Leu Arg Met Asn Gly His Asp  
 180 185 190

Leu Lys Glu Met Pro Val Asn Gly Thr Pro Ile Ser Glu Glu Leu Ser  
 195 200 205

Arg Glu Asp Gly Ile Asn Leu Asp Thr Ala Gly Val Thr Asp Ile Thr  
 210 215 220

Ala Thr Gln Pro Val Thr Val Tyr Tyr Leu Ala Glu Ser Asp Lys Gly  
 225 230 235 240

Thr Tyr Tyr Val Pro Val Thr Lys Arg Thr Ser Ala Lys Glu Lys Asp  
 245 250 255

Gln Val Thr Ala Ala Ile Lys Glu Leu Thr Glu Gly Pro Asp Asn Lys  
 260 265 270

Ser Gly Leu Leu Ser Asp Phe Gln Gly Asp Val Lys Leu Glu Asn Lys  
 275 280 285

Pro Lys Ile Glu Asp Gly His Val Thr Leu Asp Phe Asn Glu Ala Ile  
 290 295 300

Tyr Gly Ser Ala Asp Gly Gln Lys Lys Val Ile Ser Asp Glu Val Leu  
 305 310 315 320

Asn Ser Ile Val Leu Thr Leu Thr Glu Leu Pro Asp Val Lys Ser Val  
 325 330 335

Ser Val Thr Val Asn Gly Lys Ser Glu Leu Val Asn Glu Lys Gly Glu  
 340 345 350

Lys Leu Ser Lys Pro Val Ser Arg Pro Ser Lys Val Asn Thr Gly Ser  
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Phe

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<221> CDS

<222> (501)..(1667)

<400> 191

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gaattttcttt ttttatatgg gaacacggac aaaatggact ctatttttaaa cattctgatc      180
tgttgtttttt ggaagcaaaa tgctttcaca taaccgtttt ttattttcttt cacaagaatc      240
gcccgccttag aaaaaccgct ttttttcatg tatatgattt ctaccggaat gccgtcttcc      300
atggaacgat acaacagctt attcatcgtc tcacctcaca ttctatttta tacgaacatt      360
tgttcttgat caagtgtaaa caaaatgtaa attttggcat tattcgagtt catgtatgaa      420
aatattagca ttttgaagaa actttttaag gggttattgc gtcagtaa at acgtcacata      480
taaaagaagg agtaccgcgac atg gca aga aca tac aga acg cga ata aag aaa      533
                        Met Ala Arg Thr Tyr Arg Thr Arg Ile Lys Lys
                        1                5                10

aga aaa aag cag aaa aca aaa aga agg ctt atc ata ttt tcc ttt ttg      581
Arg Lys Lys Gln Lys Thr Lys Arg Arg Leu Ile Ile Phe Ser Phe Leu
                        15                20                25

gtt gtt tgt gga tta att tat ctt gca ctt cca agc ggt atg cga gat      629
Val Val Cys Gly Leu Ile Tyr Leu Ala Leu Pro Ser Gly Met Arg Asp
                        30                35                40

cac cag gaa aac caa ttg caa gca act gaa aaa aag gca cag cct gaa      677
His Gln Glu Asn Gln Leu Gln Ala Thr Glu Lys Lys Ala Gln Pro Glu
                        45                50                55

gca aag aaa aag cca aca caa aat gaa aca aaa aag agc aaa atc gtc      725
Ala Lys Lys Lys Pro Thr Gln Asn Glu Thr Lys Lys Ser Lys Ile Val
60                65                70                75

aca aaa aat gat aat gct caa ttg gat caa tat ttg aaa agc att gga      773
Thr Lys Asn Asp Asn Ala Gln Leu Asp Gln Tyr Leu Lys Ser Ile Gly
                        80                85                90

ttc agc ggc aca gca ttg atc gta gaa gat gga aaa gtg gtg aca agc      821
Phe Ser Gly Thr Ala Leu Ile Val Glu Asp Gly Lys Val Val Thr Ser
                        95                100                105

aaa ggg tat tta tat gca aac cgc gag gaa atg gtt ccc aat aca cca      869
Lys Gly Tyr Leu Tyr Ala Asn Arg Glu Glu Met Val Pro Asn Thr Pro
                        110                115                120

gat acc gtc ttt tat gtg ggg tca tca caa aaa gcg att att gca acg      917
Asp Thr Val Phe Tyr Val Gly Ser Ser Gln Lys Ala Ile Ile Ala Thr
125                130                135
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Ala Ile Leu Gln Leu Glu Glu Lys Gly Leu Leu Ser Val Asn Asp Pro	
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ggt tct aag tat ctt ccc aat ttt cca aac ggc tca aag atc acc ctt	1013
Val Ser Lys Tyr Leu Pro Asn Phe Pro Asn Gly Ser Lys Ile Thr Leu	
160 165 170	
tat cat ttc ttg acg cac aca tcc gga att agg ggt cac aaa gaa ggc	1061
Tyr His Phe Leu Thr His Thr Ser Gly Ile Arg Gly His Lys Glu Gly	
175 180 185	
cgc gga tat att tcg ccg gaa gat tta att aaa gat atc gaa aaa cgg	1109
Arg Gly Tyr Ile Ser Pro Glu Asp Leu Ile Lys Asp Ile Glu Lys Arg	
190 195 200	
ggt gta aaa tac cca aca ggg aaa tgg gat tat aga gac tcc aat tac	1157
Gly Val Lys Tyr Pro Thr Gly Lys Trp Asp Tyr Arg Asp Ser Asn Tyr	
205 210 215	
tcg gtt ctg gca tac att gtt tcc atg gta agc ggt gaa cca gtc gac	1205
Ser Val Leu Ala Tyr Ile Val Ser Met Val Ser Gly Glu Pro Val Asp	
220 225 230 235	
caa tac atc aaa aag cat att ttt aaa cct gcc ggt atg aaa cat gca	1253
Gln Tyr Ile Lys Lys His Ile Phe Lys Pro Ala Gly Met Lys His Ala	
240 245 250	
ggc ttt tat aaa aca ttt gct aaa gag tca aat cca tcg aca gga tat	1301
Gly Phe Tyr Lys Thr Phe Ala Lys Glu Ser Asn Pro Ser Thr Gly Tyr	
255 260 265	
aaa tta aac ctg caa aaa aag ctt tat acg cct gac atg ccg gat tta	1349
Lys Leu Asn Leu Gln Lys Lys Leu Tyr Thr Pro Asp Met Pro Asp Leu	
270 275 280	
tca cag ctt tac ggg gcc ggt gat att tat atg acc gct tat gac atg	1397
Ser Gln Leu Tyr Gly Ala Gly Asp Ile Tyr Met Thr Ala Tyr Asp Met	
285 290 295	
tat ttg ttt gat aaa gca ctt tac gaa aga aaa atc att tcc aat gaa	1445
Tyr Leu Phe Asp Lys Ala Leu Tyr Glu Arg Lys Ile Ile Ser Asn Glu	
300 305 310 315	
agt ttt atg aaa atg ttt acg ccg aat aaa gca aca tac ggc atg ggc	1493
Ser Phe Met Lys Met Phe Thr Pro Asn Lys Ala Thr Tyr Gly Met Gly	
320 325 330	
ttt tat gtg tct cca gga agc tat tca agc cac ggt gtc atg ccc ggc	1541
Phe Tyr Val Ser Pro Gly Ser Tyr Ser Ser His Gly Val Met Pro Gly	
335 340 345	
tac aac ata tta aac agt ttc agt ctg aca ggg agc aga tac gtc att	1589
Tyr Asn Ile Leu Asn Ser Phe Ser Leu Thr Gly Ser Arg Tyr Val Ile	
350 355 360	

cta ttt tca aac atc caa aac aac att aag tct ttt ggc agt gtg aat 1637  
 Leu Phe Ser Asn Ile Gln Asn Asn Ile Lys Ser Phe Gly Ser Val Asn  
 365 370 375

aat cgg atc ttc tct att tta aat gga ttt tgaacagcag agaaagtttt 1687  
 Asn Arg Ile Phe Ser Ile Leu Asn Gly Phe  
 380 385

tacagctaaa agggatttta attataaatg tagaagatag atgataaatg aatttttcaat 1747

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ggataaaaaat aaaagcaggc atttagcctg cttttatata ttcaataagt ctaaaagcaa 1987

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gg 2169

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<211> 389

<212> PRT

<213> Bacillus licheniformis

<400> 192

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 35 40 45

Leu Gln Ala Thr Glu Lys Lys Ala Gln Pro Glu Ala Lys Lys Lys Pro  
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Thr Gln Asn Glu Thr Lys Lys Ser Lys Ile Val Thr Lys Asn Asp Asn  
 65 70 75 80

Ala Gln Leu Asp Gln Tyr Leu Lys Ser Ile Gly Phe Ser Gly Thr Ala  
 85 90 95

Leu Ile Val Glu Asp Gly Lys Val Val Thr Ser Lys Gly Tyr Leu Tyr  
 100 105 110

Ala Asn Arg Glu Glu Met Val Pro Asn Thr Pro Asp Thr Val Phe Tyr  
 115 120 125

Val Gly Ser Ser Gln Lys Ala Ile Ile Ala Thr Ala Ile Leu Gln Leu  
 130 135 140

Glu Glu Lys Gly Leu Leu Ser Val Asn Asp Pro Val Ser Lys Tyr Leu  
 145 150 155 160

Pro Asn Phe Pro Asn Gly Ser Lys Ile Thr Leu Tyr His Phe Leu Thr  
 165 170 175

His Thr Ser Gly Ile Arg Gly His Lys Glu Gly Arg Gly Tyr Ile Ser  
 180 185 190

Pro Glu Asp Leu Ile Lys Asp Ile Glu Lys Arg Gly Val Lys Tyr Pro  
 195 200 205

Thr Gly Lys Trp Asp Tyr Arg Asp Ser Asn Tyr Ser Val Leu Ala Tyr  
 210 215 220

Ile Val Ser Met Val Ser Gly Glu Pro Val Asp Gln Tyr Ile Lys Lys  
 225 230 235 240

His Ile Phe Lys Pro Ala Gly Met Lys His Ala Gly Phe Tyr Lys Thr  
 245 250 255

Phe Ala Lys Glu Ser Asn Pro Ser Thr Gly Tyr Lys Leu Asn Leu Gln  
 260 265 270

Lys Lys Leu Tyr Thr Pro Asp Met Pro Asp Leu Ser Gln Leu Tyr Gly  
 275 280 285

Ala Gly Asp Ile Tyr Met Thr Ala Tyr Asp Met Tyr Leu Phe Asp Lys  
 290 295 300

Ala Leu Tyr Glu Arg Lys Ile Ile Ser Asn Glu Ser Phe Met Lys Met  
 305 310 315 320

Phe Thr Pro Asn Lys Ala Thr Tyr Gly Met Gly Phe Tyr Val Ser Pro  
 325 330 335

Gly Ser Tyr Ser Ser His Gly Val Met Pro Gly Tyr Asn Ile Leu Asn  
 340 345 350

Ser Phe Ser Leu Thr Gly Ser Arg Tyr Val Ile Leu Phe Ser Asn Ile  
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Gln Asn Asn Ile Lys Ser Phe Gly Ser Val Asn Asn Arg Ile Phe Ser  
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Ile Leu Asn Gly Phe  
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 gaaagccgcg aacaagagca gggatgatgcc gccgacagcc attctgacag cgccgaacac 240  
 aagaggtgcc gcctctttcg gcgcaaatgc ctgggttggt cccgtcgttc ccataaaat 300  
 tgccgcaagc aagacaaaca gaaccgatac tttcatacta acgatctctc cctactcgat 360  
 cattcagaac tttttctatt gtaagataag tttgctgatt tttgaatcgc cgcttcggaa 420  
 atttcctga aaagaggaaa tattcaacgc tggccgaatt catataatgg ccaaaaaaca 480  
 attaaagtcg gaggaagcgg atg aaa aaa cga aca gtt tta ttc ttc ttg ttg 533  
 Met Lys Lys Arg Thr Val Leu Phe Phe Leu Leu  
 1 5 10  
 atc tgg ctc gcc gga tgt gcg agc gcc caa gag gct gag gaa caa acc 581  
 Ile Trp Leu Ala Gly Cys Ala Ser Ala Gln Glu Ala Glu Glu Gln Thr  
 15 20 25  
 aaa tgg gtg aac agc gaa cag aaa gcg att gag aac ggc att cgt tat 629  
 Lys Trp Val Asn Ser Glu Gln Lys Ala Ile Glu Asn Gly Ile Arg Tyr

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Glu Ser Ile Thr Lys Asp Asp Ile Ile Asp Lys Ile Asp Leu Asn Gly			
45	50	55	
gaa caa gtc gtc gtt ttt cga ttc ggc gat tcg gag gga gag ggg att			725
Glu Gln Val Val Val Phe Arg Phe Gly Asp Ser Glu Gly Glu Gly Ile			
60	65	70	75
ggc ctc gca cac atc aaa agg gaa aac ggc aac tat caa tgg tac cgc			773
Gly Leu Ala His Ile Lys Arg Glu Asn Gly Asn Tyr Gln Trp Tyr Arg			
	80	85	90
gac tta aat tac gca att gta aaa tcg gac cac ccg aaa acg gag aat			821
Asp Leu Asn Tyr Ala Ile Val Lys Ser Asp His Pro Lys Thr Glu Asn			
	95	100	105
gcg gaa gct tcc gcg ccg ttc aca acc cct aag gga aga aag tac acg			869
Ala Glu Ala Ser Ala Pro Phe Thr Thr Pro Lys Gly Arg Lys Tyr Thr			
	110	115	120
tta tat aca ggg gat gca gat cgc ctg aat ggt aca ttt gag act gat			917
Leu Tyr Thr Gly Asp Ala Asp Arg Leu Asn Gly Thr Phe Glu Thr Asp			
	125	130	135
gac ggg ctt cat ttg gag ccg gtg gtc gat caa aaa acg ggc atg tat			965
Asp Gly Leu His Leu Glu Pro Val Val Asp Gln Lys Thr Gly Met Tyr			
	140	145	150
tat cag atc gtg cag gat tcg gac tgaaatgaaa caaaaatgct gtcgggttgt			1019
Tyr Gln Ile Val Gln Asp Ser Asp			
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tcccgcacagc atttcatttt ttacgatttc tttttccgca ctgtcaagag cagcgcagca			1079
cctccaagaa gcacggcgag gatcgacagg atcagggaag cggtttgaat cccttgctct			1139
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Cys Ala Ser Ala Gln Glu Ala Glu Glu Gln Thr Lys Trp Val Asn Ser  
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Glu Gln Lys Ala Ile Glu Asn Gly Ile Arg Tyr Glu Ser Ile Thr Lys  
 35 40 45

Asp Asp Ile Ile Asp Lys Ile Asp Leu Asn Gly Glu Gln Val Val Val  
 50 55 60

Phe Arg Phe Gly Asp Ser Glu Gly Glu Gly Ile Gly Leu Ala His Ile  
 65 70 75 80

Lys Arg Glu Asn Gly Asn Tyr Gln Trp Tyr Arg Asp Leu Asn Tyr Ala  
 85 90 95

Ile Val Lys Ser Asp His Pro Lys Thr Glu Asn Ala Glu Ala Ser Ala  
 100 105 110

Pro Phe Thr Thr Pro Lys Gly Arg Lys Tyr Thr Leu Tyr Thr Gly Asp  
 115 120 125

Ala Asp Arg Leu Asn Gly Thr Phe Glu Thr Asp Asp Gly Leu His Leu  
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aagaatctag ttgagcgggtg gagcagggga ttccttatta tgactgcgat tttgcacatt	180
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tatttttttgt ttcacaaaact ttaaggtaat tttaagaaaag aggcgatctt gccaaccccta	300
aacaggggttt ttcgaacaga atgtcaaata gattagatat ttcataagaa caaggggggaa	360
ttgtctgttt gtgatgaata aaggaggacg ggcggaattt ctgtcaggat gctcagctgg	420
gttcttagaa aaaaatgcgg ctaaatatat atttatagat tgtaaacgct gtcttgtcct	480
cgaccaacag ggggatgaag atg aag aag ctg tta gtt gtt tat gcc gtg atg	533
Met Lys Lys Leu Leu Val Val Tyr Ala Val Met	
1 5 10	
ctc tgt ttg ttt ttt ctg tat gtc tac gac tac tcc cgg ggc gat aaa	581
Leu Cys Leu Phe Phe Leu Tyr Val Tyr Asp Tyr Ser Arg Gly Asp Lys	
15 20 25	
gcc ggt tct gca gaa gaa agc agg agg cct gcg gcc gca ggc agt ctg	629
Ala Gly Ser Ala Glu Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu	
30 35 40	
tcc gaa aaa tac gtg atg gtc acg ttt caa tcg gga atc gaa tat tgg	677
Ser Glu Lys Tyr Val Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp	
45 50 55	
aag agc ggt ctg aaa ggc ttt gag gat gcc gcg cag ctt ttc aac gtc	725
Lys Ser Gly Leu Lys Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val	
60 65 70 75	
tct gtc gag tat cgg ggg gcg gcc cat tat gat gtc cat gag caa acg	773
Ser Val Glu Tyr Arg Gly Ala Ala His Tyr Asp Val His Glu Gln Thr	
80 85 90	
acc gtc ctc gag cag gtg att gca aaa aaa ccg gcg gga atc gct gtt	821
Thr Val Leu Glu Gln Val Ile Ala Lys Lys Pro Ala Gly Ile Ala Val	
95 100 105	
tcg gca ata aac cca aaa gct tta aac cct gtc atc gac aag gcg cac	869
Ser Ala Ile Asn Pro Lys Ala Leu Asn Pro Val Ile Asp Lys Ala His	
110 115 120	
gag cag ggt att ccg atc gtt tta ttt gat tca gac gcc ccg ctc agc	917
Glu Gln Gly Ile Pro Ile Val Leu Phe Asp Ser Asp Ala Pro Leu Ser	
125 130 135	
aaa gct tct aca tat atc ggc aca aat aat atg gaa gcg ggt gct gtg	965
Lys Ala Ser Thr Tyr Ile Gly Thr Asn Asn Met Glu Ala Gly Ala Val	
140 145 150 155	
gcc gca agg cga atg gcc gaa ttt ttg aat gga aag gga gaa acc gcg	1013
Ala Ala Arg Arg Met Ala Glu Phe Leu Asn Gly Lys Gly Glu Thr Ala	

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gtc att acc cag ccg cag cag tac aat cat cag gaa agg acg aag ggc			1061
Val Ile Thr Gln Pro Gln Gln Tyr Asn His Gln Glu Arg Thr Lys Gly			
175	180	185	
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Phe Glu Gln Thr Ile Lys Gln Lys Tyr Pro Asn Met Lys Val Ala Ala			
190	195	200	
gtt ttg gac gga aaa ggg gat gag ctg acg tcg aaa aaa gaa gcg gcg			1157
Val Leu Asp Gly Lys Gly Asp Glu Leu Thr Ser Lys Lys Glu Ala Ala			
205	210	215	
aag att ttg gag gaa aat ccg tcc atc aaa gga att ttc acg act gaa			1205
Lys Ile Leu Glu Glu Asn Pro Ser Ile Lys Gly Ile Phe Thr Thr Glu			
220	225	230	235
gcc aat gga gcg agc ggc gtg gcc cgt gct gtg aag gag gcg gga ctt			1253
Ala Asn Gly Ala Ser Gly Val Ala Arg Ala Val Lys Glu Ala Gly Leu			
240	245	250	
gaa ggg gaa gta tgt atc atc ggc ttt gat aaa gac aag aaa acg ctg			1301
Glu Gly Glu Val Cys Ile Ile Gly Phe Asp Lys Asp Lys Lys Thr Leu			
255	260	265	
gac ggc atc aaa aac gga tcg att tcc gcg aca atg agc cag gac aca			1349
Asp Gly Ile Lys Asn Gly Ser Ile Ser Ala Thr Met Ser Gln Asp Thr			
270	275	280	
tgg caa atg ggc tat tgg tcg ctg cac atg ctg ttt ttc tca aat cac			1397
Trp Gln Met Gly Tyr Trp Ser Leu His Met Leu Phe Phe Ser Asn His			
285	290	295	
cat ctg aag cat gaa cgc ccg ctt ccg gcc gca atc gac aca ggc att			1445
His Leu Lys His Glu Arg Pro Leu Pro Ala Ala Ile Asp Thr Gly Ile			
300	305	310	315
acc atc ata acg aaa gaa aat gtg gca gcc tat tat gcg aat gat			1490
Thr Ile Ile Thr Lys Glu Asn Val Ala Ala Tyr Tyr Ala Asn Asp			
320	325	330	
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gaatatcaga agccatgt

1988

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<212> PRT  
<213> Bacillus licheniformis

<400> 196

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Glu Ser Arg Arg Pro Ala Ala Ala Gly Ser Leu Ser Glu Lys Tyr Val  
35 40 45

Met Val Thr Phe Gln Ser Gly Ile Glu Tyr Trp Lys Ser Gly Leu Lys  
50 55 60

Gly Phe Glu Asp Ala Ala Gln Leu Phe Asn Val Ser Val Glu Tyr Arg  
65 70 75 80

Gly Ala Ala His Tyr Asp Val His Glu Gln Thr Thr Val Leu Glu Gln  
85 90 95

Val Ile Ala Lys Lys Pro Ala Gly Ile Ala Val Ser Ala Ile Asn Pro  
100 105 110

Lys Ala Leu Asn Pro Val Ile Asp Lys Ala His Glu Gln Gly Ile Pro  
115 120 125

Ile Val Leu Phe Asp Ser Asp Ala Pro Leu Ser Lys Ala Ser Thr Tyr  
130 135 140

Ile Gly Thr Asn Asn Met Glu Ala Gly Ala Val Ala Ala Arg Arg Met  
145 150 155 160

Ala Glu Phe Leu Asn Gly Lys Gly Glu Thr Ala Val Ile Thr Gln Pro  
165 170 175

Gln Gln Tyr Asn His Gln Glu Arg Thr Lys Gly Phe Glu Gln Thr Ile  
180 185 190

Lys Gln Lys Tyr Pro Asn Met Lys Val Ala Ala Val Leu Asp Gly Lys  
 195 200 205

Gly Asp Glu Leu Thr Ser Lys Lys Glu Ala Ala Lys Ile Leu Glu Glu  
 210 215 220

Asn Pro Ser Ile Lys Gly Ile Phe Thr Thr Glu Ala Asn Gly Ala Ser  
 225 230 235 240

Gly Val Ala Arg Ala Val Lys Glu Ala Gly Leu Glu Gly Glu Val Cys  
 245 250 255

Ile Ile Gly Phe Asp Lys Asp Lys Lys Thr Leu Asp Gly Ile Lys Asn  
 260 265 270

Gly Ser Ile Ser Ala Thr Met Ser Gln Asp Thr Trp Gln Met Gly Tyr  
 275 280 285

Trp Ser Leu His Met Leu Phe Phe Ser Asn His His Leu Lys His Glu  
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Arg Pro Leu Pro Ala Ala Ile Asp Thr Gly Ile Thr Ile Ile Thr Lys  
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Glu Asn Val Ala Ala Tyr Tyr Ala Asn Asp  
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 <222> (501)..(1190)

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 cattggccaa ccttttaacg cagctatcgc ccgaatgtgt atcggataca tgataaccga 180  
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Ser Val Ala Phe Val Asp Trp Lys Ile Asn Ala Gln Lys Gly Trp Arg  
190 195 200

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Tyr Ala Tyr Asp Asn Met Met Lys Gln Ala His Pro Gly Ala Ile Tyr  
205 210 215

ctg ctt cac acc gtc ttc agg cga tca ccg act tgaaaaaaga aggttatata 1210  
Leu Leu His Thr Val Phe Arg Arg Ser Pro Thr  
220 225 230

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acaatgcccc ggtgccgagg tcgcaatgcg taaaacattt gtttttcccc cccccgaaga 1330

ccccgtctca aataatataa aatagatata aaaaaaaaga atcataataa aaaaagaata 1390

tctatcccca ccaaagggag ggtggttttg ataaccagtc gcagtcgggg gaaagtgtct 1450

aaccatggaa aaggggtgtg ttttatcatt aggcaggtgt gtgacaaagg cggtaaaata 1510

cagcgaagca tccaatgttt tattaaaagc tattagcagg atggcaaagt gcatctcgct 1570

gttcaagact ttggaggggg catcgattca aaaagatatg ccgcgcgtgt tgacaaaggc 1630

tttacatcaa caacggagca tcatgatcag gccgccacgg gaatggg 1677

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<213> Bacillus licheniformis

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Phe Ser Lys Ser Lys Asn His Gln Pro Ala Asp Ala Gly Gln Glu Leu  
35 40 45

Thr Asn Leu Leu Gln Gln Tyr Asp Ala Phe Tyr Leu Gly Asn Thr Lys  
50 55 60

Glu Lys Thr Ile Tyr Leu Thr Phe Asp Asn Gly Tyr Glu Asn Gly Tyr  
65 70 75 80

Thr Pro Gln Val Leu Asp Val Leu Lys Lys Gln Asn Val Lys Ala Ala  
85 90 95

Phe Phe Val Thr Gly His Phe Val Lys Asp Gln Pro Glu Leu Ile Lys  
 100 105 110

Arg Met Ala Glu Glu Gly His Ile Ile Gly Asn His Ser Tyr His His  
 115 120 125

Pro Asp Leu Thr Thr Lys Thr Ser Arg Val Ile Gln Glu Glu Leu Glu  
 130 135 140

Ser Val Asp Glu Glu Val Tyr Lys Ile Thr Gly Glu Lys Asn Asn Leu  
 145 150 155 160

Tyr Leu Arg Pro Pro Arg Gly Ile Phe Ser Glu Arg Val Leu Glu Glu  
 165 170 175

Thr Lys Lys Leu Gly Tyr Gln Thr Val Phe Trp Ser Val Ala Phe Val  
 180 185 190

Asp Trp Lys Ile Asn Ala Gln Lys Gly Trp Arg Tyr Ala Tyr Asp Asn  
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Phe Arg Arg Ser Pro Thr  
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 taaaagaaat ttaccgtggtt ttacagggttg acggcacgct gtttctcgct gtgcatctgg 180  
 aagggcaa at gaaaaaatcg aaaaaaaciaa aaggcttttc cttataactca gaagagcaaa 240



tcaagcaact gcttgaggaa agccatttca gagacatcac ggtacatatg aacaaaaaatt	300
actgctgcat ttctgcggtta aaatcatgaa ctttgtatga tcatcccttt caatacggaa	360
gggatttttt atgtttgata gagttgaaac tggatcttaa atatcatatt tttgattttt	420
aaagaaaaagt attccattaa catagcaaac atggtttaat atcaaagtga acgttttttac	480
tatatatttcc ggaggtattt atg aac aaa agg atc gtg aaa agt tca att gtt	533
Met Asn Lys Arg Ile Val Lys Ser Ser Ile Val	
1 5 10	
ttc ttt ctc ctt gcc gca tta att ttt ggc cag ctg cct tta ccg aag	581
Phe Phe Leu Leu Ala Ala Leu Ile Phe Gly Gln Leu Pro Leu Pro Lys	
15 20 25	
aca atg gca gcg gaa gac agc gtt ccg aat aac gaa acc aca ttg acc	629
Thr Met Ala Ala Glu Asp Ser Val Pro Asn Asn Glu Thr Thr Leu Thr	
30 35 40	
agc gcg tcc cct gtt gaa gct tcg ttt caa agc gat gac gag gtg cat	677
Ser Ala Ser Pro Val Glu Ala Ser Phe Gln Ser Asp Asp Glu Val His	
45 50 55	
tgg tat aaa gtc aat cct tca aat cag gaa atc gca aac tat acg cac	725
Trp Tyr Lys Val Asn Pro Ser Asn Gln Glu Ile Ala Asn Tyr Thr His	
60 65 70 75	
ttc cgc gtc aaa ttg aaa tca gat gca gag ctg aac att tcc gtc tac	773
Phe Arg Val Lys Leu Lys Ser Asp Ala Glu Leu Asn Ile Ser Val Tyr	
80 85 90	
tcc agc ctg gaa aat gca act ggt cat caa acg ttt gac cga tac aac	821
Ser Ser Leu Glu Asn Ala Thr Gly His Gln Thr Phe Asp Arg Tyr Asn	
95 100 105	
ggc tac tcc tat gaa aat aat cct gct tta atc gat ttt ccg att gcc	869
Gly Tyr Ser Tyr Glu Asn Asn Pro Ala Leu Ile Asp Phe Pro Ile Ala	
110 115 120	
tgg aaa ggt cct tac tac ata aaa gta gaa aat cac cat gat gag gaa	917
Trp Lys Gly Pro Tyr Tyr Ile Lys Val Glu Asn His His Asp Glu Glu	
125 130 135	
aac gaa acc act tca att aca gat att tct tac acc atc agc tat gaa	965
Asn Glu Thr Thr Ser Ile Thr Asp Ile Ser Tyr Thr Ile Ser Tyr Glu	
140 145 150 155	
ggc gtc acc ctg cct ccg tca atc caa gag gca gaa gaa gag tgt ccg	1013
Gly Val Thr Leu Pro Pro Ser Ile Gln Glu Ala Glu Glu Glu Cys Pro	
160 165 170	
gca gaa tta agc gtt tcc gaa agg gaa aca ggc aag ggc ata tta aaa	1061
Ala Glu Leu Ser Val Ser Glu Arg Glu Thr Gly Lys Gly Ile Leu Lys	
175 180 185	
cag tta aga acg atc agg gat gaa gtt ctt tca aaa act gaa aaa gga	1109

Gln	Leu	Arg	Thr	Ile	Arg	Asp	Glu	Val	Leu	Ser	Lys	Thr	Glu	Lys	Gly	
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aaa	gag	ctg	tct	tcc	ctt	tac	tat	aaa	gca	gct	cca	ttc	atc	agc	gca	1157
Lys	Glu	Leu	Ser	Ser	Leu	Tyr	Tyr	Lys	Ala	Ala	Pro	Phe	Ile	Ser	Ala	
	205					210					215					
aaa	atg	ctc	ttt	aac	aaa	tcg	atg	aga	gac	agt	gtc	tac	aaa	gac	ctg	1205
Lys	Met	Leu	Phe	Asn	Lys	Ser	Met	Arg	Asp	Ser	Val	Tyr	Lys	Asp	Leu	
	220				225					230					235	
gtg	cag	ctg	aag	ccg	ctg	ttt	gca	gat	gtc	gct	aaa	aac	gga	caa	gtg	1253
Val	Gln	Leu	Lys	Pro	Leu	Phe	Ala	Asp	Val	Ala	Lys	Asn	Gly	Gln	Val	
				240					245					250		
agc	gca	tac	tcg	att	acg	aat	gat	gat	caa	aaa	gcg	atc	agt	cgc	ctg	1301
Ser	Ala	Tyr	Ser	Ile	Thr	Asn	Asp	Asp	Gln	Lys	Ala	Ile	Ser	Arg	Leu	
			255					260					265			
tac	gaa	aca	gct	cgc	gcg	tcc	gtt	ccc	gag	ccg	ttg	aaa	aaa	cag	ctg	1349
Tyr	Glu	Thr	Ala	Arg	Ala	Ser	Val	Pro	Glu	Pro	Leu	Lys	Lys	Gln	Leu	
		270					275					280				
gat	caa	gtc	gcg	aaa	gac	atc	ggc	atc	gaa	caa	tta	aca	ggc	agc	aaa	1397
Asp	Gln	Val	Ala	Lys	Asp	Ile	Gly	Ile	Glu	Gln	Leu	Thr	Gly	Ser	Lys	
	285					290					295					
gta	tcg	gct	gtg	ctt	gaa	aaa	gcg	ggg	atg	gcg	aca	gct	tca	tca	agc	1445
Val	Ser	Ala	Val	Leu	Glu	Lys	Ala	Gly	Met	Ala	Thr	Ala	Ser	Ser	Ser	
	300				305				310						315	
gcg	ccc	gaa	aac	cgt	tac	atc	gta	aaa	ttg	aaa	gaa	ggc	aaa	aaa	ccg	1493
Ala	Pro	Glu	Asn	Arg	Tyr	Ile	Val	Lys	Leu	Lys	Glu	Gly	Lys	Lys	Pro	
				320					325					330		
gga	tct	ttc	aaa	tct	aaa	gcc	caa	tca	tcc	ggc	gtc	cag	gca	tta	gag	1541
Gly	Ser	Phe	Lys	Ser	Lys	Ala	Gln	Ser	Ser	Gly	Val	Gln	Ala	Leu	Glu	
			335					340					345			
ccc	ctc	ggt	aaa	agc	aaa	acg	gca	ttt	aaa	gat	atg	tac	gtt	gtg	gaa	1589
Pro	Leu	Gly	Lys	Ser	Lys	Thr	Ala	Phe	Lys	Asp	Met	Tyr	Val	Val	Glu	
		350					355					360				
atg	aag	gaa	agc	cgt	tct	tcc	gga	ttc	aaa	gcg	gcg	gca	aag	caa	tat	1637
Met	Lys	Glu	Ser	Arg	Ser	Ser	Gly	Phe	Lys	Ala	Ala	Ala	Lys	Gln	Tyr	
	365					370					375					
cag	gcg	gca	gcc	tcc	aag	atc	gcc	aag	atg	cct	gaa	gtg	gaa	ttc	gtc	1685
Gln	Ala	Ala	Ala	Ser	Lys	Ile	Ala	Lys	Met	Pro	Glu	Val	Glu	Phe	Val	
	380				385					390					395	
gaa	cag	gtt	cag	caa	tat	gaa	gca	ctg	tca	aga	gac	acc	caa	tat	cca	1733
Glu	Gln	Val	Gln	Gln	Tyr	Glu	Ala	Leu	Ser	Arg	Asp	Thr	Gln	Tyr	Pro	
				400				405						410		
tat	caa	tgg	tcg	ctc	aaa	aat	aac	ggc	aaa	aac	cgt	gct	gcg	aat	gct	1781
Tyr	Gln	Trp	Ser	Leu	Lys	Asn	Asn	Gly	Lys	Asn	Arg	Ala	Ala	Asn	Ala	

415	420	425	
gac ata caa ttt gaa cag ctt cag aag ctg atg aaa ggc aaa aag ctg Asp Ile Gln Phe Glu Gln Leu Gln Lys Leu Met Lys Gly Lys Lys Leu 430 435 440			1829
aaa gat aca gta atc gcc gtc gtt gac aca ggc gtt gat cat acc ctt Lys Asp Thr Val Ile Ala Val Val Asp Thr Gly Val Asp His Thr Leu 445 450 455			1877
gcg gat tta agc ggc agc gtc aaa aaa gac gaa ggc tat aac tat gtc Ala Asp Leu Ser Gly Ser Val Lys Lys Asp Glu Gly Tyr Asn Tyr Val 460 465 470 475			1925
ggc cgc acg gcg gat gcg atg gat gac aat ggc cac ggc aca cac gtg Gly Arg Thr Ala Asp Ala Met Asp Asp Asn Gly His Gly Thr His Val 480 485 490			1973
tca ggc atc att gca gcc gcg caa gac aac cat ttt tcg atg gcg gga Ser Gly Ile Ile Ala Ala Ala Gln Asp Asn His Phe Ser Met Ala Gly 495 500 505			2021
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gac cac ggt gca aaa gtc atc aat tta agt ctt ggc ggc cca tac agc Asp His Gly Ala Lys Val Ile Asn Leu Ser Leu Gly Gly Pro Tyr Ser 540 545 550 555			2165
cgg gtg atg gaa tat gcg ctt aaa tat gcg gct tct aaa aat gtg acg Arg Val Met Glu Tyr Ala Leu Lys Tyr Ala Ala Ser Lys Asn Val Thr 560 565 570			2213
atc gtt gcc gcc acc gga aat gac gga gta tcg gag att tcc tac cct Ile Val Ala Ala Thr Gly Asn Asp Gly Val Ser Glu Ile Ser Tyr Pro 575 580 585			2261
gca tct tcg aaa tat acg ctt tca gtc ggg gcg acc aat aat ctc gat Ala Ser Ser Lys Tyr Thr Leu Ser Val Gly Ala Thr Asn Asn Leu Asp 590 595 600			2309
ctt gtc tcg gac tac tcc aat tat gga aaa ggt ctc gat atg gtg gcg Leu Val Ser Asp Tyr Ser Asn Tyr Gly Lys Gly Leu Asp Met Val Ala 605 610 615			2357
ccg gga acc gat att cca agc ctc gtt ccg gac ggg aat gtc act tat Pro Gly Thr Asp Ile Pro Ser Leu Val Pro Asp Gly Asn Val Thr Tyr 620 625 630 635			2405
atg agc gga aca tcg atg gcg gcg ccg cac gtg gca gct gca gca gga Met Ser Gly Thr Ser Met Ala Ala Pro His Val Ala Ala Ala Ala Gly 640 645 650			2453

ctt ctt ttg tca cag aat ccg tcc ttg aaa cca aag caa atc gca agc Leu Leu Leu Ser Gln Asn Pro Ser Leu Lys Pro Lys Gln Ile Ala Ser 655 660 665	2501
cta ttg acc gag acg aca gca gat gtg gca ttt gaa gag cag gat aat Leu Leu Thr Glu Thr Thr Ala Asp Val Ala Phe Glu Glu Gln Asp Asn 670 675 680	2549
cca aac ccg gat tat gac ctg gat ata gaa ccg gct gca caa att ccc Pro Asn Pro Asp Tyr Asp Leu Asp Ile Glu Pro Ala Ala Gln Ile Pro 685 690 695	2597
gga tat gac ttc gtc tcc ggg tgg gga agg ctg aat gtt ttt cat gca Gly Tyr Asp Phe Val Ser Gly Trp Gly Arg Leu Asn Val Phe His Ala 700 705 710 715	2645
gcc agc gtt ttt gag ctg aac atg aag gtt cat ccc gtt tta aac cgc Ala Ser Val Phe Glu Leu Asn Met Lys Val His Pro Val Leu Asn Arg 720 725 730	2693
cat acg gca gtg aca ggc aca gcc aaa agc ggt gtg acg gtc aaa atc His Thr Ala Val Thr Gly Thr Ala Lys Ser Gly Val Thr Val Lys Ile 735 740 745	2741
ttg cga ggg aag caa gta ttg ggg acg ggc acg gcc gga aaa tca ggc Leu Arg Gly Lys Gln Val Leu Gly Thr Gly Thr Ala Gly Lys Ser Gly 750 755 760	2789
gcg ttt tca gtg aaa att ccg gcc cag aag gcg ggg caa gtt ctt cat Ala Phe Ser Val Lys Ile Pro Ala Gln Lys Ala Gly Gln Val Leu His 765 770 775	2837
gtc gcg gca tcg ggc cat cag gcg gaa acc tcg ctc aga acc gtc gtg Val Ala Ala Ser Gly His Gln Ala Glu Thr Ser Leu Arg Thr Val Val 780 785 790 795	2885
gaa aaa gcg ccg aaa aac ccg tcc gtc aaa cgc atc acg aac aaa gat Glu Lys Ala Pro Lys Asn Pro Ser Val Lys Arg Ile Thr Asn Lys Asp 800 805 810	2933
act gcc gta acg ggt aga acg gca gcc ggc tac acg atc aaa gtg aaa Thr Ala Val Thr Gly Arg Thr Ala Ala Gly Tyr Thr Ile Lys Val Lys 815 820 825	2981
aac gcg tgc aaa aaa gtg atc gcg caa ggc aga gcg gat gca tcc gtg Asn Ala Cys Lys Lys Val Ile Ala Gln Gly Arg Ala Asp Ala Ser Val 830 835 840	3029
agc gtt aaa gtg aaa atc aac aag caa aaa gaa tat gcc gtt ttg tat Ser Val Lys Val Lys Ile Asn Lys Gln Lys Glu Tyr Ala Val Leu Tyr 845 850 855	3077
gtc tcc gca tct gct gat gac cac aga gaa agc ggc gat gtc aaa atg Val Ser Ala Ser Ala Asp Asp His Arg Glu Ser Gly Asp Val Lys Met 860 865 870 875	3125

acg gtc gct gac gtc atc ccg cca ggc gcc ccg aaa gtt tat cag gtt	3173
Thr Val Ala Asp Val Ile Pro Pro Gly Ala Pro Lys Val Tyr Gln Val	
880 885 890	
tcc gat aaa agt acg gtc att cag gga aaa aca gaa gca aac gcg caa	3221
Ser Asp Lys Ser Thr Val Ile Gln Gly Lys Thr Glu Ala Asn Ala Gln	
895 900 905	
gtc agc gca aaa gct aaa gga aag acg atc gct tcc ggc aaa gcg aac	3269
Val Ser Ala Lys Ala Lys Gly Lys Thr Ile Ala Ser Gly Lys Ala Asn	
910 915 920	
gga aaa ggt gaa tac aag ctg aaa atc agc agg caa aaa gcc gga acc	3317
Gly Lys Gly Glu Tyr Lys Leu Lys Ile Ser Arg Gln Lys Ala Gly Thr	
925 930 935	
gtc atc ggt gta aca gca aag gat aaa gcc gga aat gtc agc aaa gcg	3365
Val Ile Gly Val Thr Ala Lys Asp Lys Ala Gly Asn Val Ser Lys Ala	
940 945 950 955	
aca gcc gtc act gtc ctt gac aaa acc ccg ccg tct gcg ccg aag gtc	3413
Thr Ala Val Thr Val Leu Asp Lys Thr Pro Pro Ser Ala Pro Lys Val	
960 965 970	
aat ccg gtc aca aac aag agc acg gcc gtt aag ggg aaa gca gaa gcg	3461
Asn Pro Val Thr Asn Lys Ser Thr Ala Val Lys Gly Lys Ala Glu Ala	
975 980 985	
aac gcc gcc atc atc gtc aaa tca gga aag aaa acg atc gga acc ggc	3509
Asn Ala Ala Ile Ile Val Lys Ser Gly Lys Lys Thr Ile Gly Thr Gly	
990 995 1000	
aag gcc gat aaa aaa ggc gcg ttt ttt gtc aaa ata aaa aaa caa	3554
Lys Ala Asp Lys Lys Gly Ala Phe Phe Val Lys Ile Lys Lys Gln	
1005 1010 1015	
aag gca aac acc gtt tta gcg gtc act gca aaa gat aaa gcc ggc	3599
Lys Ala Asn Thr Val Leu Ala Val Thr Ala Lys Asp Lys Ala Gly	
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aat acg agc aaa gtc agc aaa ata aaa gtc aaa aag gca aaa	3641
Asn Thr Ser Lys Val Ser Lys Ile Lys Val Lys Lys Ala Lys	
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ttccgctgac ttggagggca aaatcaatgg aatcggaaag caaatatcag aagattatcg	3941
aggcttcgct cgtcctttcg cggaacagagg ctttgacgcc gcaaccattc ccatgatcgc	4001
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Asp Ser Val Pro Asn Asn Glu Thr Thr Leu Thr Ser Ala Ser Pro Val  
 35 40 45

Glu Ala Ser Phe Gln Ser Asp Asp Glu Val His Trp Tyr Lys Val Asn  
 50 55 60

Pro Ser Asn Gln Glu Ile Ala Asn Tyr Thr His Phe Arg Val Lys Leu  
 65 70 75 80

Lys Ser Asp Ala Glu Leu Asn Ile Ser Val Tyr Ser Ser Leu Glu Asn  
 85 90 95

Ala Thr Gly His Gln Thr Phe Asp Arg Tyr Asn Gly Tyr Ser Tyr Glu  
 100 105 110

Asn Asn Pro Ala Leu Ile Asp Phe Pro Ile Ala Trp Lys Gly Pro Tyr  
 115 120 125

Tyr Ile Lys Val Glu Asn His His Asp Glu Glu Asn Glu Thr Thr Ser  
 130 135 140

Ile Thr Asp Ile Ser Tyr Thr Ile Ser Tyr Glu Gly Val Thr Leu Pro  
 145 150 155 160

Pro Ser Ile Gln Glu Ala Glu Glu Glu Cys Pro Ala Glu Leu Ser Val  
 165 170 175

Ser Glu Arg Glu Thr Gly Lys Gly Ile Leu Lys Gln Leu Arg Thr Ile  
 180 185 190

Arg Asp Glu Val Leu Ser Lys Thr Glu Lys Gly Lys Glu Leu Ser Ser  
 195 200 205

Leu Tyr Tyr Lys Ala Ala Pro Phe Ile Ser Ala Lys Met Leu Phe Asn  
 210 215 220

Lys Ser Met Arg Asp Ser Val Tyr Lys Asp Leu Val Gln Leu Lys Pro  
 225 230 235 240

Leu Phe Ala Asp Val Ala Lys Asn Gly Gln Val Ser Ala Tyr Ser Ile  
 245 250 255

Thr Asn Asp Asp Gln Lys Ala Ile Ser Arg Leu Tyr Glu Thr Ala Arg  
 260 265 270

Ala Ser Val Pro Glu Pro Leu Lys Lys Gln Leu Asp Gln Val Ala Lys  
 275 280 285

Asp Ile Gly Ile Glu Gln Leu Thr Gly Ser Lys Val Ser Ala Val Leu  
 290 295 300

Glu Lys Ala Gly Met Ala Thr Ala Ser Ser Ser Ala Pro Glu Asn Arg  
 305 310 315 320

Tyr Ile Val Lys Leu Lys Glu Gly Lys Lys Pro Gly Ser Phe Lys Ser  
 325 330 335

Lys Ala Gln Ser Ser Gly Val Gln Ala Leu Glu Pro Leu Gly Lys Ser  
 340 345 350

Lys Thr Ala Phe Lys Asp Met Tyr Val Val Glu Met Lys Glu Ser Arg  
 355 360 365

Ser Ser Gly Phe Lys Ala Ala Ala Lys Gln Tyr Gln Ala Ala Ala Ser  
 370 375 380

Lys Ile Ala Lys Met Pro Glu Val Glu Phe Val Glu Gln Val Gln Gln  
 385 390 395 400

Tyr Glu Ala Leu Ser Arg Asp Thr Gln Tyr Pro Tyr Gln Trp Ser Leu  
 405 410 415

Lys Asn Asn Gly Lys Asn Arg Ala Ala Asn Ala Asp Ile Gln Phe Glu

420

425

430

Gln Leu Gln Lys Leu Met Lys Gly Lys Lys Leu Lys Asp Thr Val Ile  
 435 440 445

Ala Val Val Asp Thr Gly Val Asp His Thr Leu Ala Asp Leu Ser Gly  
 450 455 460

Ser Val Lys Lys Asp Glu Gly Tyr Asn Tyr Val Gly Arg Thr Ala Asp  
 465 470 475 480

Ala Met Asp Asp Asn Gly His Gly Thr His Val Ser Gly Ile Ile Ala  
 485 490 495

Ala Ala Gln Asp Asn His Phe Ser Met Ala Gly Ile Asn Ala Tyr Ala  
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Lys Ile Leu Pro Val Lys Val Leu Asp Ser Ser Gly Ser Gly Asp Thr  
 515 520 525

Glu Gln Ile Ala Asn Gly Ile Ile Tyr Ala Ala Asp His Gly Ala Lys  
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Val Ile Asn Leu Ser Leu Gly Gly Pro Tyr Ser Arg Val Met Glu Tyr  
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Ala Leu Lys Tyr Ala Ala Ser Lys Asn Val Thr Ile Val Ala Ala Thr  
 565 570 575

Gly Asn Asp Gly Val Ser Glu Ile Ser Tyr Pro Ala Ser Ser Lys Tyr  
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Thr Leu Ser Val Gly Ala Thr Asn Asn Leu Asp Leu Val Ser Asp Tyr  
 595 600 605

Ser Asn Tyr Gly Lys Gly Leu Asp Met Val Ala Pro Gly Thr Asp Ile  
 610 615 620

Pro Ser Leu Val Pro Asp Gly Asn Val Thr Tyr Met Ser Gly Thr Ser  
 625 630 635 640

Met Ala Ala Pro His Val Ala Ala Ala Ala Gly Leu Leu Leu Ser Gln  
 645 650 655



Asn Pro Ser Leu Lys Pro Lys Gln Ile Ala Ser Leu Leu Thr Glu Thr  
660 665 670

Thr Ala Asp Val Ala Phe Glu Glu Gln Asp Asn Pro Asn Pro Asp Tyr  
675 680 685

Asp Leu Asp Ile Glu Pro Ala Ala Gln Ile Pro Gly Tyr Asp Phe Val  
690 695 700

Ser Gly Trp Gly Arg Leu Asn Val Phe His Ala Ala Ser Val Phe Glu  
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Leu Asn Met Lys Val His Pro Val Leu Asn Arg His Thr Ala Val Thr  
725 730 735

Gly Thr Ala Lys Ser Gly Val Thr Val Lys Ile Leu Arg Gly Lys Gln  
740 745 750

Val Leu Gly Thr Gly Thr Ala Gly Lys Ser Gly Ala Phe Ser Val Lys  
755 760 765

Ile Pro Ala Gln Lys Ala Gly Gln Val Leu His Val Ala Ala Ser Gly  
770 775 780

His Gln Ala Glu Thr Ser Leu Arg Thr Val Val Glu Lys Ala Pro Lys  
785 790 795 800

Asn Pro Ser Val Lys Arg Ile Thr Asn Lys Asp Thr Ala Val Thr Gly  
805 810 815

Arg Thr Ala Ala Gly Tyr Thr Ile Lys Val Lys Asn Ala Cys Lys Lys  
820 825 830

Val Ile Ala Gln Gly Arg Ala Asp Ala Ser Val Ser Val Lys Val Lys  
835 840 845

Ile Asn Lys Gln Lys Glu Tyr Ala Val Leu Tyr Val Ser Ala Ser Ala  
850 855 860

Asp Asp His Arg Glu Ser Gly Asp Val Lys Met Thr Val Ala Asp Val  
865 870 875 880

Ile Pro Pro Gly Ala Pro Lys Val Tyr Gln Val Ser Asp Lys Ser Thr  
885 890 895

Val Ile Gln Gly Lys Thr Glu Ala Asn Ala Gln Val Ser Ala Lys Ala  
900 905 910

Lys Gly Lys Thr Ile Ala Ser Gly Lys Ala Asn Gly Lys Gly Glu Tyr  
915 920 925

Lys Leu Lys Ile Ser Arg Gln Lys Ala Gly Thr Val Ile Gly Val Thr  
930 935 940

Ala Lys Asp Lys Ala Gly Asn Val Ser Lys Ala Thr Ala Val Thr Val  
945 950 955 960

Leu Asp Lys Thr Pro Pro Ser Ala Pro Lys Val Asn Pro Val Thr Asn  
965 970 975

Lys Ser Thr Ala Val Lys Gly Lys Ala Glu Ala Asn Ala Ala Ile Ile  
980 985 990

Val Lys Ser Gly Lys Lys Thr Ile Gly Thr Gly Lys Ala Asp Lys Lys  
995 1000 1005

Gly Ala Phe Phe Val Lys Ile Lys Lys Gln Lys Ala Asn Thr Val  
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Leu Ala Val Thr Ala Lys Asp Lys Ala Gly Asn Thr Ser Lys Val  
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Ser Lys Ile Lys Val Lys Lys Ala Lys  
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39

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43

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32

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<400> 205

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caagatggcc ggcaatcata atcttcggtc cgtcagcctg tccagtcttt tttgcgatta	180
agcttcccag tctgtctgtc gtaacctcgt cggcaaacgg ttctatgtac gatttcatga	240
cttgtctggg ttctntntca ttgcgcggaa ttccttttgc atcagttaat tccttagcat	300
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ctattataca gaaacatccc ttttcaatac gaccaatata gtttacagct tttttggtta	420
aaaaatgaaa ccttgcggga actgggttcgt atatattggg atataactcaa aattactttc	480
aagggagggt ctgttttaac atg att gtc atc ata ttg aga ctg gct ttg ctg	533
Met Ile Val Ile Ile Leu Arg Leu Ala Leu Leu	
1 5 10	
gcg ctt ttg gtc tac gtc gtg tac agg gcc gtt caa ttt ttg ggg agc	581
Ala Leu Leu Val Tyr Val Val Tyr Arg Ala Val Gln Phe Leu Gly Ser	
15 20 25	
ccg gac aga agg ctg aaa tca gca cag gca aaa aag cac ttt tat gtt	629
Pro Asp Arg Arg Leu Lys Ser Ala Gln Ala Lys Lys His Phe Tyr Val	
30 35 40	
ttg gac gaa caa aag aat aca cgc aaa aat ctc aag ctg aca ttt aaa	677
Leu Asp Glu Gln Lys Asn Thr Arg Lys Asn Leu Lys Leu Thr Phe Lys	
45 50 55	
ggc gtg ctt ttc gaa gga gaa aaa cac att cct tca aaa gac cat ccg	725
Gly Val Leu Phe Glu Gly Glu Lys His Ile Pro Ser Lys Asp His Pro	
60 65 70 75	
ctg ttc atc cat acg att ttt gta tgg acg gaa gcg cct gaa gaa aag	773
Leu Phe Ile His Thr Ile Phe Val Trp Thr Glu Ala Pro Glu Glu Lys	
80 85 90	
ctc agc tct ttt acg gaa gaa gac ttc gcg gaa ctt gaa gaa aat att	821
Leu Ser Ser Phe Thr Glu Glu Asp Phe Ala Glu Leu Glu Glu Asn Ile	
95 100 105	
aaa gag cac tat ccc gat tgc aaa atc gac tgg gat tcg aac atc caa	869
Lys Glu His Tyr Pro Asp Cys Lys Ile Asp Trp Asp Ser Asn Ile Gln	
110 115 120	
aag tgg aaa aac aaa aaa gca gaa gag caa taaagcctcg tctgcttttt	919
Lys Trp Lys Asn Lys Lys Ala Glu Glu Gln	
125 130	
taattcatca tataaaagcc ggtcaaaaca gcttgacgcg cgagcaaaaa aggaatgccg	979
agcctgaagg aaaggtgttt tgtcttatgt ctgaaccgca tcatcccgaa ccagacgcct	1039
gcggagccaa aagcagccgc aacgagccag atgcggcgct cagacaccct ccatttgcct	1099

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<212> PRT  
<213> Bacillus licheniformis

<400> 206

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Lys Ser Ala Gln Ala Lys Lys His Phe Tyr Val Leu Asp Glu Gln Lys  
35 40 45

Asn Thr Arg Lys Asn Leu Lys Leu Thr Phe Lys Gly Val Leu Phe Glu  
50 55 60

Gly Glu Lys His Ile Pro Ser Lys Asp His Pro Leu Phe Ile His Thr  
65 70 75 80

Ile Phe Val Trp Thr Glu Ala Pro Glu Glu Lys Leu Ser Ser Phe Thr  
85 90 95

Glu Glu Asp Phe Ala Glu Leu Glu Glu Asn Ile Lys Glu His Tyr Pro  
100 105 110

Asp Cys Lys Ile Asp Trp Asp Ser Asn Ile Gln Lys Trp Lys Asn Lys  
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Lys Ala Glu Glu Gln  
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<212> DNA

<213> *Bacillus licheniformis*

<220>

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<222> (501)..(1682)

<400> 207

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aaacagccag gcaggaagcc ggcttaaaac aagttgacag cgtggagacg tttgtcggta      180
aagaaaagca gtacattggt acaggggacg acaaaaaagg cgacaaaatg tatgtttggg      240
tgcttgcgtga caaaaagcag aaaacgcttt acaaaaaagc atcagccggc attaccggcc      300
gccaggctgc aaaagctggt caggatgagg gcctgatgtc tgagcttaaa gaggtgcacc      360
ttgcaaggga aggcaatggt ctattgtggg aagttacata cttaaataaa gatgggcagt      420
acagtttaag ctatgtggac tttataaacg gaaaaattca caaaaatatt acgccttaga      480
cgaaacaggg ggaaatcgag ttg aat cta gct aaa aga gta tca gcg tta aca      533
                        Leu Asn Leu Ala Lys Arg Val Ser Ala Leu Thr
                        1             5             10

cca tct gca aca ttg gca atc act gca aaa gca aaa gaa tta aaa gcg      581
Pro Ser Ala Thr Leu Ala Ile Thr Ala Lys Ala Lys Glu Leu Lys Ala
                        15             20             25

gca ggg cac gac gtc atc ggt ctt ggg gca ggt gag ccg gat ttt aat      629
Ala Gly His Asp Val Ile Gly Leu Gly Ala Gly Glu Pro Asp Phe Asn
                        30             35             40

acg cct gag cac atc att gaa gcg gct gtc cgt tcg atg aac gaa gga      677
Thr Pro Glu His Ile Ile Glu Ala Ala Val Arg Ser Met Asn Glu Gly
                        45             50             55

cat acc aaa tac acg cct tcc ggc ggt ctt gcg gcg ctg aaa gac agc      725
His Thr Lys Tyr Thr Pro Ser Gly Gly Leu Ala Ala Leu Lys Asp Ser
60             65             70             75

atc cgc gat aaa ttc aag cgc gat cag gga att gaa tac agc caa tcg      773
Ile Arg Asp Lys Phe Lys Arg Asp Gln Gly Ile Glu Tyr Ser Gln Ser
                        80             85             90

gaa gtt att gtg tgc aca ggt gca aag cat gct ctt tac acc cta ttt      821
Glu Val Ile Val Cys Thr Gly Ala Lys His Ala Leu Tyr Thr Leu Phe
                        95             100            105

caa gtg ctc ctc gac gaa ggg gac gaa gtg att att ccg act ccg tac      869
Gln Val Leu Leu Asp Glu Gly Asp Glu Val Ile Ile Pro Thr Pro Tyr
110            115            120
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tgg gtc agc tat cct gaa caa gtc aag ctt gca ggc ggc aaa cct gtg	917
Trp Val Ser Tyr Pro Glu Gln Val Lys Leu Ala Gly Gly Lys Pro Val	
125 130 135	
ttt gtg gaa ggc ctt gag gaa aac agc ttc aag att tct ccg gag cag	965
Phe Val Glu Gly Leu Glu Glu Asn Ser Phe Lys Ile Ser Pro Glu Gln	
140 145 150 155	
ctc gaa aaa gcc gtc aca gaa aaa acg aag gct gtg atc atc aat tcc	1013
Leu Glu Lys Ala Val Thr Glu Lys Thr Lys Ala Val Ile Ile Asn Ser	
160 165 170	
cca agc aat ccg aca ggg atg atg tat acg gaa gaa gag ctc aaa gct	1061
Pro Ser Asn Pro Thr Gly Met Met Tyr Thr Glu Glu Glu Leu Lys Ala	
175 180 185	
ctc ggt gaa gta tgc ctt cga cgc aac gtt tta atc gta tct gat gaa	1109
Leu Gly Glu Val Cys Leu Arg Arg Asn Val Leu Ile Val Ser Asp Glu	
190 195 200	
ata tat gaa aag ctg att tac ggc gga aaa aaa cat gta tcc att gca	1157
Ile Tyr Glu Lys Leu Ile Tyr Gly Gly Lys Lys His Val Ser Ile Ala	
205 210 215	
cag ctt tct cca gaa ctt aaa aac caa acc gtg atc atc aac ggg gtt	1205
Gln Leu Ser Pro Glu Leu Lys Asn Gln Thr Val Ile Ile Asn Gly Val	
220 225 230 235	
tcc aag tca cac agc atg acc ggc tgg aga atc ggt tat gca gca ggc	1253
Ser Lys Ser His Ser Met Thr Gly Trp Arg Ile Gly Tyr Ala Ala Gly	
240 245 250	
agc gaa ccg atc att aaa gcg atg acg aac cta gcc agc cac agc acg	1301
Ser Glu Pro Ile Ile Lys Ala Met Thr Asn Leu Ala Ser His Ser Thr	
255 260 265	
tca aat ccg aca tct gtc gct caa tat gga gcc att gcc gct tac aat	1349
Ser Asn Pro Thr Ser Val Ala Gln Tyr Gly Ala Ile Ala Ala Tyr Asn	
270 275 280	
ggg cca aac gag cct gtt gag gag atg aga aaa gct ttt gaa gaa cgg	1397
Gly Pro Asn Glu Pro Val Glu Glu Met Arg Lys Ala Phe Glu Glu Arg	
285 290 295	
ctg aac aag gtg tat gaa ctg ctt gtt gac att ccg gga tta aca tgc	1445
Leu Asn Lys Val Tyr Glu Leu Leu Val Asp Ile Pro Gly Leu Thr Cys	
300 305 310 315	
ctg aag cct gaa gga gcc ttc tac ttg ttc ccg aat gca aaa aaa gcg	1493
Leu Lys Pro Glu Gly Ala Phe Tyr Leu Phe Pro Asn Ala Lys Lys Ala	
320 325 330	
gca gaa tcg tgc ggc ttt tca agc gtt gat gaa ttc gcc gaa gcg ctt	1541
Ala Glu Ser Cys Gly Phe Ser Ser Val Asp Glu Phe Ala Glu Ala Leu	
335 340 345	
ttg gaa gaa gaa aag gtt gcg atc gtt cct ggt tca ggg ttc ggc gca	1589

Leu Glu Glu Glu Lys Val Ala Ile Val Pro Gly Ser Gly Phe Gly Ala  
 350 355 360  
 ccg gac aac atc cgt ctg tgc tat gcg aca tcc ctg tca ctt ttg gaa 1637  
 Pro Asp Asn Ile Arg Leu Ser Tyr Ala Thr Ser Leu Ser Leu Leu Glu  
 365 370 375  
 gaa gcg gtt gaa cgc atc cgc cgc ttt gtc gtg aat cgc agc cgc 1682  
 Glu Ala Val Glu Arg Ile Arg Arg Phe Val Val Asn Arg Ser Arg  
 380 385 390  
 tagaaattaa aaagcgtccg caggcggacg cttttttcat gcacacaacc tgcattgacc 1742  
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 35 40 45

Ile Glu Ala Ala Val Arg Ser Met Asn Glu Gly His Thr Lys Tyr Thr  
 50 55 60

Pro Ser Gly Gly Leu Ala Ala Leu Lys Asp Ser Ile Arg Asp Lys Phe  
 65 70 75 80



Lys Arg Asp Gln Gly Ile Glu Tyr Ser Gln Ser Glu Val Ile Val Cys  
85 90 95

Thr Gly Ala Lys His Ala Leu Tyr Thr Leu Phe Gln Val Leu Leu Asp  
100 105 110

Glu Gly Asp Glu Val Ile Ile Pro Thr Pro Tyr Trp Val Ser Tyr Pro  
115 120 125

Glu Gln Val Lys Leu Ala Gly Gly Lys Pro Val Phe Val Glu Gly Leu  
130 135 140

Glu Glu Asn Ser Phe Lys Ile Ser Pro Glu Gln Leu Glu Lys Ala Val  
145 150 155 160

Thr Glu Lys Thr Lys Ala Val Ile Ile Asn Ser Pro Ser Asn Pro Thr  
165 170 175

Gly Met Met Tyr Thr Glu Glu Glu Leu Lys Ala Leu Gly Glu Val Cys  
180 185 190

Leu Arg Arg Asn Val Leu Ile Val Ser Asp Glu Ile Tyr Glu Lys Leu  
195 200 205

Ile Tyr Gly Gly Lys Lys His Val Ser Ile Ala Gln Leu Ser Pro Glu  
210 215 220

Leu Lys Asn Gln Thr Val Ile Ile Asn Gly Val Ser Lys Ser His Ser  
225 230 235 240

Met Thr Gly Trp Arg Ile Gly Tyr Ala Ala Gly Ser Glu Pro Ile Ile  
245 250 255

Lys Ala Met Thr Asn Leu Ala Ser His Ser Thr Ser Asn Pro Thr Ser  
260 265 270

Val Ala Gln Tyr Gly Ala Ile Ala Ala Tyr Asn Gly Pro Asn Glu Pro  
275 280 285

Val Glu Glu Met Arg Lys Ala Phe Glu Glu Arg Leu Asn Lys Val Tyr  
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Glu Leu Leu Val Asp Ile Pro Gly Leu Thr Cys Leu Lys Pro Glu Gly

305

310

315

320

Ala Phe Tyr Leu Phe Pro Asn Ala Lys Lys Ala Ala Glu Ser Cys Gly  
 325 330 335

Phe Ser Ser Val Asp Glu Phe Ala Glu Ala Leu Leu Glu Glu Glu Lys  
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Val Ala Ile Val Pro Gly Ser Gly Phe Gly Ala Pro Asp Asn Ile Arg  
 355 360 365

Leu Ser Tyr Ala Thr Ser Leu Ser Leu Leu Glu Glu Ala Val Glu Arg  
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Ile Arg Arg Phe Val Val Asn Arg Ser Arg  
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&lt;210&gt; 209

&lt;211&gt; 1663

&lt;212&gt; DNA

&lt;213&gt; Bacillus licheniformis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (501)..(1163)

&lt;400&gt; 209

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tccggacatg tcaaatacaga tgacgggggtt ttggaccata acattgtcat gccaaatgaa 120

aaaaaagaag gcgaatcagg gacaaatcct gaacagctct ttgcggcgagg atacgcggcg 180

tgcttcggcg gcgcattgga acatgtcgca aaacaaaaag gcattgacat cgattctgag 240

gtcgaaggcc atgtgagctt gctgaaggat gagagtgcg gcggttttta aatcggcgctc 300

aagctgatcg tcacagcagg cggggtagaa aaagaaaaag cgaaagagct ggtcgaagcc 360

gctcatgact tttgccctta ttcaaaagcg acgagaggaa atatcgacgt caatcttgaa 420

gtaaaataaaa taaacgggaa agatgaaaac gagaaagcaa acaaagcttg tttgctttct 480

tttttagaaa ggagcagcat atg gca tat ctt aaa aaa gcg ctt gtg ttc tcc 533

Met Ala Tyr Leu Lys Lys Ala Leu Val Phe Ser  
 1 5 10

gtg ctt tct ctc gct att gtc ctt gca gga tgc gga acc gga gcg gcg 581

Val Leu Ser Leu Ala Ile Val Leu Ala Gly Cys Gly Thr Gly Ala Ala  
 15 20 25

gag aag aac aac ggc aat caa tcc ccg gct gat acg gcc aag cag aaa	629
Glu Lys Asn Asn Gly Asn Gln Ser Pro Ala Asp Thr Ala Lys Gln Lys	
30 35 40	
gca cct gat ttg aaa aca tat tcc ctt gac aaa aat atc cgg tct gaa	677
Ala Pro Asp Leu Lys Thr Tyr Ser Leu Asp Lys Asn Ile Arg Ser Glu	
45 50 55	
gaa gat ttt gat ttg ata ggc aag tat gtt cat gct gaa gat gac caa	725
Glu Asp Phe Asp Leu Ile Gly Lys Tyr Val His Ala Glu Asp Asp Gln	
60 65 70 75	
atc acg ctc gaa ata aag gat aag gaa ctg att gtt ccg aaa agc agc	773
Ile Thr Leu Glu Ile Lys Asp Lys Glu Leu Ile Val Pro Lys Ser Ser	
80 85 90	
cgc ttt cac agc gaa gaa gac cat gat gac tta atc ggg aag ctt gtg	821
Arg Phe His Ser Glu Glu Asp His Asp Asp Leu Ile Gly Lys Leu Val	
95 100 105	
aag gta gag gtg gat gga aaa acg caa gaa gcg gaa gaa gcc gag ctt	869
Lys Val Glu Val Asp Gly Lys Thr Gln Glu Ala Glu Glu Ala Glu Leu	
110 115 120	
atg ccg cag tca aaa gcc gac caa aat ggc gta tat gag gag gag aaa	917
Met Pro Gln Ser Lys Ala Asp Gln Asn Gly Val Tyr Glu Glu Glu Lys	
125 130 135	
gac ggc agc cga aaa atc atc gcc acg ttt gtc agc gag tcg gag caa	965
Asp Gly Ser Arg Lys Ile Ile Ala Thr Phe Val Ser Glu Ser Glu Gln	
140 145 150 155	
aac att aca atc aaa aca aaa gca ggg gaa aaa act tat cag aaa aca	1013
Asn Ile Thr Ile Lys Thr Lys Ala Gly Glu Lys Thr Tyr Gln Lys Thr	
160 165 170	
gcc gat ttt gag agg gat gtc gcc gaa gca cct gaa aaa ctg aaa ggg	1061
Ala Asp Phe Glu Arg Asp Val Ala Glu Ala Pro Glu Lys Leu Lys Gly	
175 180 185	
aaa att gtc agg ctt gaa att gaa aag gat gga aaa gca gaa agc ctt	1109
Lys Ile Val Arg Leu Glu Ile Glu Lys Asp Gly Lys Ala Glu Ser Leu	
190 195 200	
gat ttg gaa tcg gaa gat caa aag ctt gaa tgg tat gag ccg tct gct	1157
Asp Leu Glu Ser Glu Asp Gln Lys Leu Glu Trp Tyr Glu Pro Ser Ala	
205 210 215	
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Ser Lys	
220	
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<211> 221

<212> PRT

<213> *Bacillus licheniformis*

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 35 40 45

Thr Tyr Ser Leu Asp Lys Asn Ile Arg Ser Glu Glu Asp Phe Asp Leu  
 50 55 60

Ile Gly Lys Tyr Val His Ala Glu Asp Asp Gln Ile Thr Leu Glu Ile  
 65 70 75 80

Lys Asp Lys Glu Leu Ile Val Pro Lys Ser Ser Arg Phe His Ser Glu  
 85 90 95

Glu Asp His Asp Asp Leu Ile Gly Lys Leu Val Lys Val Glu Val Asp  
 100 105 110

Gly Lys Thr Gln Glu Ala Glu Glu Ala Glu Leu Met Pro Gln Ser Lys  
 115 120 125

Ala Asp Gln Asn Gly Val Tyr Glu Glu Glu Lys Asp Gly Ser Arg Lys  
 130 135 140

Ile Ile Ala Thr Phe Val Ser Glu Ser Glu Gln Asn Ile Thr Ile Lys

145 150 155 160

Thr Lys Ala Gly Glu Lys Thr Tyr Gln Lys Thr Ala Asp Phe Glu Arg  
165 170 175

Asp Val Ala Glu Ala Pro Glu Lys Leu Lys Gly Lys Ile Val Arg Leu  
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Glu Ile Glu Lys Asp Gly Lys Ala Glu Ser Leu Asp Leu Glu Ser Glu  
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gtggaagcgc atgctgaaca tcccgaata tgtcttctcc gttctgaaag aggaaagagt 420  
tcaaaaacag cggcactact atccggagca gatcaaagag caatctaaaa tcgatttgta 480  
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Met Asn Ile Arg Ser Leu Leu Val Met Val Tyr  
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tcg gcc ggt ctc gct ttg acc ggt ttt att ttc aga ttg gta aaa gcg 581  
Ser Ala Gly Leu Ala Leu Thr Gly Phe Ile Phe Arg Leu Val Lys Ala  
15 20 25  
cgc gac aga gct gta ttg ctt gtt tcc ttt ccg gat aat gcg cgc gcg 629  
Arg Asp Arg Ala Val Leu Leu Val Ser Phe Pro Asp Asn Ala Arg Ala  
30 35 40

ctg ctt gat gag tat gtc agc agc agc cgg ccg ttt gaa atg gaa gtc Leu Leu Asp Glu Tyr Val Ser Ser Ser Arg Pro Phe Glu Met Glu Val 45 50 55	677
ctc tat aca agg cac gcc gtt tcc ctt gca gat gaa tat cct tcc gtt Leu Tyr Thr Arg His Ala Val Ser Leu Ala Asp Glu Tyr Pro Ser Val 60 65 70 75	725
cga tcg caa gtg atc aac gag aaa aat ccg att cat ctc ata aaa gcc Arg Ser Gln Val Ile Asn Glu Lys Asn Pro Ile His Leu Ile Lys Ala 80 85 90	773
gta tac cga atg ttc agg tgt aaa ttc gtg ttg acg gat aat tat ttt Val Tyr Arg Met Phe Arg Cys Lys Phe Val Leu Thr Asp Asn Tyr Phe 95 100 105	821
ctg ctg aca agt gtt ttg aat aaa cgc cct cag acg aca tgc att caa Leu Leu Thr Ser Val Leu Asn Lys Arg Pro Gln Thr Thr Cys Ile Gln 110 115 120	869
att tgg cat gcg tcc ggc gct ttg aag aag ttc gga ctc gaa gat atc Ile Trp His Ala Ser Gly Ala Leu Lys Lys Phe Gly Leu Glu Asp Ile 125 130 135	917
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att ttc aag ccg tca ttc ggc ttg gga gat gac cgt ttt ttg ccg acg Ile Phe Lys Arg Ser Phe Gly Leu Gly Asp Asp Arg Phe Leu Arg Thr 175 180 185	1061
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ggg gaa ctg cag gga gaa ttt ttg ctg ctg gtc aaa ctg cat ccg gcc Gly Glu Leu Gln Gly Glu Phe Leu Leu Val Lys Leu His Pro Ala 240 245 250	1253
gtg cgg gaa cag att gct ttt gaa gag cac gaa ggg ctg atc aaa gac Val Arg Glu Gln Ile Ala Phe Glu Glu His Glu Gly Leu Ile Lys Asp 255 260 265	1301

gta tca gac gtt ccg tta aag gat ttg ctg atg gaa agc gac atc ctg 1349  
Val Ser Asp Val Pro Leu Lys Asp Leu Leu Met Glu Ser Asp Ile Leu  
270 275 280

att tcc gac tac tcg tcg gtc gcc ttt gag tac gct ttg tta aat aaa 1397  
Ile Ser Asp Tyr Ser Ser Val Ala Phe Glu Tyr Ala Leu Leu Asn Lys  
285 290 295

ccg att ttg ttt ttc acg tat gat atg gca gag tat aat gaa aaa cgc 1445  
Pro Ile Leu Phe Phe Thr Tyr Asp Met Ala Glu Tyr Asn Glu Lys Arg  
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gga ctg atc gat gat ttt gaa gca gtc att ccc ggc aaa gcc tgc atg 1493  
Gly Leu Ile Asp Asp Phe Glu Ala Val Ile Pro Gly Lys Ala Cys Met  
320 325 330

gac agc gaa atg ctg ctg aaa gaa atc aaa gaa atg tcc gat aca aag 1541  
Asp Ser Glu Met Leu Leu Lys Glu Ile Lys Glu Met Ser Asp Thr Lys  
335 340 345

gaa gag atc aag aag ttt gcg gaa gag tgg cat caa tat tca aca ggt 1589  
Glu Glu Ile Lys Lys Phe Ala Glu Glu Trp His Gln Tyr Ser Thr Gly  
350 355 360

gat gcc agc atg cgc ctg ttg aac ttt atg agc gag cat atg acg gca 1637  
Asp Ala Ser Met Arg Leu Leu Asn Phe Met Ser Glu His Met Thr Ala  
365 370 375

aat gaa aaa aga ccg gcc ggt tcc taatggaaca tggccggtct ttttatgatg 1691  
Asn Glu Lys Arg Pro Ala Gly Ser  
380 385

attaccgata aaccggcaca tcatagtaca gcgtatattg atcgagcaat gtatacagac 1751

tgtacattct cccacactgc ttacaagccc atccgacatc tgtcgcatat tggatgaagg 1811

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atttttcacc gatgaatttg gctccgcca taatggcggc ctcaggtgtg aaccaccctt 1931

gttcataggc gtatttttgcg ccgtagtaaa gcgggttgct gtcgtaagcc ccgacgccgt 1991

acatattgta aacctttttg ccggtgaaca tcgttccttt agccaactcg gaagttccgt 2051

tgcccgctctc aaggagcggag tgtgaaatga ggtacagttc attgatgctg tatgctctcg 2111

ccgcgtcgat gaacgcttgc cctttgcctg tcaaaacccc tttattataa 2161

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<212> PRT

<213> Bacillus licheniformis

<400> 212

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Leu Leu Val Ser Phe Pro Asp Asn Ala Arg Ala Leu Leu Asp Glu Tyr  
 35 40 45

Val Ser Ser Ser Arg Pro Phe Glu Met Glu Val Leu Tyr Thr Arg His  
 50 55 60

Ala Val Ser Leu Ala Asp Glu Tyr Pro Ser Val Arg Ser Gln Val Ile  
 65 70 75 80

Asn Glu Lys Asn Pro Ile His Leu Ile Lys Ala Val Tyr Arg Met Phe  
 85 90 95

Arg Cys Lys Phe Val Leu Thr Asp Asn Tyr Phe Leu Leu Thr Ser Val  
 100 105 110

Leu Asn Lys Arg Pro Gln Thr Thr Cys Ile Gln Ile Trp His Ala Ser  
 115 120 125

Gly Ala Leu Lys Lys Phe Gly Leu Glu Asp Ile Gly Asn Arg Tyr Arg  
 130 135 140

Ser Ala Gly Asp Ile Lys Arg Phe Lys Lys Val Tyr Arg Ser Phe Asp  
 145 150 155 160

His Ile Val Val Gly Ser Glu Lys Met Ala Asp Ile Phe Lys Arg Ser  
 165 170 175

Phe Gly Leu Gly Asp Asp Arg Phe Leu Arg Thr Gly Val Pro Leu Thr  
 180 185 190

Asp Glu Tyr Phe His Ala Gly Arg Gln Thr Ala Glu Arg Pro Asp Gln  
 195 200 205

Lys Val Ile Leu Tyr Ala Pro Thr Tyr Arg Asp Tyr Cys Leu Thr Ser  
 210 215 220

Val Arg Leu Pro Phe Ser Lys Glu Gln Leu Ser Gly Glu Leu Gln Gly  
 225 230 235 240



Glu Phe Leu Leu Leu Val Lys Leu His Pro Ala Val Arg Glu Gln Ile  
245 250 255

Ala Phe Glu Glu His Glu Gly Leu Ile Lys Asp Val Ser Asp Val Pro  
260 265 270

Leu Lys Asp Leu Leu Met Glu Ser Asp Ile Leu Ile Ser Asp Tyr Ser  
275 280 285

Ser Val Ala Phe Glu Tyr Ala Leu Leu Asn Lys Pro Ile Leu Phe Phe  
290 295 300

Thr Tyr Asp Met Ala Glu Tyr Asn Glu Lys Arg Gly Leu Ile Asp Asp  
305 310 315 320

Phe Glu Ala Val Ile Pro Gly Lys Ala Cys Met Asp Ser Glu Met Leu  
325 330 335

Leu Lys Glu Ile Lys Glu Met Ser Asp Thr Lys Glu Glu Ile Lys Lys  
340 345 350

Phe Ala Glu Glu Trp His Gln Tyr Ser Thr Gly Asp Ala Ser Met Arg  
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370 375 380

Ala Gly Ser  
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<213> Bacillus licheniformis

<220>  
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<222> (501)..(2606)

<400> 213  
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agctgctgct gataaaagaa aagctttttt cataaacagt aatcctccta aatgttgtag	180
tagttgttgt ttcgtacact agaatacataa catggctttt ttgaaataat agatccatat	240
attccctttg acaaggtatt attgttaatt ttgacataaa aaaagaaaaa ccctttgctg	300
ccaatatgca accagatcgt tcttttacac gtcttgatcat aaacgtggta aaattttaaat	360
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aacaaccatt acaaaagtgt tacaatatat ctcagttaat taatgtaaaa ttgaatattg	480
tgagaggaga gagagtttca gtg aca gaa tct caa cat gat ccg gct gaa atc	533
Val Thr Glu Ser Gln His Asp Pro Ala Glu Ile	
1 5 10	
aaa aag agc agg cgt tgc cgt tta tgg cgg atc aac ctg tac ttc ttt	581
Lys Lys Ser Arg Arg Ser Arg Leu Trp Arg Ile Asn Leu Tyr Phe Phe	
15 20 25	
gcg gtg ttc act ttg ttc gct gcg ctg att gtc aag ctg ggc ctc gtg	629
Ala Val Phe Thr Leu Phe Ala Ala Leu Ile Val Lys Leu Gly Leu Val	
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caa atc gtc aat gga gag gcg tat gag cag gaa gct tgc aaa acc gag	677
Gln Ile Val Asn Gly Glu Ala Tyr Glu Gln Glu Ala Ser Lys Thr Glu	
45 50 55	
gcg aaa att gcg tca tac ccg gca ccg cgg ggt aaa atg tat gac aga	725
Ala Lys Ile Ala Ser Tyr Pro Ala Pro Arg Gly Lys Met Tyr Asp Arg	
60 65 70 75	
tac ggg cgg gtg gtt gtc gac aac caa agc gtt ccc gcg atc aca tat	773
Tyr Gly Arg Val Val Val Asp Asn Gln Ser Val Pro Ala Ile Thr Tyr	
80 85 90	
acg atg atg act agc aca aaa acg gag gaa aaa atc agc aca gcc aaa	821
Thr Met Met Thr Ser Thr Lys Thr Glu Glu Lys Ile Ser Thr Ala Lys	
95 100 105	
aaa ctc gca gaa ttg atc gat atc gat act tgc ttt ctg aaa gag aga	869
Lys Leu Ala Glu Leu Ile Asp Ile Asp Thr Ser Phe Leu Lys Glu Arg	
110 115 120	
gat ctg aaa gat tac tgg ctt gcc aga cac ccg aaa aaa gct gct gca	917
Asp Leu Lys Asp Tyr Trp Leu Ala Arg His Pro Lys Lys Ala Ala Ala	
125 130 135	
ctt ctg aaa gac agc gag aaa acc ctc aag tct gat caa aca tac aag	965
Leu Leu Lys Asp Ser Glu Lys Thr Leu Lys Ser Asp Gln Thr Tyr Lys	
140 145 150 155	
ctt cag gtg gac cgc gtt ccg gcg gaa gag atc aaa gcg ctg gaa aag	1013
Leu Gln Val Asp Arg Val Pro Ala Glu Glu Ile Lys Ala Leu Glu Lys	
160 165 170	
gac aaa gat gag ctt aaa gtc gca gcg att ttc aga aga ttt tct ggc	1061

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ggc	tat	gcg	tat	gag	ccg	caa	atc	gtc	aag	gcg	atg	agc	ccg	aaa	acc		1109
Gly	Tyr	Ala	Tyr	Glu	Pro	Gln	Ile	Val	Lys	Ala	Met	Ser	Pro	Lys	Thr		
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gcg	ggg	aaa	aac	gat	gcg	cag	ctc	ctt	gat	gag	aag	gct	tct	aaa	cag		1157
Ala	Gly	Lys	Asn	Asp	Ala	Gln	Leu	Leu	Asp	Glu	Lys	Ala	Ser	Lys	Gln		
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Met	Pro	Ala	Asn	Asp	Leu	Thr	Tyr	Glu	Glu	Val	Ser	Arg	Val	Ser	Glu		
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cat	ctt	gag	gaa	ctg	ccc	ggc	gtc	gac	gtc	atc	atg	gac	tgg	acc	agg		1253
His	Leu	Glu	Glu	Leu	Pro	Gly	Val	Asp	Val	Ile	Met	Asp	Trp	Thr	Arg		
				240					245					250			
aaa	tat	cct	tat	gaa	aaa	acg	ctc	tac	tcc	att	ttc	gga	ggc	gtc	aca		1301
Lys	Tyr	Pro	Tyr	Glu	Lys	Thr	Leu	Tyr	Ser	Ile	Phe	Gly	Gly	Val	Thr		
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acg	cct	gaa	caa	ggg	ctt	atc	aag	gac	cgg	gaa	gac	ttt	tac	ctg	aca		1349
Thr	Pro	Glu	Gln	Gly	Leu	Ile	Lys	Asp	Arg	Glu	Asp	Phe	Tyr	Leu	Thr		
		270					275					280					
agg	gga	tat	gcc	cgg	aat	gac	aga	gtg	gga	aaa	agc	tat	ctc	gag	tat		1397
Arg	Gly	Tyr	Ala	Arg	Asn	Asp	Arg	Val	Gly	Lys	Ser	Tyr	Leu	Glu	Tyr		
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caa	tat	gaa	gaa	tat	tta	aat	ccg	aaa	aaa	gcg	aaa	gtc	caa	tat	acc		1445
Gln	Tyr	Glu	Glu	Tyr	Leu	Asn	Pro	Lys	Lys	Ala	Lys	Val	Gln	Tyr	Thr		
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gaa	aac	cgt	tca	gga	aag	gtt	atc	agc	cag	gaa	acg	gtt	gat	gaa	gga		1493
Glu	Asn	Arg	Ser	Gly	Lys	Val	Ile	Ser	Gln	Glu	Thr	Val	Asp	Glu	Gly		
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aga	cgc	ggc	tac	gat	ctg	cag	ctg	acg	ttc	gac	atg	gag	ctc	caa	aag		1541
Arg	Arg	Gly	Tyr	Asp	Leu	Gln	Leu	Thr	Phe	Asp	Met	Glu	Leu	Gln	Lys		
			335					340					345				
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Lys	Val	Glu	Glu	Ala	Ile	Glu	Glu	Glu	Leu	Asn	Lys	Phe	Arg	Gly	Ser		
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aac	tac	atg	ctg	gac	aga	gcg	ttc	gtc	gtc	atg	atg	gac	ccg	aat	aac		1637
Asn	Tyr	Met	Leu	Asp	Arg	Ala	Phe	Val	Val	Met	Met	Asp	Pro	Asn	Asn		
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gga	gac	att	ctg	tcc	atg	gcc	gga	aag	cgg	atc	gtc	gac	ggc	aaa	atc		1685
Gly	Asp	Ile	Leu	Ser	Met	Ala	Gly	Lys	Arg	Ile	Val	Asp	Gly	Lys	Ile		
	380				385				390						395		
acc	gac	tat	gca	atc	ggc	gcg	ttt	aca	acc	cag	tac	gaa	atg	gga	tcg		1733
Thr	Asp	Tyr	Ala	Ile	Gly	Ala	Phe	Thr	Thr	Gln	Tyr	Glu	Met	Gly	Ser		

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aaa aaa ggt tcc tac aga gga aac act atc ggt tgg gct aat gaa gtt Lys Lys Gly Ser Tyr Arg Gly Asn Thr Ile Gly Trp Ala Asn Glu Val 445 450 455			1877
aga gcg ctg gaa aaa agt tca aac gtt tat atg ttc tat gtg gca atg Arg Ala Leu Glu Lys Ser Ser Asn Val Tyr Met Phe Tyr Val Ala Met 460 465 470 475			1925
aga atg gca gga att acg tat gta ccg aac ggc ccg ctt ccg gcg aac Arg Met Ala Gly Ile Thr Tyr Val Pro Asn Gly Pro Leu Pro Ala Asn 480 485 490			1973
cta gag gac tta aag aaa atg agg tat tac ttc aat caa ttt ggc ctt Leu Glu Asp Leu Lys Lys Met Arg Tyr Tyr Phe Asn Gln Phe Gly Leu 495 500 505			2021
ggg gta aaa aca ggc atc gac ttg ccg cag gag tcg gcc ggg atg cag Gly Val Lys Thr Gly Ile Asp Leu Pro Gln Glu Ser Ala Gly Met Gln 510 515 520			2069
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cag ttt gac acg tac acg cct ttg cag ctc gcc caa tat gtt tca acg Gln Phe Asp Thr Tyr Thr Pro Leu Gln Leu Ala Gln Tyr Val Ser Thr 540 545 550 555			2165
atc gcc aac ggc gga tac agg ttg cag ccg aga gtc gtg aaa agc att Ile Ala Asn Gly Gly Tyr Arg Leu Gln Pro Arg Val Val Lys Ser Ile 560 565 570			2213
cac cag cca gaa agc gaa aaa ctc ggt ccg gtc att gaa gag cgc tct His Gln Pro Glu Ser Glu Lys Leu Gly Pro Val Ile Glu Glu Arg Ser 575 580 585			2261
gcc aat gtg ctg aat cgt atc aac aat tct caa agc gac atc gcc atc Ala Asn Val Leu Asn Arg Ile Asn Asn Ser Gln Ser Asp Ile Ala Ile 590 595 600			2309
gtc aag caa gga ttt aaa cga gta acc cag acg gga act gca gcc ggc Val Lys Gln Gly Phe Lys Arg Val Thr Gln Thr Gly Thr Ala Ala Gly 605 610 615			2357
gca ttc ggt tcg ctt gac gta tca ggc aaa acc gga acg gcg cag acg Ala Phe Gly Ser Leu Asp Val Ser Gly Lys Thr Gly Thr Ala Gln Thr 620 625 630 635			2405

caa tac tac ggc aca aac cga aac tgg tgg ggg act agg act tac aat	2453
Gln Tyr Tyr Gly Thr Asn Arg Asn Trp Trp Gly Thr Arg Thr Tyr Asn	
640 645 650	

atc acc ttt gcc ggc tat tac ccg tcg gaa aat ccg cag gtc gcc ttc	2501
Ile Thr Phe Ala Gly Tyr Tyr Pro Ser Glu Asn Pro Gln Val Ala Phe	
655 660 665	

agc gtt gtc gtc ccg aat gtc gac gac aaa acg aag atg aac aaa aac	2549
Ser Val Val Val Pro Asn Val Asp Asp Lys Thr Lys Met Asn Lys Asn	
670 675 680	

atc gcc gcc aaa atc gtc aaa gcc tat gtc gat ctg caa aaa aaa tac	2597
Ile Ala Ala Lys Ile Val Lys Ala Tyr Val Asp Leu Gln Lys Lys Tyr	
685 690 695	

agc aaa gat tagacaaaaa agaacacgga ttttttccgg gttctttttt	2646
Ser Lys Asp	
700	

tgttatcaaa atttgacgaa tgctagaagt tttgaaggag atttctcgca ttttagcgaa	2706
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tccttttaag caaaatagtt ttaatgaatg ctgggtcatga ataggggtata aaggagggat	2766
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atgatggaac aaaaaacaaa acgttttgag caatataagc ctcatatgaa tttacaggca	2826
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gtcctgtcag ctaacggccg ttttatatac atatctgcaa attgcaaaga gctcttaagc	2886
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tacgagcaga atgaactgat cggtacgtat ttgaaggact atttacacga agacgatctt	2946
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tttctggtag aaagctatth ttacaatgag catcatttgc tgccctgcac cttcagattt	3006
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gtgaaaaaag actacacgat gatctggatc gaagcatcga tcgatttcgt gacgacccat	3066
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gttggagaaa aagaacgcga aattgtactc aaaatgaaag	3106
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<211> 702

<212> PRT

<213> Bacillus licheniformis

<400> 214

Val Thr Glu Ser Gln His Asp Pro Ala Glu Ile Lys Lys Ser Arg Arg
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20 25 30

Phe Ala Ala Leu Ile Val Lys Leu Gly Leu Val Gln Ile Val Asn Gly
35 40 45

Glu Ala Tyr Glu Gln Glu Ala Ser Lys Thr Glu Ala Lys Ile Ala Ser  
50 55 60

Tyr Pro Ala Pro Arg Gly Lys Met Tyr Asp Arg Tyr Gly Arg Val Val  
65 70 75 80

Val Asp Asn Gln Ser Val Pro Ala Ile Thr Tyr Thr Met Met Thr Ser  
85 90 95

Thr Lys Thr Glu Glu Lys Ile Ser Thr Ala Lys Lys Leu Ala Glu Leu  
100 105 110

Ile Asp Ile Asp Thr Ser Phe Leu Lys Glu Arg Asp Leu Lys Asp Tyr  
115 120 125

Trp Leu Ala Arg His Pro Lys Lys Ala Ala Ala Leu Leu Lys Asp Ser  
130 135 140

Glu Lys Thr Leu Lys Ser Asp Gln Thr Tyr Lys Leu Gln Val Asp Arg  
145 150 155 160

Val Pro Ala Glu Glu Ile Lys Ala Leu Glu Lys Asp Lys Asp Glu Leu  
165 170 175

Lys Val Ala Ala Ile Phe Arg Arg Phe Ser Gly Gly Tyr Ala Tyr Glu  
180 185 190

Pro Gln Ile Val Lys Ala Met Ser Pro Lys Thr Ala Gly Lys Asn Asp  
195 200 205

Ala Gln Leu Leu Asp Glu Lys Ala Ser Lys Gln Met Pro Ala Asn Asp  
210 215 220

Leu Thr Tyr Glu Glu Val Ser Arg Val Ser Glu His Leu Glu Glu Leu  
225 230 235 240

Pro Gly Val Asp Val Ile Met Asp Trp Thr Arg Lys Tyr Pro Tyr Glu  
245 250 255

Lys Thr Leu Tyr Ser Ile Phe Gly Gly Val Thr Thr Pro Glu Gln Gly  
260 265 270

Leu Ile Lys Asp Arg Glu Asp Phe Tyr Leu Thr Arg Gly Tyr Ala Arg

275

280

285

Asn Asp Arg Val Gly Lys Ser Tyr Leu Glu Tyr Gln Tyr Glu Glu Tyr  
 290 295 300

Leu Asn Pro Lys Lys Ala Lys Val Gln Tyr Thr Glu Asn Arg Ser Gly  
 305 310 315 320

Lys Val Ile Ser Gln Glu Thr Val Asp Glu Gly Arg Arg Gly Tyr Asp  
 325 330 335

Leu Gln Leu Thr Phe Asp Met Glu Leu Gln Lys Lys Val Glu Glu Ala  
 340 345 350

Ile Glu Glu Glu Leu Asn Lys Phe Arg Gly Ser Asn Tyr Met Leu Asp  
 355 360 365

Arg Ala Phe Val Val Met Met Asp Pro Asn Asn Gly Asp Ile Leu Ser  
 370 375 380

Met Ala Gly Lys Arg Ile Val Asp Gly Lys Ile Thr Asp Tyr Ala Ile  
 385 390 395 400

Gly Ala Phe Thr Thr Gln Tyr Glu Met Gly Ser Ala Val Lys Gly Ala  
 405 410 415

Thr Val Leu Ala Gly Tyr Gln Asp Gly Met Pro His Gly Gln Ser Tyr  
 420 425 430

Leu Asp Gln Glu Leu Ser Phe Ala Gly Gly Val Lys Lys Gly Ser Tyr  
 435 440 445

Arg Gly Asn Thr Ile Gly Trp Ala Asn Glu Val Arg Ala Leu Glu Lys  
 450 455 460

Ser Ser Asn Val Tyr Met Phe Tyr Val Ala Met Arg Met Ala Gly Ile  
 465 470 475 480

Thr Tyr Val Pro Asn Gly Pro Leu Pro Ala Asn Leu Glu Asp Leu Lys  
 485 490 495

Lys Met Arg Tyr Tyr Phe Asn Gln Phe Gly Leu Gly Val Lys Thr Gly  
 500 505 510

Ile Asp Leu Pro Gln Glu Ser Ala Gly Met Gln Thr Asn Pro Lys Ile  
515 520 525

Val Gly Gly Leu Leu Leu Asp Glu Ala Ile Gly Gln Phe Asp Thr Tyr  
530 535 540

Thr Pro Leu Gln Leu Ala Gln Tyr Val Ser Thr Ile Ala Asn Gly Gly  
545 550 555 560

Tyr Arg Leu Gln Pro Arg Val Val Lys Ser Ile His Gln Pro Glu Ser  
565 570 575

Glu Lys Leu Gly Pro Val Ile Glu Glu Arg Ser Ala Asn Val Leu Asn  
580 585 590

Arg Ile Asn Asn Ser Gln Ser Asp Ile Ala Ile Val Lys Gln Gly Phe  
595 600 605

Lys Arg Val Thr Gln Thr Gly Thr Ala Ala Gly Ala Phe Gly Ser Leu  
610 615 620

Asp Val Ser Gly Lys Thr Gly Thr Ala Gln Thr Gln Tyr Tyr Gly Thr  
625 630 635 640

Asn Arg Asn Trp Trp Gly Thr Arg Thr Tyr Asn Ile Thr Phe Ala Gly  
645 650 655

Tyr Tyr Pro Ser Glu Asn Pro Gln Val Ala Phe Ser Val Val Val Pro  
660 665 670

Asn Val Asp Asp Lys Thr Lys Met Asn Lys Asn Ile Ala Ala Lys Ile  
675 680 685

Val Lys Ala Tyr Val Asp Leu Gln Lys Lys Tyr Ser Lys Asp  
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<211> 1489

<212> DNA

<213> Bacillus licheniformis

<220>



<221> CDS

<222> (501)..(989)

<400> 215

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ctttgaggat tgatgtcttc aacgtacaga ttaacgcttg gttctgcctc gataaaatat      360
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aagaaacgga ggggtgttca atg atg gca ctt ctg aga agt ctg gcg ata tcg      533
                Met Met Ala Leu Leu Arg Ser Leu Ala Ile Ser
                1             5             10

ttt gtc ctc att ctg cct gcg gca gcg gcc tac gca caa gta cct tat      581
Phe Val Leu Ile Leu Pro Ala Ala Ala Ala Tyr Ala Gln Val Pro Tyr
                15             20             25

cca tgc agc gtc gtt ctt gat cca gtc cga gat att ccc aat gcc cgc      629
Pro Cys Ser Val Val Leu Asp Pro Val Arg Asp Ile Pro Asn Ala Arg
                30             35             40

gga acg gct tta att gcg aaa gtg aag aaa ccg tat acc gaa gcc ccc      677
Gly Thr Ala Leu Ile Ala Lys Val Lys Lys Pro Tyr Thr Glu Ala Pro
                45             50             55

ggg agt cct gtc agg gaa agg cag agt gtc ggc atc tac gct gat tgg      725
Gly Ser Pro Val Arg Glu Arg Gln Ser Val Gly Ile Tyr Ala Asp Trp
        60             65             70             75

ctt ccg gac cct gct tca ttt gga gat tat gat caa ttt gaa gga att      773
Leu Pro Asp Pro Ala Ser Phe Gly Asp Tyr Asp Gln Phe Glu Gly Ile
                80             85             90

gcc cgg ata cct gac cag atc agc tgg cgt ttc acc atg cat caa gtc      821
Ala Arg Ile Pro Asp Gln Ile Ser Trp Arg Phe Thr Met His Gln Val
                95             100             105

caa gaa gac gcg ccg agc tgg ttt ggc gga agt cct tgg gcg ggc aaa      869
Gln Glu Asp Ala Pro Ser Trp Phe Gly Gly Ser Pro Trp Ala Gly Lys
                110             115             120

ttt gac gaa ata tca tca gag ctg act gtg aat acc caa gtc gaa gtg      917
Phe Asp Glu Ile Ser Ser Glu Leu Thr Val Asn Thr Gln Val Glu Val
                125             130             135

cgc cct ttc aat tcg aag acg aaa aag gcc ggc gaa gct gtt ttg cgt      965
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Arg Pro Phe Asn Ser Lys Thr Lys Lys Ala Gly Glu Ala Val Leu Arg  
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Gly Asn Leu Gln Gly Cys Arg Ser  
160

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caagaaacta aaaatccgtc cattttcccc gcctttttgc taaaaagtgt ttctcagatg 1439  
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<211> 163  
<212> PRT  
<213> Bacillus licheniformis

<400> 216

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35 40 45

Ala Lys Val Lys Lys Pro Tyr Thr Glu Ala Pro Gly Ser Pro Val Arg  
50 55 60

Glu Arg Gln Ser Val Gly Ile Tyr Ala Asp Trp Leu Pro Asp Pro Ala  
65 70 75 80

Ser Phe Gly Asp Tyr Asp Gln Phe Glu Gly Ile Ala Arg Ile Pro Asp  
85 90 95

Gln Ile Ser Trp Arg Phe Thr Met His Gln Val Gln Glu Asp Ala Pro  
100 105 110

Ser Trp Phe Gly Gly Ser Pro Trp Ala Gly Lys Phe Asp Glu Ile Ser  
 115 120 125

Ser Glu Leu Thr Val Asn Thr Gln Val Glu Val Arg Pro Phe Asn Ser  
 130 135 140

Lys Thr Lys Lys Ala Gly Glu Ala Val Leu Arg Gly Asn Leu Gln Gly  
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Cys Arg Ser

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 Ser Asp Ala Ala Ala Lys Pro Ala Leu Thr Ser Met Lys Glu Gln Ala  
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Ile	Tyr	Ser	Gly	Ser	Glu	Thr	Pro	Leu	Lys	Ala	Asp	Val	Glu	Asp	Asp	
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Thr	Tyr	Glu	Ala	Ala	Val	Thr	Val	Ser	Glu	Gly	Lys	Thr	Leu	Ser	Tyr	
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Trp	Glu	Arg	Gly	Ile	Pro	Gln	Ser	Gly	Pro	Asn	Ala	Ala	Ala	Ser	Gly	
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Asn	Met	Asn	Leu	Leu	Met	Pro	Pro	Val	Ser	Val	Pro	Lys	Asn	Gln	Lys	
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Leu	Tyr	Leu	Thr	Tyr	Lys	Tyr	Trp	Arg	Asp	Ile	Glu	Glu	Asp	Phe	Asp	
700					705				710						715	
tac	ggc	ttc	gtt	tac	gta	cag	cct	gaa	gga	aaa	ggt	gaa	tgg	atc	ccg	2693
Tyr	Gly	Phe	Val	Tyr	Val	Gln	Pro	Glu	Gly	Lys	Gly	Glu	Trp	Ile	Pro	
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Lys Asp Phe Tyr Leu Val Tyr Val Gln Lys Glu Asp Leu Ala Asn	
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Ser Pro Gly Leu Ala Thr Asp Glu Asp Gly Glu Tyr Ser Gly Arg	
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Pro	Leu	Thr	Asn	Phe	Lys	Thr	Ala	Ala	Gln	Asn	Val	Thr	Glu	Leu	
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Pro	Ile	Arg	Glu	Val	Ser	Lys	Gly	Lys	Tyr	Glu	Gly	Tyr	Trp	Thr	

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Val Arg Asp Asp Tyr Gly Asn	Glu Thr Arg Gln Thr	Ala Lys Gly	
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Thr Phe Leu Ile Lys Leu Lys Asp Gln Val Asp Thr Pro Lys Val Ala			
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Lys Gln Gly Asp Val Lys Lys Ile Arg Ser Tyr Tyr Ile Val Asn Gly  
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Met Ala Val His Ala Thr Lys Glu Val Met Glu Gln Val Ala Ala Phe  
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Pro Glu Val Glu Lys Val Leu Pro Asn Glu Lys Arg Gln Leu Ile Lys  
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Pro Thr Lys Gln Ser Val Lys Lys Ser Ala Ala Lys Asp Glu Lys Glu  
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Ile Glu Trp Asn Ile Asn Arg Val Asp Ala Pro Lys Ala Trp Lys Leu  
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Gly Tyr Asp Gly Ser Gly Thr Val Val Ala Ser Ile Asp Thr Gly Val  
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Gln Trp Asp His Pro Ala Leu Lys Glu Lys Tyr Arg Gly Tyr Asp Pro  
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370 375 380

Asn Pro Ala Asn Tyr Pro Glu Ala Phe Ala Thr Gly Ala Thr Asp Ile  
385 390 395 400

Asp Asn Arg Leu Ala Asp Phe Ser Leu Gln Gly Pro Ser Pro Tyr Asp  
405 410 415

Glu Thr Lys Pro Glu Ile Ser Ala Pro Gly Val Asn Ile Arg Ser Ser  
420 425 430

Val Pro Gly Ser Gly Tyr Gln Asp Gly Trp Asp Gly Thr Ser Met Ala  
435 440 445

Gly Pro His Val Ala Ala Ala Ala Ala Leu Ile Lys Gln Ala Asp Ser  
450 455 460

Ser Ile Thr Val Asp Glu Thr Glu Lys Ile Leu Met Glu Thr Ala Thr  
465 470 475 480

Pro Leu Thr Asp Ser Lys Phe Thr Glu Ser Pro Asn Asn Gly Tyr Gly  
485 490 495

His Gly Leu Val Asn Val Phe Asp Ala Val Ser Ala Val Thr Asp Gly  
500 505 510

Leu Gly Arg Ala Glu Gly Gln Val Gly Lys Glu Gly Glu Asp Lys Ser  
515 520 525

Pro Pro Ala Leu Asn His Gln Glu Ile Thr Glu Ile Tyr Ser Gly Ser

530		535		540
Glu Thr Pro Leu Lys Ala Asp Val Glu Asp Asp Val Ser Ile Ile Ser				
545		550		555
Val Lys Leu Ser Tyr Lys Thr Asp Asp Ala Asp Trp Glu Thr Ile Ala				
		565		570
Ala Lys Gln Thr Ser Gly Asp Tyr Lys Lys Gly Thr Tyr Glu Ala Ala				
		580		585
Val Thr Val Ser Glu Gly Lys Thr Leu Ser Tyr Lys Trp Ile Val Thr				
		595		600
Asp Phe Gly Gly Asn Lys Thr Glu Ser Lys Val Tyr Glu Val Pro Ile				
		610		615
Ser Pro Ala Val Thr Thr Gly Tyr Lys Gln Asp Phe Glu Asn Ser Ala				
		625		630
Ser Gly Trp Leu Thr Ser Gly Val Lys Asn Ser Trp Glu Arg Gly Ile				
		645		650
Pro Gln Ser Gly Pro Asn Ala Ala Ala Ser Gly Lys Asn Val Phe Ala				
		660		665
Thr Asn Leu Thr Gly Pro Tyr Glu Ser Ser Ala Asn Met Asn Leu Leu				
		675		680
Met Pro Pro Val Ser Val Pro Lys Asn Gln Lys Leu Tyr Leu Thr Tyr				
		690		695
Lys Tyr Trp Arg Asp Ile Glu Glu Asp Phe Asp Tyr Gly Phe Val Tyr				
		705		710
Val Gln Pro Glu Gly Lys Gly Glu Trp Ile Pro Ala Ala Glu Tyr Ser				
		725		730
Gly Lys Thr Ser Glu Trp Lys Asp Gly Gln Ile Asp Leu Ser Glu Tyr				
		740		745
Gly Gly Gln Thr Ile Lys Val Met Phe Asn Leu Gln Ser Asp Asp Ser				
		755		760

Ile Glu Gly Asp Gly Leu Tyr Ile Asp Asp Val Ala Leu Val Lys Glu  
770 775 780

Val Lys Ser Ala Gly Thr Lys Lys Arg Leu Gly Val Glu Lys Gln Pro  
785 790 795 800

Ala Lys Met Lys Asp Lys Lys Thr Lys Lys Arg Met Ile Asp Pro Lys  
805 810 815

Lys Ala Lys Pro Ala Glu Ala Leu Gln Glu Lys Thr Glu Thr Lys Lys  
820 825 830

Ala Ala Pro Ala Val Leu Pro Val Arg Ala Gln Val Ser Val Leu Glu  
835 840 845

Thr Gly Lys Ser Thr Tyr Ser Asn Gln Ala Thr Gly Ala Tyr Ser Leu  
850 855 860

Ala His Ala Pro Gly Thr Tyr Thr Leu Lys Ala Glu Ala Tyr Gly Tyr  
865 870 875 880

Glu Ser Thr Ala Gln Thr Val Lys Ile Glu Ser Asp Lys Thr Thr Thr  
885 890 895

Ala Asp Phe Val Leu Lys Glu Leu Lys Lys Gly Thr Leu Thr Gly Thr  
900 905 910

Ile Lys Asn Lys Lys Thr Gly Glu Pro Val Arg His Ala Lys Leu Tyr  
915 920 925

Ile Val Glu Asp Ala Ala Val Lys Pro Val Gln Thr Asp Asp Asp Gly  
930 935 940

Ser Tyr Ser Leu Thr Ala Tyr Glu Gly Ser Tyr Thr Val Lys Val Ser  
945 950 955 960

Ala Asn Gly Tyr Tyr Ser Ser Glu Phe Ser Val Asp Leu Lys Gly Asp  
965 970 975

Val Ser Lys Asp Ile Asp Leu Asp Pro Phe Ile Gly Tyr Pro Gly Glu  
980 985 990

Ile Gly Tyr Asp Asp Gly Thr Gly Glu Asn Ala Trp Ala Phe Tyr Glu  
 995 1000 1005

Ser Gly Asn Gly Leu Ala Val Lys Met Thr Leu Glu Asn Gly Gln  
 1010 1015 1020

Glu Lys Ala Met Leu Lys Gly Gly Leu Phe Lys Phe Trp Asp Thr  
 1025 1030 1035

Glu Phe Pro Asp Pro Gly Gly Thr Asp Phe Ala Val Glu Val Tyr  
 1040 1045 1050

Asp Ala Ser Gly Glu Lys Gly Ser Pro Gly Lys Lys Ile Ala Gly  
 1055 1060 1065

Pro Phe Lys Ala Glu Ala Leu Arg Thr Gly Glu Trp Thr Thr Val  
 1070 1075 1080

Asp Leu Gly Asp Glu Gly Ile Ile Val Gly Lys Asp Phe Tyr Leu  
 1085 1090 1095

Val Tyr Val Gln Lys Glu Asp Leu Ala Asn Ser Pro Gly Leu Ala  
 1100 1105 1110

Thr Asp Glu Asp Gly Glu Tyr Ser Gly Arg Asn Trp Gln Tyr Thr  
 1115 1120 1125

Asp Gly Ser Trp Ser Lys Ala Pro Ser Asp Gln Gly Asn Phe Met  
 1130 1135 1140

Ile Arg Ala Leu Val Asp Tyr Glu Leu Ser Val Pro Val Ile Thr  
 1145 1150 1155

Ser Pro Lys Asp Gly Phe Ile Thr Asn Gln Lys Asn Ala Val Ile  
 1160 1165 1170

Glu Gly Thr Ser Ser Pro Asn Thr Thr Val His Leu Phe Asn Gly  
 1175 1180 1185

Asp Glu Glu Ala Gly Thr Ala Glu Thr Ala Ala Asp Gly Thr Phe  
 1190 1195 1200

Ser	Lys	Glu	Ile	Pro	Leu	Asn	Lys	Gly	Glu	Asn	Val	Ile	Thr	Ala
1205						1210					1215			
Lys	Ser	Ser	Ser	Ala	Ser	Gly	Thr	Thr	Asp	Ala	Ser	Glu	Pro	Val
1220						1225					1230			
Arg	Ile	Val	Leu	Asp	Gln	Lys	Lys	Pro	Lys	Leu	Thr	Ile	Asp	Thr
1235						1240					1245			
Pro	Glu	Ser	Gly	Ser	Lys	Leu	Asn	Lys	Glu	Thr	Val	Thr	Val	Lys
1250						1255					1260			
Gly	Thr	Val	Ser	Asp	Asp	His	Leu	Glu	Ser	Val	His	Val	Asn	Gly
1265						1270					1275			
Lys	Lys	Ala	Ala	Val	Asp	Asn	Gly	Glu	Tyr	Ser	Ala	Arg	Ile	Met
1280						1285					1290			
Leu	Asp	Asn	Gly	Lys	Asn	Glu	Ile	Lys	Val	Thr	Ala	Ser	Asp	Ala
1295						1300					1305			
Ala	Gly	Asn	Lys	Thr	Thr	Lys	Lys	Val	Thr	Val	Asp	Val	Asn	Phe
1310						1315					1320			
Glu	Ala	Pro	Gln	Ile	Thr	Gly	Leu	Lys	Pro	Ala	Glu	Asp	Leu	Glu
1325						1330					1335			
Leu	Lys	Thr	Gly	Glu	Thr	Val	Lys	Ile	Glu	Phe	Glu	Ser	Ala	Ala
1340						1345					1350			
Asp	Leu	Asp	Ala	Val	Phe	Val	Ile	Arg	Met	Pro	Leu	Thr	Asn	Phe
1355						1360					1365			
Lys	Thr	Ala	Ala	Gln	Asn	Val	Thr	Glu	Leu	Pro	Ile	Arg	Glu	Val
1370						1375					1380			
Ser	Lys	Gly	Lys	Tyr	Glu	Gly	Tyr	Trp	Thr	Ala	Thr	Ser	Thr	Ala
1385						1390					1395			
Lys	Ala	Lys	Gly	Ala	Glu	Ile	Glu	Val	Ile	Val	Arg	Asp	Asp	Tyr
1400						1405					1410			
Gly	Asn	Glu	Thr	Arg	Gln	Thr	Ala	Lys	Gly	Lys	Leu	Tyr	Ile	Asn



1415

1420

1425

Glu Lys Leu Lys  
1430

<210> 219  
<211> 2092  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(1592)

<400> 219  
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ctgtccgccc gtaaaacacg gcttcacccc atagctgaat aaatgccaca aaaaatggct 120  
caccaagatc gcgtcccttt ccggaagctc catgcttgcg gcaaaacggt tttcccacgt 180  
ttttctcaag taagagcccc acttcggtat ttctgtcact ttcacatttt gtctttcaag 240  
cttgctgatg atgtacattc aggccctccg tttattttat ttttccaagc gctagcacac 300  
ccgctagttc tcttctacat tccccctttt aaaaatcaat acgaaaatcc tgctattgat 360  
ggaaaaacat tttattattg gacttacgtc ctgttttttg atagtccaaa aagatcaaat 420  
aaatctagca atctccattt tttcatttat aataaataag tcaaaatcat tactcaaaaa 480  
aacattcggg gtgatctatc gtg aaa gca ccc gtg agg tat ata tgg att ggt 533  
Val Lys Ala Pro Val Arg Tyr Ile Trp Ile Gly  
1 5 10  
atg atc ctg tgc ttt tta tcc gtc agt ctg gcc gtc ggc tgc atc aaa 581  
Met Ile Leu Cys Phe Leu Ser Val Ser Leu Ala Val Gly Cys Ile Lys  
15 20 25  
gct gaa gat cag tca gat gat gag aaa aat gat gaa gcg ctt cag cct 629  
Ala Glu Asp Gln Ser Asp Asp Glu Lys Asn Asp Glu Ala Leu Gln Pro  
30 35 40  
gcc gaa cac ttc gtt tac cgt cat tta atg agc gat cag ggg ctg atc 677  
Ala Glu His Phe Val Tyr Arg His Leu Met Ser Asp Gln Gly Leu Ile  
45 50 55  
aaa acc ggc ttt tcc gac cag cct gtt tac ttg tcg gaa tcg ctt ggc 725  
Lys Thr Gly Phe Ser Asp Gln Pro Val Tyr Leu Ser Glu Ser Leu Gly  
60 65 70 75  
ttg tgg atg gag ttt ttg atc agc aaa aaa gac ggc gag cat ttc cat 773  
Leu Trp Met Glu Phe Leu Ile Ser Lys Lys Asp Gly Glu His Phe His  
80 85 90

gag caa tat cag cac ctg aac gaa tcc ttc ctt atg aac aac aac ctg	821
Glu Gln Tyr Gln His Leu Asn Glu Ser Phe Leu Met Asn Asn Asn Leu	
95 100 105	
gtg tca tgg caa atc caa aac ggc cag gca agc ggg gtg aac gcc ctg	869
Val Ser Trp Gln Ile Gln Asn Gly Gln Ala Ser Gly Val Asn Ala Leu	
110 115 120	
atc gat gat ctc aga atc atg gtg agc ctc gat caa gcg gca gct cta	917
Ile Asp Asp Leu Arg Ile Met Val Ser Leu Asp Gln Ala Ala Ala Leu	
125 130 135	
tgg gga aac agc gag tat aaa caa acc gct cgg aac atc ggt gcc gca	965
Trp Gly Asn Ser Glu Tyr Lys Gln Thr Ala Arg Asn Ile Gly Ala Ala	
140 145 150 155	
tta aga aaa tac aac atg aac aac ggg ata ttg acg gac ttt tac gac	1013
Leu Arg Lys Tyr Asn Met Asn Asn Gly Ile Leu Thr Asp Phe Tyr Asp	
160 165 170	
tcc gcc tct caa tcc gcg gca aaa gat atc acg ctt tcc tat atc atg	1061
Ser Ala Ser Gln Ser Ala Ala Lys Asp Ile Thr Leu Ser Tyr Ile Met	
175 180 185	
ccg gat gcg cta tcc atc ttg aaa aag aat gga gtg ata aat aaa gaa	1109
Pro Asp Ala Leu Ser Ile Leu Lys Lys Asn Gly Val Ile Asn Lys Glu	
190 195 200	
ctc gaa agt cgg aat gcc agc att ctt tat ctc gcc cct ttg aaa aac	1157
Leu Glu Ser Arg Asn Ala Ser Ile Leu Tyr Leu Ala Pro Leu Lys Asn	
205 210 215	
ggg ttt ctc cca aaa gca tac agt aca gaa acg aaa gca tac acc tat	1205
Gly Phe Leu Pro Lys Ala Tyr Ser Thr Glu Thr Lys Ala Tyr Thr Tyr	
220 225 230 235	
gac cat gaa gtc aat ctc att gat cag ctt tac gca gct tgg cat tta	1253
Asp His Glu Val Asn Leu Ile Asp Gln Leu Tyr Ala Ala Trp His Leu	
240 245 250	
cct ccg aag gat caa aaa gcc gct gta tta gcg gat tgg ctc aaa cag	1301
Pro Pro Lys Asp Gln Lys Ala Ala Val Leu Ala Asp Trp Leu Lys Gln	
255 260 265	
acg ttt caa acc ggc gga aaa ctg tat ggc cgg tat tcg ctc gat aca	1349
Thr Phe Gln Thr Gly Gly Lys Leu Tyr Gly Arg Tyr Ser Leu Asp Thr	
270 275 280	
aaa aag ccg gcg gtc caa tac gag tct cca tcc gtc tac gcg ttg gcg	1397
Lys Lys Pro Ala Val Gln Tyr Glu Ser Pro Ser Val Tyr Ala Leu Ala	
285 290 295	
att tta ttc ttc atc aac caa aac gaa gat aaa acc gtc att aaa gcg	1445
Ile Leu Phe Phe Ile Asn Gln Asn Glu Asp Lys Thr Val Ile Lys Ala	
300 305 310 315	

ctg tat gat cga atg aat gat ttt gaa att ctt gat tcg tcc gag acg 1493  
 Leu Tyr Asp Arg Met Asn Asp Phe Glu Ile Leu Asp Ser Ser Glu Thr  
                   320                  325                  330

tat tat ggg gga tat atg agc gga aat gat acg cat tct ttt gat aat 1541  
 Tyr Tyr Gly Gly Tyr Met Ser Gly Asn Asp Thr His Ser Phe Asp Asn  
                   335                  340                  345

ctg ctg ccc cta tta gcc gaa agg aag ctt tta aat gaa aat ctc att 1589  
 Leu Leu Pro Leu Leu Ala Glu Arg Lys Leu Leu Asn Glu Asn Leu Ile  
                   350                  355                  360

caa tgaatcgcat aaaatgttcg cttatatgac aggacttgca gcagcgcttg 1642  
 Gln

cgttgttcat ccattatatc tcagtccagc ggttcgaacc cgttctcatc atttgcata 1702

cacttgccat catcgagca ggaatatggc tcggatcgat ttacgcactg gctgggacca 1762

tcatcgctcct gtttggttctc ggcaatttga tgatgttttt tcacacaggc caaggagaag 1822

ctgcttcgtc tgaaaccgga ctgcaaatgc tcgtcatctg gggagtggcg ctgttgctgt 1882

tttcctttat gtcagggaga atacacgaca tcgcatcgcg acttcaccgc tccgtcaaac 1942

accttcaaga cgaaatcaaa agctttgttg cgattgacag ggtgacaggc tttgataata 2002

aacagaggat gaagctggag ctgtcagaag aaatcaagcg ggcggagcgg tatggcaact 2062

cgtttggttt tttactgctt catatgcatt 2092

<210> 220

<211> 364

<212> PRT

<213> Bacillus licheniformis

<400> 220

Val Lys Ala Pro Val Arg Tyr Ile Trp Ile Gly Met Ile Leu Cys Phe  
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Leu Ser Val Ser Leu Ala Val Gly Cys Ile Lys Ala Glu Asp Gln Ser  
                   20                  25                  30

Asp Asp Glu Lys Asn Asp Glu Ala Leu Gln Pro Ala Glu His Phe Val  
                   35                  40                  45

Tyr Arg His Leu Met Ser Asp Gln Gly Leu Ile Lys Thr Gly Phe Ser  
                   50                  55                  60

Asp Gln Pro Val Tyr Leu Ser Glu Ser Leu Gly Leu Trp Met Glu Phe

65

70

75

80

Leu Ile Ser Lys Lys Asp Gly Glu His Phe His Glu Gln Tyr Gln His  
85 90 95

Leu Asn Glu Ser Phe Leu Met Asn Asn Asn Leu Val Ser Trp Gln Ile  
100 105 110

Gln Asn Gly Gln Ala Ser Gly Val Asn Ala Leu Ile Asp Asp Leu Arg  
115 120 125

Ile Met Val Ser Leu Asp Gln Ala Ala Ala Leu Trp Gly Asn Ser Glu  
130 135 140

Tyr Lys Gln Thr Ala Arg Asn Ile Gly Ala Ala Leu Arg Lys Tyr Asn  
145 150 155 160

Met Asn Asn Gly Ile Leu Thr Asp Phe Tyr Asp Ser Ala Ser Gln Ser  
165 170 175

Ala Ala Lys Asp Ile Thr Leu Ser Tyr Ile Met Pro Asp Ala Leu Ser  
180 185 190

Ile Leu Lys Lys Asn Gly Val Ile Asn Lys Glu Leu Glu Ser Arg Asn  
195 200 205

Ala Ser Ile Leu Tyr Leu Ala Pro Leu Lys Asn Gly Phe Leu Pro Lys  
210 215 220

Ala Tyr Ser Thr Glu Thr Lys Ala Tyr Thr Tyr Asp His Glu Val Asn  
225 230 235 240

Leu Ile Asp Gln Leu Tyr Ala Ala Trp His Leu Pro Pro Lys Asp Gln  
245 250 255

Lys Ala Ala Val Leu Ala Asp Trp Leu Lys Gln Thr Phe Gln Thr Gly  
260 265 270

Gly Lys Leu Tyr Gly Arg Tyr Ser Leu Asp Thr Lys Lys Pro Ala Val  
275 280 285

Gln Tyr Glu Ser Pro Ser Val Tyr Ala Leu Ala Ile Leu Phe Phe Ile  
290 295 300

Asn Gln Asn Glu Asp Lys Thr Val Ile Lys Ala Leu Tyr Asp Arg Met  
 305 310 315 320

Asn Asp Phe Glu Ile Leu Asp Ser Ser Glu Thr Tyr Tyr Gly Gly Tyr  
 325 330 335

Met Ser Gly Asn Asp Thr His Ser Phe Asp Asn Leu Leu Pro Leu Leu  
 340 345 350

Ala Glu Arg Lys Leu Leu Asn Glu Asn Leu Ile Gln  
 355 360

<210> 221  
 <211> 1420  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(920)

<400> 221  
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 gcatacatatt acgcgcacgc agtcattcct gaatgagttt gccgaaagcc tcaagaaagc 120  
 cgattatgta tatctttgcg atatattcgg atctgcccgg gaaaacgcag gaaagctgac 180  
 gatcgggtgat ttgcaggaga aaattccgca ggccaagctg atcgatgaaa atgacacatc 240  
 aatttttaaag gagcatgaaa atgcggtgtt aattttcatg ggcgaggtg acattcaaaa 300  
 gtattttaaga gcatatgaaa atgtattagc ataacaagaa aaaggcagtg tgagtcaatc 360  
 cgctgctttt ttgtacatat gaagcgggag tttctgttaa aggaattcac ccgtgcgtat 420  
 agaaaaagta aatatagagg tttacgattt aaacaattgg gtatacatca attgtaagcc 480  
 cttagctgaa ggaggataag atg att att att ctg tat tta agc gct gca ctc 533  
 Met Ile Ile Ile Leu Tyr Leu Ser Ala Ala Leu  
 1 5 10  
 atc gct gtt agc ttt ctt att ttg gtt atc tat tta tca aaa aca tta 581  
 Ile Ala Val Ser Phe Leu Ile Leu Val Ile Tyr Leu Ser Lys Thr Leu  
 15 20 25  
 aaa tcg ctt caa gtc aca ctt aat cat gtt gca tca acg ctg gaa ggt 629  
 Lys Ser Leu Gln Val Thr Leu Asn His Val Ala Ser Thr Leu Glu Gly  
 30 35 40

gtg gaa gga caa atg aaa ggc atc acc gct gaa aca acg gag ctg ctg 677  
Val Glu Gly Gln Met Lys Gly Ile Thr Ala Glu Thr Thr Glu Leu Leu  
45 50 55

aat aag acg aat cgg ctg gct gat gat att cag gaa aaa tct ttg aag 725  
Asn Lys Thr Asn Arg Leu Ala Asp Asp Ile Gln Glu Lys Ser Leu Lys  
60 65 70 75

ctg aat acg gtc gtg gat gcc gtt cag gaa gtc ggc aca tcg gtc agg 773  
Leu Asn Thr Val Val Asp Ala Val Gln Glu Val Gly Thr Ser Val Arg  
80 85 90

cag ttt aac aac tcc att cag cag gtt tca cag tcc gtc aca tca gcc 821  
Gln Phe Asn Asn Ser Ile Gln Gln Val Ser Gln Ser Val Thr Ser Ala  
95 100 105

gca gag caa aac cgt gaa aaa att tct caa gtt gtc agc tgg agc aat 869  
Ala Glu Gln Asn Arg Glu Lys Ile Ser Gln Val Val Ser Trp Ser Asn  
110 115 120

gca gct ttg gaa att tgg aat aga tgg aaa caa aag aag atg agg gag 917  
Ala Ala Leu Glu Ile Trp Asn Arg Trp Lys Gln Lys Lys Met Arg Glu  
125 130 135

gaa taataaatga gtaaagacgg aatgaatact aaggattttt taatcggcac 970  
Glu  
140

gtttgtaggc ggaatcatcg gggcggctgc agctttatatt tttagcgccg aagtcgggga 1030

aagagcttcg cgatgacctt ggaaatcagg ccgtcgtttt aaaggataag accggaaagc 1090

tcacaagcga agcgagggag agaggctctg agtacgtcag catcgccaaa gagaagacat 1150

cttcgatttc acagcttggt gccgaccagt cttcacagat tatggataaa gtcaaagact 1210

tgcgaaagcaa ggggtgccgaa aaagctggtg aactaaagga agaagcatcg tctgcaatcg 1270

aagaacaggc tgaagaagcc aaaaatgaaa tagaagatga agcaaggaaa acagcagata 1330

ccgctcagaa ataactgtgg aaaggagat caccgtgtcg aaacagctca ttcaaacaga 1390

ggatgaattt aaaaggcttg cagaaaacaa 1420

<210> 222

<211> 140

<212> PRT

<213> Bacillus licheniformis

<400> 222

Met Ile Ile Ile Leu Tyr Leu Ser Ala Ala Leu Ile Ala Val Ser Phe  
1 5 10 15

Leu Ile Leu Val Ile Tyr Leu Ser Lys Thr Leu Lys Ser Leu Gln Val

20

25

30

Thr Leu Asn His Val Ala Ser Thr Leu Glu Gly Val Glu Gly Gln Met  
 35 40 45

Lys Gly Ile Thr Ala Glu Thr Thr Glu Leu Leu Asn Lys Thr Asn Arg  
 50 55 60

Leu Ala Asp Asp Ile Gln Glu Lys Ser Leu Lys Leu Asn Thr Val Val  
 65 70 75 80

Asp Ala Val Gln Glu Val Gly Thr Ser Val Arg Gln Phe Asn Asn Ser  
 85 90 95

Ile Gln Gln Val Ser Gln Ser Val Thr Ser Ala Ala Glu Gln Asn Arg  
 100 105 110

Glu Lys Ile Ser Gln Val Val Ser Trp Ser Asn Ala Ala Leu Glu Ile  
 115 120 125

Trp Asn Arg Trp Lys Gln Lys Lys Met Arg Glu Glu  
 130 135 140

<210> 223

<211> 2641

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (501)..(2141)

<400> 223

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 accgccggct tatttcacaa tggattggac aaaagcagca gattcggttc ggaagctggc 180  
 aggattaaaa ccggctgcat tattgacggg acacggtgta ccgatgaaag gaagcgattt 240  
 ttccgaagcg ctccttgatc tatcagaccg cttgcccgcc tctgattcgt aaattgtcat 300  
 atgctgcgct taaaacattc agccaggctg aatgtttttt tatagggaaa aactaaccat 360  
 tttacatgtg atgatggccg tccattgttc taaattccgg atgttgatgt ataccaaagg 420  
 aatcattttc tgaaatttta gacaaaatat gttgatattt catttataat gcaggatatgc 480

ctgaaaggag ctgagaaaaag atg aaa att caa aaa agg gtc caa gct ttg ctg	533
Met Lys Ile Gln Lys Arg Val Gln Ala Leu Leu	
1 5 10	
gca act tcg gca atg ttt gca gga ctg atg ctg tcc gat gcg gtg tac	581
Ala Thr Ser Ala Met Phe Ala Gly Leu Met Leu Ser Asp Ala Val Tyr	
15 20 25	
gct gcg gaa acc cct tac tat gga aag aac tat act cag cca gag caa	629
Ala Ala Glu Thr Pro Tyr Tyr Gly Lys Asn Tyr Thr Gln Pro Glu Gln	
30 35 40	
gtg tca tca tta tat ccg gag cct gaa gaa aca ttc tca acc cct gct	677
Val Ser Ser Leu Tyr Pro Glu Pro Glu Glu Thr Phe Ser Thr Pro Ala	
45 50 55	
ttt gta aaa gaa ggg gaa gcc ttt acg aca caa gaa gaa atg atg aag	725
Phe Val Lys Glu Gly Glu Ala Phe Thr Thr Gln Glu Glu Met Met Lys	
60 65 70 75	
ttt ata acc agt ctg aca aag aaa agc ccg aat gtc aaa atc ggg aat	773
Phe Ile Thr Ser Leu Thr Lys Lys Ser Pro Asn Val Lys Ile Gly Asn	
80 85 90	
atc ggt ttt tca att gaa aaa aga aat att cct gtg ctt tac ttc aca	821
Ile Gly Phe Ser Ile Glu Lys Arg Asn Ile Pro Val Leu Tyr Phe Thr	
95 100 105	
aag gac aag caa ata cgt tcc ata tca aaa aaa cca acc gtc tgg ctg	869
Lys Asp Lys Gln Ile Arg Ser Ile Ser Lys Lys Pro Thr Val Trp Leu	
110 115 120	
caa gga cag ata cat gga aat gag ccg gca gcg gga gaa tct gct ctg	917
Gln Gly Gln Ile His Gly Asn Glu Pro Ala Ala Gly Glu Ser Ala Leu	
125 130 135	
gcg ata gct gaa aaa ctg gcc gga ccg tat ggc gac aaa gtg ttg gac	965
Ala Ile Ala Glu Lys Leu Ala Gly Pro Tyr Gly Asp Lys Val Leu Asp	
140 145 150 155	
aag atc aat gtc atc gtt gtt ccg cgg gtc aat cct gac gga tca tat	1013
Lys Ile Asn Val Ile Val Val Pro Arg Val Asn Pro Asp Gly Ser Tyr	
160 165 170	
cag ttc aac aga cgg ctg gcg aac gga atc gac gga aac agg gat cat	1061
Gln Phe Asn Arg Arg Leu Ala Asn Gly Ile Asp Gly Asn Arg Asp His	
175 180 185	
gtc aag ctc gag tct cca gaa gtg cgc gcc att cac caa gaa ttc aat	1109
Val Lys Leu Glu Ser Pro Glu Val Arg Ala Ile His Gln Glu Phe Asn	
190 195 200	
aag tat tcg cct gaa gtc gtt atc gat gcc cat gaa tac ggt gtc ggc	1157
Lys Tyr Ser Pro Glu Val Val Ile Asp Ala His Glu Tyr Gly Val Gly	
205 210 215	



caa aac gaa ttt cag agc ata ggc gaa aaa ggg tca tta aaa tac cat	1205
Gln Asn Glu Phe Gln Ser Ile Gly Glu Lys Gly Ser Leu Lys Tyr His	
220 225 230 235	
gat att tta att tta tca gga aaa aat tta aac att ccc aag tcg atc	1253
Asp Ile Leu Ile Leu Ser Gly Lys Asn Leu Asn Ile Pro Lys Ser Ile	
240 245 250	
agg cat gcg tcc gac agc ctt tat gtg aac ggc gtc aga gct aaa ctt	1301
Arg His Ala Ser Asp Ser Leu Tyr Val Asn Gly Val Arg Ala Lys Leu	
255 260 265	
gat gaa aaa gga ttt tct aat gat gct tat tat acg aca gga aaa agc	1349
Asp Glu Lys Gly Phe Ser Asn Asp Ala Tyr Tyr Thr Thr Gly Lys Ser	
270 275 280	
aag gac gga aaa atc gaa atc tat gaa ggc ggt aca gaa gcg aga atc	1397
Lys Asp Gly Lys Ile Glu Ile Tyr Glu Gly Gly Thr Glu Ala Arg Ile	
285 290 295	
ggg cgt aat gca ttc gcc ctc cag cct gcc ctt tcc ttc ctg gtg gaa	1445
Gly Arg Asn Ala Phe Ala Leu Gln Pro Ala Leu Ser Phe Leu Val Glu	
300 305 310 315	
agc agg gga ata gac atc gga cgc gaa aat ttt gca aga aga gtc gcg	1493
Ser Arg Gly Ile Asp Ile Gly Arg Glu Asn Phe Ala Arg Arg Val Ala	
320 325 330	
gct cag gtt gct aca cat gag acg atc atc gac acg aca gtg aag cat	1541
Ala Gln Val Ala Thr His Glu Thr Ile Ile Asp Thr Thr Val Lys His	
335 340 345	
gca gcc gag atc aag cgc ctt gtc tcc aaa gaa aaa tta aag ctg ata	1589
Ala Ala Glu Ile Lys Arg Leu Val Ser Lys Glu Lys Leu Lys Leu Ile	
350 355 360	
caa aac ggc gct aaa gtg agc gat aaa gac caa gtg gtc atc aac agt	1637
Gln Asn Gly Ala Lys Val Ser Asp Lys Asp Gln Val Val Ile Asn Ser	
365 370 375	
gag ttt gca ggc ccg ttt aaa gac acg ctt aaa gtc gct gat att gcc	1685
Glu Phe Ala Gly Pro Phe Lys Asp Thr Leu Lys Val Ala Asp Ile Ala	
380 385 390 395	
tca gga caa gca gtt gac gtt cct gtc caa tat tac agc gcc tca gag	1733
Ser Gly Gln Ala Val Asp Val Pro Val Gln Tyr Tyr Ser Ala Ser Glu	
400 405 410	
gcc gtt cct gtg ctg tca aga act cgg ccg acc gct tac ctt gtc ctt	1781
Ala Val Pro Val Leu Ser Arg Thr Arg Pro Thr Ala Tyr Leu Val Leu	
415 420 425	
ccg ggc cat caa gat atc gaa cag aag ctg aag gat cag gga tta aag	1829
Pro Gly His Gln Asp Ile Glu Gln Lys Leu Lys Asp Gln Gly Leu Lys	
430 435 440	
agc gtg aca ctg gct ttc aaa caa aaa ctc acc gct gaa gcg tat gag	1877

Ser Val Thr Leu Ala Phe Lys Gln Lys Leu Thr Ala Glu Ala Tyr Glu	
445 450 455	
gtt tta tcg aaa gaa aca gcg gga gaa tct gag ggc cgg cca gtg atc	1925
Val Leu Ser Lys Glu Thr Ala Gly Glu Ser Glu Gly Arg Pro Val Ile	
460 465 470 475	
aag gta gaa acg aag ctc aaa aaa cag aaa aaa gag ttt cct aaa gga	1973
Lys Val Glu Thr Lys Leu Lys Lys Gln Lys Lys Glu Phe Pro Lys Gly	
480 485 490	
aca aaa atc tat ttt aca gct cag cag caa agc aat ctg ctg tca atc	2021
Thr Lys Ile Tyr Phe Thr Ala Gln Gln Gln Ser Asn Leu Leu Ser Ile	
495 500 505	
gca ctt gag ccg gag tcg gtt gac agt tat gta agc aca ggt tac att	2069
Ala Leu Glu Pro Glu Ser Val Asp Ser Tyr Val Ser Thr Gly Tyr Ile	
510 515 520	
cct tct caa aaa ggc aaa gag ctg ccg gtt tac cgc ttc atg ctg aac	2117
Pro Ser Gln Lys Gly Lys Glu Leu Pro Val Tyr Arg Phe Met Leu Asn	
525 530 535	
acc aaa acg ctt aat ttt aag gaa taatcaccag gcatccgtct ttgacggatg	2171
Thr Lys Thr Leu Asn Phe Lys Glu	
540 545	
cttttttagcg gttttttgtt ttttcataca taattgtttt aaactgagat cgaaacctat	2231
acaataaaata tcagtctgaa atctggaagg agagaatccg gttggaatca catgaagaat	2291
tatggaggga agccaaggcc ttcacgcgagc tctgctacgg ggaactgtcg aagtccgaag	2351
aagaaacaag gatgcgctta cataaaatag ataaagaaat cagagaaacc ggaagctata	2411
cacatacatt agaagaaatc gaacatggag ccagaatggc gtggagaaac agcagccgct	2471
gcatcggcag gctgtttttgg cactctctta ctgtcatcga tcaaagaggc gttcaaaccg	2531
aggcagaggt gcgggatgcg cttttccacc atattcagct tgcaacaaac ggagggaaaa	2591
tcagaccgtt cattacggtt ttcccccg aacaaaacgg acaaaaaaaaa	2641

<210> 224

<211> 547

<212> PRT

<213> Bacillus licheniformis

<400> 224

Met Lys Ile Gln Lys Arg Val Gln Ala Leu Leu Ala Thr Ser Ala Met
1 5 10 15

Phe Ala Gly Leu Met Leu Ser Asp Ala Val Tyr Ala Ala Glu Thr Pro
20 25 30

Tyr Tyr Gly Lys Asn Tyr Thr Gln Pro Glu Gln Val Ser Ser Leu Tyr  
 35 40 45

Pro Glu Pro Glu Glu Thr Phe Ser Thr Pro Ala Phe Val Lys Glu Gly  
 50 55 60

Glu Ala Phe Thr Thr Gln Glu Glu Met Met Lys Phe Ile Thr Ser Leu  
 65 70 75 80

Thr Lys Lys Ser Pro Asn Val Lys Ile Gly Asn Ile Gly Phe Ser Ile  
 85 90 95

Glu Lys Arg Asn Ile Pro Val Leu Tyr Phe Thr Lys Asp Lys Gln Ile  
 100 105 110

Arg Ser Ile Ser Lys Lys Pro Thr Val Trp Leu Gln Gly Gln Ile His  
 115 120 125

Gly Asn Glu Pro Ala Ala Gly Glu Ser Ala Leu Ala Ile Ala Glu Lys  
 130 135 140

Leu Ala Gly Pro Tyr Gly Asp Lys Val Leu Asp Lys Ile Asn Val Ile  
 145 150 155 160

Val Val Pro Arg Val Asn Pro Asp Gly Ser Tyr Gln Phe Asn Arg Arg  
 165 170 175

Leu Ala Asn Gly Ile Asp Gly Asn Arg Asp His Val Lys Leu Glu Ser  
 180 185 190

Pro Glu Val Arg Ala Ile His Gln Glu Phe Asn Lys Tyr Ser Pro Glu  
 195 200 205

Val Val Ile Asp Ala His Glu Tyr Gly Val Gly Gln Asn Glu Phe Gln  
 210 215 220

Ser Ile Gly Glu Lys Gly Ser Leu Lys Tyr His Asp Ile Leu Ile Leu  
 225 230 235 240

Ser Gly Lys Asn Leu Asn Ile Pro Lys Ser Ile Arg His Ala Ser Asp  
 245 250 255

Ser Leu Tyr Val Asn Gly Val Arg Ala Lys Leu Asp Glu Lys Gly Phe  
 260 265 270

Ser Asn Asp Ala Tyr Tyr Thr Thr Gly Lys Ser Lys Asp Gly Lys Ile  
 275 280 285

Glu Ile Tyr Glu Gly Gly Thr Glu Ala Arg Ile Gly Arg Asn Ala Phe  
 290 295 300

Ala Leu Gln Pro Ala Leu Ser Phe Leu Val Glu Ser Arg Gly Ile Asp  
 305 310 315 320

Ile Gly Arg Glu Asn Phe Ala Arg Arg Val Ala Ala Gln Val Ala Thr  
 325 330 335

His Glu Thr Ile Ile Asp Thr Thr Val Lys His Ala Ala Glu Ile Lys  
 340 345 350

Arg Leu Val Ser Lys Glu Lys Leu Lys Leu Ile Gln Asn Gly Ala Lys  
 355 360 365

Val Ser Asp Lys Asp Gln Val Val Ile Asn Ser Glu Phe Ala Gly Pro  
 370 375 380

Phe Lys Asp Thr Leu Lys Val Ala Asp Ile Ala Ser Gly Gln Ala Val  
 385 390 395 400

Asp Val Pro Val Gln Tyr Tyr Ser Ala Ser Glu Ala Val Pro Val Leu  
 405 410 415

Ser Arg Thr Arg Pro Thr Ala Tyr Leu Val Leu Pro Gly His Gln Asp  
 420 425 430

Ile Glu Gln Lys Leu Lys Asp Gln Gly Leu Lys Ser Val Thr Leu Ala  
 435 440 445

Phe Lys Gln Lys Leu Thr Ala Glu Ala Tyr Glu Val Leu Ser Lys Glu  
 450 455 460

Thr Ala Gly Glu Ser Glu Gly Arg Pro Val Ile Lys Val Glu Thr Lys  
 465 470 475 480

Leu Lys Lys Gln Lys Lys Glu Phe Pro Lys Gly Thr Lys Ile Tyr Phe  
485 490 495

Thr Ala Gln Gln Gln Ser Asn Leu Leu Ser Ile Ala Leu Glu Pro Glu  
500 505 510

Ser Val Asp Ser Tyr Val Ser Thr Gly Tyr Ile Pro Ser Gln Lys Gly  
515 520 525

Lys Glu Leu Pro Val Tyr Arg Phe Met Leu Asn Thr Lys Thr Leu Asn  
530 535 540

Phe Lys Glu  
545

<210> 225  
<211> 1381  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(881)

<400> 225  
ttgattatta ttttaagtaa tcgcagaaag aaaggctcgt ctatggcaag ctatttaaaa 60  
tccagaatcg tatcttatct gtttattctt ttggaagtgg ggaccggatt cgcaatttgc 120  
gaggtgtcaa tggaaaaatcc gaattactcc tcagcttgcg cggtctttat catagggtttt 180  
acgattgggg aatgcttcat gattagaaaaa tggtaaattt tgatcatgac gggatactct 240  
ttaccctctt ctataaaagt gggacagaca gttgaaaagc cggtaaattc atagccttgt 300  
atttcaacag taacttcttc tatatgcggg tttcattttt tcatctttgc ttaatacatt 360  
aaatcacctc ctttatacag tatttgtcca ttaaagaaga acaggatctt cttgtcaaat 420  
atctttatta gatcatattg tcatgtataa tgaagggtat agcatgtgac attcatactg 480  
tataagaaag gatatgacca gtg aaa atg ttg aaa aag gct gtg ttg ata gcc 533  
Val Lys Met Leu Lys Lys Ala Val Leu Ile Ala  
1 5 10  
gct gtt ttc ttg ctg gcc gca ttt gcc ggg agt aca gaa gcc ttt gct 581  
Ala Val Phe Leu Leu Ala Ala Phe Ala Gly Ser Thr Glu Ala Phe Ala  
15 20 25  
atg cct tcc aaa ggc gcg gtg aaa ttc agg acg gat gcc aat aca tat 629  
Met Pro Ser Lys Gly Ala Val Lys Phe Arg Thr Asp Ala Asn Thr Tyr

30	35	40	
acg aaa tca gcc act tcg atc gtt gtc act gga aaa agc cct gtt acg			677
Thr Lys Ser Ala Thr Ser Ile Val Val Thr Gly Lys Ser Pro Val Thr			
45	50	55	
gga acg atg att gcc gtc agg ctg atc aat aaa aaa ggg act gtc ctg			725
Gly Thr Met Ile Ala Val Arg Leu Ile Asn Lys Lys Gly Thr Val Leu			
60	65	70	75
atc tat cga gat gtt cat tta acg cgc gga aag cct cat ttt cgg gtg			773
Ile Tyr Arg Asp Val His Leu Thr Arg Gly Lys Pro His Phe Arg Val			
80	85	90	
agc ttt ccg acg aaa aag ctg aaa ccg ggc aag tat gac gtc tgg gtg			821
Ser Phe Pro Thr Lys Lys Leu Lys Pro Gly Lys Tyr Asp Val Trp Val			
95	100	105	
gat gcc gtc aaa gga aag aag tgg cac ggg gaa ttg aag cgc tac att			869
Asp Ala Val Lys Gly Lys Lys Trp His Gly Glu Leu Lys Arg Tyr Ile			
110	115	120	
gtc atc aag cat tgatctcttt tatgatggac ggagggctgt gtaatgactg			921
Val Ile Lys His			
125			
tcgtggggttt ttgcgtatta ttatgttctg catttatcca tgcacgtgg aactatcttt			981
ctaaaaaagc cgatggaggc gttccgttta tctggctgtt cacagcgatt gcagccgtca			1041
tctacacgcc gttggccata ggtgtcgtca tatatgaaaa gcctgagatc ggcatctggc			1101
agcttgtcat catcatggcg agcatccttg ctcaacttggg cttttttctt gttcttcaaa			1161
aaggatacaa aaagggcgat ctctcccttg tctatccgat cgcgaggggg acaggcccgc			1221
tgctcacctg catgctggcg gtcgcctttt ttggcgagac gttgacgctg cccgctatta			1281
tagggattct attgattgtg atcagcattc ttttttttac agggggagtg aagcgggtaa			1341
aagaatcagg ctcgttcaca ccggttcttt acgggctggc			1381

<210> 226

<211> 127

<212> PRT

<213> Bacillus licheniformis

<400> 226

Val Lys Met Leu Lys Lys Ala Val Leu Ile Ala Ala Val Phe Leu Leu
1 5 10 15

Ala Ala Phe Ala Gly Ser Thr Glu Ala Phe Ala Met Pro Ser Lys Gly
20 25 30

Ala Val Lys Phe Arg Thr Asp Ala Asn Thr Tyr Thr Lys Ser Ala Thr  
 35 40 45

Ser Ile Val Val Thr Gly Lys Ser Pro Val Thr Gly Thr Met Ile Ala  
 50 55 60

Val Arg Leu Ile Asn Lys Lys Gly Thr Val Leu Ile Tyr Arg Asp Val  
 65 70 75 80

His Leu Thr Arg Gly Lys Pro His Phe Arg Val Ser Phe Pro Thr Lys  
 85 90 95

Lys Leu Lys Pro Gly Lys Tyr Asp Val Trp Val Asp Ala Val Lys Gly  
 100 105 110

Lys Lys Trp His Gly Glu Leu Lys Arg Tyr Ile Val Ile Lys His  
 115 120 125

<210> 227  
 <211> 1687  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1187)

<400> 227  
 caatgtcaat gaaatgaaag acccgttttt gaaaaaaggc ctgctccttg ccatcgacgg 60  
 atgggatgag gagacgatcc gcaatgtgat gaactcgga attgccgcga tggaagaacg 120  
 acacagaaag gggagaagga tctttgaaaa agcaggagaa tttgcgcctg catggggaat 180  
 gatcggaacg cttgtcggtc tcgtcatgat gctcaaaaac ctgaacaagc cggaaacgct 240  
 cgggccgaat atggcaatcg cccttttgac gacgctttac ggatcacttt tagccaacat 300  
 gctgtttata ccgatcgccg cgaagcttga agaaaagacg gagaatgaaa tctttaagaa 360  
 gcaagtcatg atcgaaggca tcatcggcat ccaatcgga agaaatccgc gaaatcttga 420  
 aagtcagctt gtcgtttttca gttcaaaaaga agaattggaca aaaaagcggg cggaccgcat 480  
 gaaacaaaag gacaggcctc atg aag ctt aga cat gaa cga agg aag cgc gag 533  
 Met Lys Leu Arg His Glu Arg Arg Lys Arg Glu  
 1 5 10  
 cag ggc cgc aaa tcg cca aac tgg atc atc acg ttt tcg gat ttg att 581

Gln	Gly	Arg	Lys	Ser	Pro	Asn	Trp	Ile	Ile	Thr	Phe	Ser	Asp	Leu	Ile		
			15					20					25				
acg	ctc	atc	ctc	gtg	ttc	ttt	att	tta	ctg	ttt	tcg	atg	tcg	caa	atc	629	
Thr	Leu	Ile	Leu	Val	Phe	Phe	Ile	Leu	Leu	Phe	Ser	Met	Ser	Gln	Ile		
			30				35					40					
gat	tta	aac	aaa	ttc	aaa	gca	gca	gtc	ggg	tca	ttt	caa	gac	agg	gcc	677	
Asp	Leu	Asn	Lys	Phe	Lys	Ala	Ala	Val	Gly	Ser	Phe	Gln	Asp	Arg	Ala		
			45			50					55						
gac	ggc	aaa	tcc	gcc	gca	gag	ttg	aaa	aaa	gac	gcg	ggc	gat	cag	aag	725	
Asp	Gly	Lys	Ser	Ala	Ala	Glu	Leu	Lys	Lys	Asp	Ala	Gly	Asp	Gln	Lys		
					65					70					75		
gct	gaa	aaa	acg	gct	aaa	agc	caa	gat	gat	tta	tta	aag	aaa	atc	aat	773	
Ala	Glu	Lys	Thr	Ala	Lys	Ser	Gln	Asp	Asp	Leu	Leu	Lys	Lys	Ile	Asn		
				80					85					90			
gac	tat	att	gaa	aaa	aac	gaa	ctg	tca	agt	ttg	att	gcg	gcc	aag	cgt	821	
Asp	Tyr	Ile	Glu	Lys	Asn	Glu	Leu	Ser	Ser	Leu	Ile	Ala	Ala	Lys	Arg		
			95					100					105				
gac	gaa	cgg	ggc	gtc	att	ctc	gtc	ctt	cag	gaa	gcg	gtt	ttg	ttt	gat	869	
Asp	Glu	Arg	Gly	Val	Ile	Leu	Val	Leu	Gln	Glu	Ala	Val	Leu	Phe	Asp		
			110				115					120					
tca	ggg	aaa	gcg	gat	ctg	aaa	gac	caa	gct	cac	ccg	ctt	ttg	cat	aaa	917	
Ser	Gly	Lys	Ala	Asp	Leu	Lys	Asp	Gln	Ala	His		Pro	Leu	Leu	His	Lys	
			125			130					135						
atc	gcc	gtc	ctt	ctc	aaa	tcg	gtg	tcc	aac	ccg	att	cgt	gtg	gag	ggg	965	
Ile	Ala	Val	Leu	Leu	Lys	Ser	Val	Ser	Asn	Pro	Ile	Arg	Val	Glu	Gly		
					145					150					155		
cat	acg	gac	agc	cgc	ccg	att	tcg	act	tac	cgt	ttt	cca	tcc	aat	tgg	1013	
His	Thr	Asp	Ser	Arg	Pro	Ile	Ser	Thr	Tyr	Arg	Phe	Pro	Ser	Asn	Trp		
				160					165					170			
gag	ctt	tct	gca	gca	agg	gcg	agc	act	gtg	atc	ggc	tac	ttt	acg	tcg	1061	
Glu	Leu	Ser	Ala	Ala	Arg	Ala	Ser	Thr	Val	Ile	Gly	Tyr	Phe	Thr	Ser		
				175				180					185				
aag	gaa	aag	ctc	gac	tcg	tcg	cgt	ttt	ctt	gcc	atc	ggg	tat	gcg	gat	1109	
Lys	Glu	Lys	Leu	Asp	Ser	Ser	Arg	Phe	Leu	Ala	Ile	Gly	Tyr	Ala	Asp		
			190				195					200					
aca	aaa	ccg	gtc	agg	gac	aac	cgc	act	gag	agc	cat	atg	aag	gaa	aac	1157	
Thr	Lys	Pro	Val	Arg	Asp	Asn	Arg	Thr	Glu	Ser	His	Met	Lys	Glu	Asn		
			205			210					215						
agg	cgc	gtc	gag	att	gtc	atc	gca	aaa	caa	taatgagaag	aaagcaaggt					1207	
Arg	Arg	Val	Glu	Ile	Val	Ile	Ala	Lys	Gln								
			220			225											
cttgacaaaa	agcaaggcct	tttctgtgtg	ccgcaatttt	catattaagt	gggtacgctgg											1267	



gcagagcgaa tcggataaag ggctttggca acggtttgtg cgtttttttc cgttatttcg 1327  
gttttttcttg gaattggagg atacaaatct tccgggtcgg accagttggc aggaagccgg 1387  
acagatgcct gtttccccca ttttttcagc catttttcag gcattttctc ctctgggtcc 1447  
atccctttca tttcaagcca gattcttgcc catgccctcg gtacgacgcg ccaaagtgcg 1507  
tagccgcctc cgccgacagc gatccatctt ccgctgcaat aggtgtgtgc aagttcgtga 1567  
gcgagctttg gaatctcttc gtaaactctc atcgtcgtgc acaagtgtgt cagcggatcg 1627  
tagtaatgtg cgtcagctcc gttttgcgac aaaatgacat ccggtttgaa aaactcggct 1687

<210> 228

<211> 229

<212> PRT

<213> Bacillus licheniformis

<400> 228

Met Lys Leu Arg His Glu Arg Arg Lys Arg Glu Gln Gly Arg Lys Ser  
1 5 10 15

Pro Asn Trp Ile Ile Thr Phe Ser Asp Leu Ile Thr Leu Ile Leu Val  
20 25 30

Phe Phe Ile Leu Leu Phe Ser Met Ser Gln Ile Asp Leu Asn Lys Phe  
35 40 45

Lys Ala Ala Val Gly Ser Phe Gln Asp Arg Ala Asp Gly Lys Ser Ala  
50 55 60

Ala Glu Leu Lys Lys Asp Ala Gly Asp Gln Lys Ala Glu Lys Thr Ala  
65 70 75 80

Lys Ser Gln Asp Asp Leu Leu Lys Lys Ile Asn Asp Tyr Ile Glu Lys  
85 90 95

Asn Glu Leu Ser Ser Leu Ile Ala Ala Lys Arg Asp Glu Arg Gly Val  
100 105 110

Ile Leu Val Leu Gln Glu Ala Val Leu Phe Asp Ser Gly Lys Ala Asp  
115 120 125

Leu Lys Asp Gln Ala His Pro Leu Leu His Lys Ile Ala Val Leu Leu  
130 135 140

Lys Ser Val Ser Asn Pro Ile Arg Val Glu Gly His Thr Asp Ser Arg  
 145 150 155 160

Pro Ile Ser Thr Tyr Arg Phe Pro Ser Asn Trp Glu Leu Ser Ala Ala  
 165 170 175

Arg Ala Ser Thr Val Ile Gly Tyr Phe Thr Ser Lys Glu Lys Leu Asp  
 180 185 190

Ser Ser Arg Phe Leu Ala Ile Gly Tyr Ala Asp Thr Lys Pro Val Arg  
 195 200 205

Asp Asn Arg Thr Glu Ser His Met Lys Glu Asn Arg Arg Val Glu Ile  
 210 215 220

Val Ile Ala Lys Gln  
 225

<210> 229  
 <211> 2602  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(2102)

<400> 229  
 tatctgattg ccccaaaagc gatattcccg ttgattttga ttttgtcggg cgccgggggg 60  
 caggcgattc ttgaaacgtt tgtcgggtgc gccacaaaac ttgtcggctt tttctccgat 120  
 ttaaagaagt aaaccattcc aagcggatgg ttttattttt ttgtcaataa agtgatacaa 180  
 acagcagaga gaacgtgtca gttttatgaa cttttcacag cgatttttcc cggatgcggc 240  
 attttaggca gagaggaagc atctcattgt aaagatttca gtttttaaaa tttagaattg 300  
 agagaaaaag gatgtgcaaa gtccccggcc atttgtttta aaagcttgcg gtcactagta 360  
 ttcagacctc ccattttata cgaaaagagg aaatagatag attttttaag cgccaaaaaa 420  
 caagaaatat ggttgataga caatcgggtga atagtttatt tacaatcagt tcgtgctaca 480  
 ggcaaggaaa ggagtgaaaa atg gct gcg gaa aaa gta ttt tcg aaa aat aaa 533  
 Met Ala Ala Glu Lys Val Phe Ser Lys Asn Lys  
 1 5 10  
 atc att gga gga aaa aga atg tca tat atg aaa cgt tcc atc tct gtc 581

Ile	Ile	Gly	Gly	Lys	Arg	Met	Ser	Tyr	Met	Lys	Arg	Ser	Ile	Ser	Val	
			15					20					25			
ttc	atc	gcc	tgt	ttt	atg	gta	gcg	gcg	ctt	ggc	atc	agc	ggg	atc	att	629
Phe	Ile	Ala	Cys	Phe	Met	Val	Ala	Ala	Leu	Gly	Ile	Ser	Gly	Ile	Ile	
		30					35					40				
gca	ccg	aaa	gcg	gct	gcc	gct	tct	aaa	aca	ccc	ggt	gct	gta	aac	gga	677
Ala	Pro	Lys	Ala	Ala	Ala	Ala	Ser	Lys	Thr	Pro	Val	Ala	Val	Asn	Gly	
		45				50					55					
cag	ctt	acc	tta	aaa	ggg	acg	cag	ctc	gtc	aat	caa	aac	gga	aaa	gcg	725
Gln	Leu	Thr	Leu	Lys	Gly	Thr	Gln	Leu	Val	Asn	Gln	Asn	Gly	Lys	Ala	
60					65				70					75		
ggt	cag	ctg	aaa	gga	atc	agc	tcc	cac	ggg	cta	cag	tgg	tat	ggc	gat	773
Val	Gln	Leu	Lys	Gly	Ile	Ser	Ser	His	Gly	Leu	Gln	Trp	Tyr	Gly	Asp	
			80						85					90		
tat	gtc	aac	aaa	gac	tcg	tta	aaa	tgg	ctg	aga	gac	gac	tgg	ggc	atc	821
Tyr	Val	Asn	Lys	Asp	Ser	Leu	Lys	Trp	Leu	Arg	Asp	Asp	Trp	Gly	Ile	
			95					100					105			
aat	gtc	ttc	cgc	gcg	gcc	atg	tat	aca	gct	gaa	ggc	ggc	tat	att	gac	869
Asn	Val	Phe	Arg	Ala	Ala	Met	Tyr	Thr	Ala	Glu	Gly	Gly	Tyr	Ile	Asp	
		110					115					120				
aat	ccg	tcg	gtt	aaa	aac	aaa	gtg	aag	gaa	gcc	gtc	gaa	gcg	gca	aaa	917
Asn	Pro	Ser	Val	Lys	Asn	Lys	Val	Lys	Glu	Ala	Val	Glu	Ala	Ala	Lys	
		125				130					135					
gaa	ctc	gga	atc	tat	gtg	atc	att	gac	tgg	cac	ata	ctg	agc	gat	ggc	965
Glu	Leu	Gly	Ile	Tyr	Val	Ile	Ile	Asp	Trp	His	Ile	Leu	Ser	Asp	Gly	
140					145				150					155		
aat	cca	aac	caa	aac	aaa	gcg	aaa	gca	aaa	gaa	ttt	ttt	aac	gaa	atg	1013
Asn	Pro	Asn	Gln	Asn	Lys	Ala	Lys	Ala	Lys	Glu	Phe	Phe	Asn	Glu	Met	
			160					165						170		
tca	aga	ctt	tat	ggc	aag	acg	cca	aac	gtc	att	ttt	gaa	att	gcc	aac	1061
Ser	Arg	Leu	Tyr	Gly	Lys	Thr	Pro	Asn	Val	Ile	Phe	Glu	Ile	Ala	Asn	
			175					180					185			
gag	ccg	aac	ggc	gat	gtc	aac	tgg	aat	cgc	gac	att	aaa	cct	tac	gcc	1109
Glu	Pro	Asn	Gly	Asp	Val	Asn	Trp	Asn	Arg	Asp	Ile	Lys	Pro	Tyr	Ala	
		190					195					200				
gaa	gaa	atc	ctg	tcc	gtg	att	cgc	aaa	aac	tct	ccg	aaa	aat	att	gtg	1157
Glu	Glu	Ile	Leu	Ser	Val	Ile	Arg	Lys	Asn	Ser	Pro	Lys	Asn	Ile	Val	
		205				210					215					
att	gtc	gga	aca	ggc	acc	tgg	agc	cag	gat	gtc	aat	gat	gcg	gcg	gac	1205
Ile	Val	Gly	Thr	Gly	Thr	Trp	Ser	Gln	Asp	Val	Asn	Asp	Ala	Ala	Asp	
220					225					230					235	
aat	cag	ctg	aaa	gac	ggc	aat	gtc	atg	tac	gcg	ctc	cat	ttt	tat	gcg	1253
Asn	Gln	Leu	Lys	Asp	Gly	Asn	Val	Met	Tyr	Ala	Leu	His	Phe	Tyr	Ala	

240	245	250	
ggc acg cac ggt cag tct ttg cgg gat	aaa gcc gat tat gca ctc agc	1301	
Gly Thr His Gly Gln Ser Leu Arg Asp	Lys Ala Asp Tyr Ala Leu Ser		
255	260	265	
aaa gga gcg ccg att ttc gtc aca gaa tgg gga acg agc gat gct tca	1349		
Lys Gly Ala Pro Ile Phe Val Thr Glu Trp Gly Thr Ser Asp Ala Ser			
270	275	280	
gga aac ggc ggg gtc tac ctt gac caa tcc agg gag tgg ctg aaa tat	1397		
Gly Asn Gly Gly Val Tyr Leu Asp Gln Ser Arg Glu Trp Leu Lys Tyr			
285	290	295	
tta gac agc aaa aaa atc agc tgg gta aac tgg aac tta tcc gac aaa	1445		
Leu Asp Ser Lys Lys Ile Ser Trp Val Asn Trp Asn Leu Ser Asp Lys			
300	305	310	315
caa gag tcg tca gca gct tta aac cca ggc gcc tct aaa aac gga gga	1493		
Gln Glu Ser Ser Ala Ala Leu Asn Pro Gly Ala Ser Lys Asn Gly Gly			
320	325	330	
tgg tcg caa tcc gac ttg tcc cca tca ggc aaa ttc gtc agg gat aac	1541		
Trp Ser Gln Ser Asp Leu Ser Pro Ser Gly Lys Phe Val Arg Asp Asn			
335	340	345	
atc cgc agc ggg tca aac ggt tcg tca gga gac tct gga tcg aat tcg	1589		
Ile Arg Ser Gly Ser Asn Gly Ser Ser Gly Asp Ser Gly Ser Asn Ser			
350	355	360	
aaa ggg tca gat caa aaa gac caa aaa aag gat cag gat aaa cca ggt	1637		
Lys Gly Ser Asp Gln Lys Asp Gln Lys Lys Asp Gln Asp Lys Pro Gly			
365	370	375	
caa gac agc ggc gct gca gcc aac acg ata gca gta caa tac aga gcg	1685		
Gln Asp Ser Gly Ala Ala Ala Asn Thr Ile Ala Val Gln Tyr Arg Ala			
380	385	390	395
ggg gac aac aat gta aac ggc aac caa atc cgc cct cag ctc aac att	1733		
Gly Asp Asn Asn Val Asn Gly Asn Gln Ile Arg Pro Gln Leu Asn Ile			
400	405	410	
aaa aac aac agc aaa aaa acc gtg tct tta aat cga atc act gtc cgc	1781		
Lys Asn Asn Ser Lys Lys Thr Val Ser Leu Asn Arg Ile Thr Val Arg			
415	420	425	
tac tgg tat aaa acg aat cgc aaa gga caa aat ttt gac tgc gac tat	1829		
Tyr Trp Tyr Lys Thr Asn Arg Lys Gly Gln Asn Phe Asp Cys Asp Tyr			
430	435	440	
gcc caa atc ggc tgc agc aaa atc acg cac aaa ttc gtt caa tta aaa	1877		
Ala Gln Ile Gly Cys Ser Lys Ile Thr His Lys Phe Val Gln Leu Lys			
445	450	455	
aaa gcg gta aac gga gca gac acg tat ctt gaa gta gga ttt aaa aat	1925		
Lys Ala Val Asn Gly Ala Asp Thr Tyr Leu Glu Val Gly Phe Lys Asn			
460	465	470	475

ggt aca ttg gcg ccg ggg gct gat act ggc gaa atc cag atc cgt ctt 1973  
 Gly Thr Leu Ala Pro Gly Ala Asp Thr Gly Glu Ile Gln Ile Arg Leu  
                     480                    485                    490

cac aat gac ggc tgg agc aat tat gcc caa agc ggc gac tat tca ttt 2021  
 His Asn Asp Gly Trp Ser Asn Tyr Ala Gln Ser Gly Asp Tyr Ser Phe  
                     495                    500                    505

ttt aat tca aac acg ttt aaa aat acg aaa aaa atc acg ttg tat gag 2069  
 Phe Asn Ser Asn Thr Phe Lys Asn Thr Lys Lys Ile Thr Leu Tyr Glu  
                     510                    515                    520

aac gga aag ctg att tgg ggc act gaa cct aaa taacggcact ttgacggaca 2122  
 Asn Gly Lys Leu Ile Trp Gly Thr Glu Pro Lys  
                     525                    530

ccggatatgg tgtccgtttt cgtatatatt ataatggaag gaatgaggaa tattttttgta 2182

aacatgaaag gagatggatg tatgaatgaa acattgcagc aatacatgat gcttgtcaag 2242

gaacactatg acacgatcaa tggaccggat tacacaggca aggaggaaga cattgaaaag 2302

agaaaggaac aaatcgagct ttacgccaaa acgcttcagc aaggcttttc aacagatgat 2362

gactatgatg aattcgcaga tgccgtgatt aaatgcgcat acggagatct gacggtggaa 2422

gaattagaaa cggtttatcg ggaattaacg tctccataat caataaaata agggggagga 2482

gaagcatgaa agacatgatc atgaagacag accggcttat tttgcgaaaa atgaggcgcg 2542

atgacgccga aaacctgctc gaaatctttt ctgaccgat agcaatggaa tattatccat 2602

<210> 230

<211> 534

<212> PRT

<213> Bacillus licheniformis

<400> 230

Met Ala Ala Glu Lys Val Phe Ser Lys Asn Lys Ile Ile Gly Gly Lys  
 1                    5                    10                    15

Arg Met Ser Tyr Met Lys Arg Ser Ile Ser Val Phe Ile Ala Cys Phe  
                     20                    25                    30

Met Val Ala Ala Leu Gly Ile Ser Gly Ile Ile Ala Pro Lys Ala Ala  
                     35                    40                    45

Ala Ala Ser Lys Thr Pro Val Ala Val Asn Gly Gln Leu Thr Leu Lys  
                     50                    55                    60

Gly Thr Gln Leu Val Asn Gln Asn Gly Lys Ala Val Gln Leu Lys Gly  
65 70 75 80

Ile Ser Ser His Gly Leu Gln Trp Tyr Gly Asp Tyr Val Asn Lys Asp  
85 90 95

Ser Leu Lys Trp Leu Arg Asp Asp Trp Gly Ile Asn Val Phe Arg Ala  
100 105 110

Ala Met Tyr Thr Ala Glu Gly Gly Tyr Ile Asp Asn Pro Ser Val Lys  
115 120 125

Asn Lys Val Lys Glu Ala Val Glu Ala Ala Lys Glu Leu Gly Ile Tyr  
130 135 140

Val Ile Ile Asp Trp His Ile Leu Ser Asp Gly Asn Pro Asn Gln Asn  
145 150 155 160

Lys Ala Lys Ala Lys Glu Phe Phe Asn Glu Met Ser Arg Leu Tyr Gly  
165 170 175

Lys Thr Pro Asn Val Ile Phe Glu Ile Ala Asn Glu Pro Asn Gly Asp  
180 185 190

Val Asn Trp Asn Arg Asp Ile Lys Pro Tyr Ala Glu Glu Ile Leu Ser  
195 200 205

Val Ile Arg Lys Asn Ser Pro Lys Asn Ile Val Ile Val Gly Thr Gly  
210 215 220

Thr Trp Ser Gln Asp Val Asn Asp Ala Ala Asp Asn Gln Leu Lys Asp  
225 230 235 240

Gly Asn Val Met Tyr Ala Leu His Phe Tyr Ala Gly Thr His Gly Gln  
245 250 255

Ser Leu Arg Asp Lys Ala Asp Tyr Ala Leu Ser Lys Gly Ala Pro Ile  
260 265 270

Phe Val Thr Glu Trp Gly Thr Ser Asp Ala Ser Gly Asn Gly Gly Val  
275 280 285

Tyr Leu Asp Gln Ser Arg Glu Trp Leu Lys Tyr Leu Asp Ser Lys Lys

290		295		300
Ile Ser Trp Val Asn Trp Asn Leu Ser Asp Lys Gln Glu Ser Ser Ala				
305		310		315 320
Ala Leu Asn Pro Gly Ala Ser Lys Asn Gly Gly Trp Ser Gln Ser Asp				
		325		330 335
Leu Ser Pro Ser Gly Lys Phe Val Arg Asp Asn Ile Arg Ser Gly Ser				
		340		345 350
Asn Gly Ser Ser Gly Asp Ser Gly Ser Asn Ser Lys Gly Ser Asp Gln				
		355		360 365
Lys Asp Gln Lys Lys Asp Gln Asp Lys Pro Gly Gln Asp Ser Gly Ala				
		370		375 380
Ala Ala Asn Thr Ile Ala Val Gln Tyr Arg Ala Gly Asp Asn Asn Val				
385		390		395 400
Asn Gly Asn Gln Ile Arg Pro Gln Leu Asn Ile Lys Asn Asn Ser Lys				
		405		410 415
Lys Thr Val Ser Leu Asn Arg Ile Thr Val Arg Tyr Trp Tyr Lys Thr				
		420		425 430
Asn Arg Lys Gly Gln Asn Phe Asp Cys Asp Tyr Ala Gln Ile Gly Cys				
		435		440 445
Ser Lys Ile Thr His Lys Phe Val Gln Leu Lys Lys Ala Val Asn Gly				
		450		455 460
Ala Asp Thr Tyr Leu Glu Val Gly Phe Lys Asn Gly Thr Leu Ala Pro				
465		470		475 480
Gly Ala Asp Thr Gly Glu Ile Gln Ile Arg Leu His Asn Asp Gly Trp				
		485		490 495
Ser Asn Tyr Ala Gln Ser Gly Asp Tyr Ser Phe Phe Asn Ser Asn Thr				
		500		505 510
Phe Lys Asn Thr Lys Lys Ile Thr Leu Tyr Glu Asn Gly Lys Leu Ile				
		515		520 525

Trp Gly Thr Glu Pro Lys  
530

<210> 231  
<211> 2437  
<212> DNA  
<213> Bacillus licheniformis

<220>  
<221> CDS  
<222> (501)..(1937)

<400> 231  
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taatcgggaac cgtgctctct tctctgacct ttttgcatat cgtgacccca tccatcgacg 120  
gcagcatgat atcgatgatc agcaaatccc aatcacctga tttaaaacgg ttatatacctt 180  
cgagtccgtc atggacgaac tctgtttcaa atccttcttt tgcaaaaaaac atctctgtca 240  
tagtacatac gcttaaatta tcttcaatca ttaatatatt catcgtaaaa gtgcctccgc 300  
tagacaaacg ttagattcat ttacatagg gccagccat ttctcaattc cattctgaac 360  
atttaaaggt ctggcaacag tttggtcata atttattcat aagtagcggc taagatgaaa 420  
tcaagcataa ggcaaaagtc ctgctgccgt tagatttggc agcaataata aatgaaatag 480  
atacggagga atcacgcgtt atg aat ttt ttc aaa cga gcc ttt tgg agc atg 533  
Met Asn Phe Phe Lys Arg Ala Phe Trp Ser Met  
1 5 10  
aaa gcg aaa aaa gga aaa aca ctt tta caa ttg ttt gtt ttc acg atg 581  
Lys Ala Lys Lys Gly Lys Thr Leu Leu Gln Leu Phe Val Phe Thr Met  
15 20 25  
att tgc gtg ctc gtg ctg aca gga att acg atc cag tcg gca gcc gtg 629  
Ile Cys Val Leu Val Leu Thr Gly Ile Thr Ile Gln Ser Ala Ala Val  
30 35 40  
aaa tcg agc gaa ctg gcg agg gaa cag ctc gga ggc agc gtc acg ctc 677  
Lys Ser Ser Glu Leu Ala Arg Glu Gln Leu Gly Gly Ser Val Thr Leu  
45 50 55  
aaa gtt gac agg gaa aaa atg atg aaa gaa cag cag gac tca gga gac 725  
Lys Val Asp Arg Glu Lys Met Met Lys Glu Gln Gln Asp Ser Gly Asp  
60 65 70 75  
cgg aaa agg ttt gaa tcg acc ccc gtt tct ctc aaa tca gcc gag aaa 773  
Arg Lys Arg Phe Glu Ser Thr Pro Val Ser Leu Lys Ser Ala Glu Lys  
80 85 90



ctt gcg agc ctt tac cat gtc aaa agc tat aac ttc atc tcc tca aca	821
Leu Ala Ser Leu Tyr His Val Lys Ser Tyr Asn Phe Ile Ser Ser Thr	
95 100 105	
tct gct tta gcg gac aac ttc gat ccg atc gaa agc ggt gac gag gat	869
Ser Ala Leu Ala Asp Asn Phe Asp Pro Ile Glu Ser Gly Asp Glu Asp	
110 115 120	
tca acg gac tca aac agc gat cag ccg gcc gga tcg ggc ggc aat gaa	917
Ser Thr Asp Ser Asn Ser Asp Gln Pro Ala Gly Ser Gly Gly Asn Glu	
125 130 135	
cag ggc ggc cgg caa atg atg cag gct gac gta tca atc gaa ggt gtg	965
Gln Gly Gly Arg Gln Met Met Gln Ala Asp Val Ser Ile Glu Gly Val	
140 145 150 155	
aca agc aca gcc ctc gtc gac gaa ttt gcc gac ggg acg tcc aag atc	1013
Thr Ser Thr Ala Leu Val Asp Glu Phe Ala Asp Gly Thr Ser Lys Ile	
160 165 170	
acg gaa ggc cgt gct tta aca aag gat gat gtg aat gaa aaa gtc gcc	1061
Thr Glu Gly Arg Ala Leu Thr Lys Asp Asp Val Asn Glu Lys Val Ala	
175 180 185	
gtg att gaa gaa acg ctt gcc gaa gaa aac gag ctg aag gtc ggc gat	1109
Val Ile Glu Glu Thr Leu Ala Glu Glu Asn Glu Leu Lys Val Gly Asp	
190 195 200	
acg atc aaa gtc aaa gcg agc agc gat gaa gat gca acg atc aat tta	1157
Thr Ile Lys Val Lys Ala Ser Ser Asp Glu Asp Ala Thr Ile Asn Leu	
205 210 215	
aaa atc gtc gga atc tat aaa acg act tca tcc gga gac aat caa gcg	1205
Lys Ile Val Gly Ile Tyr Lys Thr Thr Ser Ser Gly Asp Asn Gln Ala	
220 225 230 235	
caa aac ttc gcc ttt tta aac cct tat aac aaa atc tat aca cca tat	1253
Gln Asn Phe Ala Phe Leu Asn Pro Tyr Asn Lys Ile Tyr Thr Pro Tyr	
240 245 250	
acg gcg gca tcg gcc tta aaa ggc gac gat tat caa aac gcg ata gat	1301
Thr Ala Ala Ser Ala Leu Lys Gly Asp Asp Tyr Gln Asn Ala Ile Asp	
255 260 265	
gaa gcg gtc tac aat atg gac gac gcc tcc aac atc gac gct ttc att	1349
Glu Ala Val Tyr Asn Met Asp Asp Ala Ser Asn Ile Asp Ala Phe Ile	
270 275 280	
gcg gct gcc aag aaa aca ggc att gat ttg gat aca ttc aca ttg gac	1397
Ala Ala Ala Lys Lys Thr Gly Ile Asp Leu Asp Thr Phe Thr Leu Asp	
285 290 295	
gcc aat gac cag ttg tac cag cag atg gtc ggc ccg att gaa aat gtc	1445
Ala Asn Asp Gln Leu Tyr Gln Gln Met Val Gly Pro Ile Glu Asn Val	
300 305 310 315	
gcc tcc ttc tcg aaa aat gtc gtc tat ctt gtc acg gtc gcc ggg gcg	1493

Ala Ser Phe Ser Lys Asn Val Val Tyr Leu Val Thr Val Ala Gly Ala	
320 325 330	
gtg att ctc gga ctg atc gtc atg atg tca atc agg gag aga aaa tac	1541
Val Ile Leu Gly Leu Ile Val Met Met Ser Ile Arg Glu Arg Lys Tyr	
335 340 345	
gaa atg ggt gtt ctg atg gcg atc ggc gaa aaa cgc cgg aaa ctc atc	1589
Glu Met Gly Val Leu Met Ala Ile Gly Glu Lys Arg Arg Lys Leu Ile	
350 355 360	
gga cag ttt tta acc gaa atc tta atg atc gca gtg ctt gcc atc ggg	1637
Gly Gln Phe Leu Thr Glu Ile Leu Met Ile Ala Val Leu Ala Ile Gly	
365 370 375	
atc tca gca tta acc ggc agc ctg att gca aag caa atc ggg aac cag	1685
Ile Ser Ala Leu Thr Gly Ser Leu Ile Ala Lys Gln Ile Gly Asn Gln	
380 385 390 395	
ctc ttg agc cag caa atc gaa caa acg tca gct agc cag tct gca ggc	1733
Leu Leu Ser Gln Gln Ile Glu Gln Thr Ser Ala Ser Gln Ser Ala Gly	
400 405 410	
gga atg atg ggc cca ggc ggc gga ggc ttc ttc gga caa agt act gct	1781
Gly Met Met Gly Pro Gly Gly Gly Gly Phe Phe Gly Gln Ser Thr Ala	
415 420 425	
caa gtc tca gcc att gat cag ctc gac att caa gta tcc ttc ggg aac	1829
Gln Val Ser Ala Ile Asp Gln Leu Asp Ile Gln Val Ser Phe Gly Asn	
430 435 440	
tta atg gca ctt ggc gga atc ggc ctt tta att gcg atg ttc gcg aca	1877
Leu Met Ala Leu Gly Gly Ile Gly Leu Leu Ile Ala Met Phe Ala Thr	
445 450 455	
ctc ctt ccg tcc ata tct gtt tta agg ctc cat ccg aaa acg att tta	1925
Leu Leu Pro Ser Ile Ser Val Leu Arg Leu His Pro Lys Thr Ile Leu	
460 465 470 475	
aca aaa caa gaa tagaaagaag tgaagattat gggcagtatt ttagaatttc	1977
Thr Lys Gln Glu	
agaatgtcgg ctattggtat aaaaatcagg atcagcctct attcgaggat atcagcattc	2037
aattcagcca aggactctta tatacgattg tcgggacttc cggttccggc aaaaccacct	2097
ttttatcggt ggcgggcgga cttgacgcgc caaaagaggg gaacatcctc tacaaaggag	2157
aaaacatttc aaaaatcgga ctgaccagct tccgcaatca atatgtatcg atcgtttttc	2217
agtcctataa cctgctgccg tatatgacgg ctctccaaaa tatcacgtcg gccatggaaa	2277
tcaccggatc tcaggtcaaa aacaaggaac aatacgcttt ggagatgctc gaaaaggctc	2337
gcacgcggca aaagcaggcc agacagaaag tattgacatt aagcggcggc cagcagcagc	2397

gtgtctccat catcagagcg ttctgctgtg acacggattt

2437

<210> 232

<211> 479

<212> PRT

<213> Bacillus licheniformis

<400> 232

Met Asn Phe Phe Lys Arg Ala Phe Trp Ser Met Lys Ala Lys Lys Gly  
1 5 10 15

Lys Thr Leu Leu Gln Leu Phe Val Phe Thr Met Ile Cys Val Leu Val  
20 25 30

Leu Thr Gly Ile Thr Ile Gln Ser Ala Ala Val Lys Ser Ser Glu Leu  
35 40 45

Ala Arg Glu Gln Leu Gly Gly Ser Val Thr Leu Lys Val Asp Arg Glu  
50 55 60

Lys Met Met Lys Glu Gln Gln Asp Ser Gly Asp Arg Lys Arg Phe Glu  
65 70 75 80

Ser Thr Pro Val Ser Leu Lys Ser Ala Glu Lys Leu Ala Ser Leu Tyr  
85 90 95

His Val Lys Ser Tyr Asn Phe Ile Ser Ser Thr Ser Ala Leu Ala Asp  
100 105 110

Asn Phe Asp Pro Ile Glu Ser Gly Asp Glu Asp Ser Thr Asp Ser Asn  
115 120 125

Ser Asp Gln Pro Ala Gly Ser Gly Gly Asn Glu Gln Gly Gly Arg Gln  
130 135 140

Met Met Gln Ala Asp Val Ser Ile Glu Gly Val Thr Ser Thr Ala Leu  
145 150 155 160

Val Asp Glu Phe Ala Asp Gly Thr Ser Lys Ile Thr Glu Gly Arg Ala  
165 170 175

Leu Thr Lys Asp Asp Val Asn Glu Lys Val Ala Val Ile Glu Glu Thr  
180 185 190

Leu Ala Glu Glu Asn Glu Leu Lys Val Gly Asp Thr Ile Lys Val Lys  
 195 200 205

Ala Ser Ser Asp Glu Asp Ala Thr Ile Asn Leu Lys Ile Val Gly Ile  
 210 215 220

Tyr Lys Thr Thr Ser Ser Gly Asp Asn Gln Ala Gln Asn Phe Ala Phe  
 225 230 235 240

Leu Asn Pro Tyr Asn Lys Ile Tyr Thr Pro Tyr Thr Ala Ala Ser Ala  
 245 250 255

Leu Lys Gly Asp Asp Tyr Gln Asn Ala Ile Asp Glu Ala Val Tyr Asn  
 260 265 270

Met Asp Asp Ala Ser Asn Ile Asp Ala Phe Ile Ala Ala Ala Lys Lys  
 275 280 285

Thr Gly Ile Asp Leu Asp Thr Phe Thr Leu Asp Ala Asn Asp Gln Leu  
 290 295 300

Tyr Gln Gln Met Val Gly Pro Ile Glu Asn Val Ala Ser Phe Ser Lys  
 305 310 315 320

Asn Val Val Tyr Leu Val Thr Val Ala Gly Ala Val Ile Leu Gly Leu  
 325 330 335

Ile Val Met Met Ser Ile Arg Glu Arg Lys Tyr Glu Met Gly Val Leu  
 340 345 350

Met Ala Ile Gly Glu Lys Arg Arg Lys Leu Ile Gly Gln Phe Leu Thr  
 355 360 365

Glu Ile Leu Met Ile Ala Val Leu Ala Ile Gly Ile Ser Ala Leu Thr  
 370 375 380

Gly Ser Leu Ile Ala Lys Gln Ile Gly Asn Gln Leu Leu Ser Gln Gln  
 385 390 395 400

Ile Glu Gln Thr Ser Ala Ser Gln Ser Ala Gly Gly Met Met Gly Pro  
 405 410 415

Gly Gly Gly Gly Phe Phe Gly Gln Ser Thr Ala Gln Val Ser Ala Ile  
 420 425 430

Asp Gln Leu Asp Ile Gln Val Ser Phe Gly Asn Leu Met Ala Leu Gly  
 435 440 445

Gly Ile Gly Leu Leu Ile Ala Met Phe Ala Thr Leu Leu Pro Ser Ile  
 450 455 460

Ser Val Leu Arg Leu His Pro Lys Thr Ile Leu Thr Lys Gln Glu  
 465 470 475

<210> 233  
 <211> 1789  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1289)

<400> 233  
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 cgatcgctcg aaacgcggca gagcatgctt ccgccgtcat tatggcctat aaggacaaaa 180  
 tggatgtcgc ggttgaaatt gcgatcggat caacgcttca gatcgcgatg tttgtcgccc 240  
 ctgttcttgt catcagctct ttgttttttc caacgagcat gccgctcgtc tttaccttgc 300  
 cggagctggg cgccatgggt tccgccgtcc ttttgatgat catcatttcc aacgacgggg 360  
 acacgaactg gtttgaaggc gcgacattgc tggccgctta tatcatcatg ggaatcggtt 420  
 ttttccttct ttaaaaaaat cgggataaac agagagcatc cggaaaacaa taaggaaaaa 480  
 gaaacagaaa gagtgatagt atg aaa aag ctt ttg tgt ttt acg ctg act gcg 533  
 Met Lys Lys Leu Leu Cys Phe Thr Leu Thr Ala  
 1 5 10  
 ttt tta tcc ttt agt ttt ttc gct gta cag gaa gct gac gca gcc aag 581  
 Phe Leu Ser Phe Ser Phe Phe Ala Val Gln Glu Ala Asp Ala Ala Lys  
 15 20 25  
 ccg atc aag att cca agc tct gtc acg aat att tcc aaa gag aac aca 629  
 Pro Ile Lys Ile Pro Ser Ser Val Thr Asn Ile Ser Lys Glu Asn Thr  
 30 35 40  
 tac cct aac gcc tct cag gat cag ccg agg ctg cag ccg agc gaa tta 677  
 Tyr Pro Asn Ala Ser Gln Asp Gln Pro Arg Leu Gln Pro Ser Glu Leu

45	50	55	
gcc gaa gag ctg ctg aaa aca acc gat att gcg att gaa aat ccg cat			725
Ala Glu Glu Leu Leu Lys Thr Thr Asp Ile Ala Ile Glu Asn Pro His			
60	65	70	75
ctg att aaa atg ctg aat gag tca agc att tcc gcc aca ccg ctg gca			773
Leu Ile Lys Met Leu Asn Glu Ser Ser Ile Ser Gly Thr Pro Leu Ala			
	80	85	90
atc gcc tat cgg gcg acg att tat ttg gcc aga tgg gcg cta ggt tac			821
Ile Gly Tyr Arg Ala Thr Ile Tyr Leu Gly Arg Trp Ala Leu Gly Tyr			
	95	100	105
acc tcg aat gaa acc gtt gcg aac tgg gaa tac cgc aaa atc aac aca			869
Thr Ser Asn Glu Thr Val Ala Asn Trp Glu Tyr Arg Lys Ile Asn Thr			
	110	115	120
aac cgc ttt gac aac cgg gcc ggg aaa gca cct gca gaa ctc acg tat			917
Asn Arg Phe Asp Asn Arg Gly Gly Lys Ala Pro Ala Glu Leu Thr Tyr			
	125	130	135
tcc cag gaa cag acg agc aaa atc aaa gcc gcc tta aca gcg aaa gtt			965
Ser Gln Glu Gln Thr Ser Lys Ile Lys Gly Gly Leu Thr Ala Lys Val			
140	145	150	155
cca aag gcg gaa gat gtc aaa aat atg atg atg ctc aaa gcc atg gaa			1013
Pro Lys Ala Glu Asp Val Lys Asn Met Met Met Leu Lys Ala Met Glu			
	160	165	170
aaa aca aag ctg ccg ctc gcc ttt gaa aca gtg gtc gcc tcc ggt aca			1061
Lys Thr Lys Leu Pro Leu Ala Phe Glu Thr Val Val Gly Ser Gly Thr			
	175	180	185
aaa cgc gat cag att tat aaa gtg cag ccg aaa aaa ctg gga aat tta			1109
Lys Arg Asp Gln Ile Tyr Lys Val Gln Pro Lys Lys Leu Gly Asn Leu			
	190	195	200
cac gcc tat gca cct gcc gtc aat gaa aaa gga aaa gtc acc tac gcc			1157
His Ala Tyr Ala Pro Ala Val Asn Glu Lys Gly Lys Val Thr Tyr Gly			
205	210	215	
gaa gtg tac atc gta tta aaa gcc aac aaa aga aag cta gtc gtc aaa			1205
Glu Val Tyr Ile Val Leu Lys Gly Asn Lys Arg Lys Leu Val Val Lys			
220	225	230	235
aat atc acc tcg caa gga atc gcc gct tgg att cct gta cag gat cac			1253
Asn Ile Thr Ser Gln Gly Ile Gly Ala Trp Ile Pro Val Gln Asp His			
	240	245	250
ctg aca ttc gcc ttt cag ctc agc cat cag ccg aaa taaaaaagca			1299
Leu Thr Phe Gly Phe Gln Leu Ser His Gln Pro Lys			
	255	260	
agcctttgcg gcttgctttt ttcatactct tgctgttctg gaagtaaaat caacatcttg			1359
ataatagctg tttttgacga gcacattcgg tccgaggcac cggacgtgcg ggcagtggca			1419

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 cggcagagtg ccgaacagca tccacgtatt ttcgtcgcga atgtcaagaa ggcgggtggat 1719  
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Ser Ser Val Thr Asn Ile Ser Lys Glu Asn Thr Tyr Pro Asn Ala Ser  
 35 40 45

Gln Asp Gln Pro Arg Leu Gln Pro Ser Glu Leu Ala Glu Glu Leu Leu  
 50 55 60

Lys Thr Thr Asp Ile Ala Ile Glu Asn Pro His Leu Ile Lys Met Leu  
 65 70 75 80

Asn Glu Ser Ser Ile Ser Gly Thr Pro Leu Ala Ile Gly Tyr Arg Ala  
 85 90 95

Thr Ile Tyr Leu Gly Arg Trp Ala Leu Gly Tyr Thr Ser Asn Glu Thr  
 100 105 110

Val Ala Asn Trp Glu Tyr Arg Lys Ile Asn Thr Asn Arg Phe Asp Asn  
 115 120 125

Arg Gly Gly Lys Ala Pro Ala Glu Leu Thr Tyr Ser Gln Glu Gln Thr  
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Ser Lys Ile Lys Gly Gly Leu Thr Ala Lys Val Pro Lys Ala Glu Asp  
 145 150 155 160

Val Lys Asn Met Met Met Leu Lys Ala Met Glu Lys Thr Lys Leu Pro  
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Leu Ala Phe Glu Thr Val Val Gly Ser Gly Thr Lys Arg Asp Gln Ile  
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Tyr Lys Val Gln Pro Lys Lys Leu Gly Asn Leu His Ala Tyr Ala Pro  
 195 200 205

Ala Val Asn Glu Lys Gly Lys Val Thr Tyr Gly Glu Val Tyr Ile Val  
 210 215 220

Leu Lys Gly Asn Lys Arg Lys Leu Val Val Lys Asn Ile Thr Ser Gln  
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Gln Leu Ser His Gln Pro Lys  
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 tttgtccgct atttttcaca ggctgcgctg atcgggtctcg ttcgcccttt gacgacggcc 180  
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 ccattttatg gtgtcagttt gtttgctctt gtatcgatgt ttatcgaca tcgctgtttt 300  
 ttgcgtctgg aaggctagct gaactgtgca aaaatgagaa aatcgggcaa aaaaatatca 360



attggaagg ctgaaccgct taagaccgga cttgaacaca tcttttcct tcggcaaaaa 420

agtgcaattg aataaaaaatg gaagccgtaa tagaatccct tttgagtaag cgtttataaaa 480

aatggtgaag ggagaagatg atg aaa aaa gga aag aaa agg tgg aag aac ctg 533  
Met Lys Lys Gly Lys Lys Arg Trp Lys Asn Leu  
1 5 10

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Leu Ala Ala Ser Ser Leu Leu Leu Ile Thr Leu Val Thr Gly Phe Ser  
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gag caa gct gag gca gac ggg cgg acg gct gcg cag gca agg caa atg 629  
Glu Gln Ala Glu Ala Asp Gly Arg Thr Ala Ala Gln Ala Arg Gln Met  
30 35 40

gaa tcg ctt aac agg ggg ctt gtc gct gtt aaa acg ggg aac ggt gtc 677  
Glu Ser Leu Asn Arg Gly Leu Val Ala Val Lys Thr Gly Asn Gly Val  
45 50 55

ttt gtc agc tgg cgg ctt ctg gga acc gag ccg tct tct gtt tca ttt 725  
Phe Val Ser Trp Arg Leu Leu Gly Thr Glu Pro Ser Ser Val Ser Phe  
60 65 70 75

aat gtg tat cga aac gga aag aag ctg aac ggt tct ccg att aca tcg 773  
Asn Val Tyr Arg Asn Gly Lys Lys Leu Asn Gly Ser Pro Ile Thr Ser  
80 85 90

agc aca aac tat cag gat gca ggc ggg gat ttg aac gcc gtt tac cag 821  
Ser Thr Asn Tyr Gln Asp Ala Gly Gly Asp Leu Asn Ala Val Tyr Gln  
95 100 105

gtg cgc gcc gtt ttg aac ggc agg gag cag gct cct tct gaa tcc gtc 869  
Val Arg Ala Val Leu Asn Gly Arg Glu Gln Ala Pro Ser Glu Ser Val  
110 115 120

ggc gta ttg aat aaa caa tat aaa tct gtt ccg ctg caa aaa ccg gcc 917  
Gly Val Leu Asn Lys Gln Tyr Lys Ser Val Pro Leu Gln Lys Pro Ala  
125 130 135

gga gga aaa acg cct gat ggg gtg tca tac aca tac agc gcc aat gat 965  
Gly Gly Lys Thr Pro Asp Gly Val Ser Tyr Thr Tyr Ser Ala Asn Asp  
140 145 150 155

gcg agc gta ggc gac ctt gat gga gac ggc caa tat gaa atc att ctc 1013  
Ala Ser Val Gly Asp Leu Asp Gly Asp Gly Gln Tyr Glu Ile Ile Leu  
160 165 170

aag tgg gat cct tcc aat tca aag gat aat tca cag gac gga tac acg 1061  
Lys Trp Asp Pro Ser Asn Ser Lys Asp Asn Ser Gln Asp Gly Tyr Thr  
175 180 185

gga gat gtg ctg att gac gca tac aag ctt gac ggc acc atg atg tgg 1109  
Gly Asp Val Leu Ile Asp Ala Tyr Lys Leu Asp Gly Thr Met Met Trp  
190 195 200

aga atc aac ctt ggc aaa aat att cgc gcc ggc gcc cat tat acg cag 1157

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Phe	Leu	Val	Tyr	Asp	Phe	Asp	Gly	Asp	Gly	Lys	Ala	Glu	Ile	Ala	Met	
220					225					230					235	
aag	acg	gca	gac	ggg	acg	aag	gac	ggc	aaa	ggg	aag	gtg	atc	ggc	aat	1253
Lys	Thr	Ala	Asp	Gly	Thr	Lys	Asp	Gly	Lys	Gly	Lys	Val	Ile	Gly	Asn	
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Ala	Asn	Ala	Asp	Tyr	Arg	Asn	Ala	Gln	Gly	Arg	Ile	Leu	Ser	Gly	Pro	
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gag	tat	ttg	acg	gtt	ttt	aaa	ggc	gat	aca	ggc	gct	gag	ctt	aca	acg	1349
Glu	Tyr	Leu	Thr	Val	Phe	Lys	Gly	Asp	Thr	Gly	Ala	Glu	Leu	Thr	Thr	
		270					275					280				
gtc	aac	tac	gaa	cct	gcc	cgg	gga	aat	gta	gcc	gat	tgg	gga	gac	agc	1397
Val	Asn	Tyr	Glu	Pro	Ala	Arg	Gly	Asn	Val	Ala	Asp	Trp	Gly	Asp	Ser	
		285					290				295					
tac	ggc	aac	agg	gtt	gac	cgc	ttt	ctg	gcc	ggt	gtc	gca	tac	ctt	gac	1445
Tyr	Gly	Asn	Arg	Val	Asp	Arg	Phe	Leu	Ala	Gly	Val	Ala	Tyr	Leu	Asp	
300					305					310					315	
ggg	gag	cgg	ccg	agt	ttt	gtc	atg	gca	cgc	ggt	tat	tac	acg	aga	aca	1493
Gly	Glu	Arg	Pro	Ser	Phe	Val	Met	Ala	Arg	Gly	Tyr	Tyr	Thr	Arg	Thr	
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Val	Leu	Val	Ala	Tyr	Asn	Phe	Arg	Gly	Gly	Lys	Leu	Thr	Lys	Leu	Trp	
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Thr	Phe	Asp	Ser	Asp	Ala	Pro	Gly	Asn	Gly	Ala	Tyr	Ala	Gly	Gln	Gly	
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aac	cac	agt	ttg	agc	gtc	gcc	gac	gtt	gac	gga	gat	gga	aag	gac	gag	1637
Asn	His	Ser	Leu	Ser	Val	Ala	Asp	Val	Asp	Gly	Asp	Gly	Lys	Asp	Glu	
		365					370				375					
atc	ata	tac	gga	gcg	atg	gct	gtc	gat	cat	gac	gga	aaa	ggc	ctc	tac	1685
Ile	Ile	Tyr	Gly	Ala	Met	Ala	Val	Asp	His	Asp	Gly	Lys	Gly	Leu	Tyr	
380					385					390					395	
tca	acc	ggc	tgg	gga	cat	ggg	gat	gcc	atg	cat	aca	ggg	aac	ctg	gac	1733
Ser	Thr	Gly	Trp	Gly	His	Gly	Asp	Ala	Met	His	Thr	Gly	Asn	Leu	Asp	
				400					405					410		
ccg	tca	agg	cct	gga	ctg	gaa	gtc	ttc	caa	gtc	cat	gaa	aac	agc	aat	1781
Pro	Ser	Arg	Pro	Gly	Leu	Glu	Val	Phe	Gln	Val	His	Glu	Asn	Ser	Asn	
			415					420					425			
tct	cct	tat	ggc	ttg	tcc	ttc	cgc	gat	gcg	aaa	aca	gga	aag	atc	atc	1829
Ser	Pro	Tyr	Gly	Leu	Ser	Phe	Arg	Asp	Ala	Lys	Thr	Gly	Lys	Ile	Ile	

430	435	440	
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atc gat ccg cgc tac gaa gga gcg gaa gta tgg gcg aac ggc agt ctt Ile Asp Pro Arg Tyr Glu Gly Ala Glu Val Trp Ala Asn Gly Ser Leu 460 465 470 475			1925
tat acg gca aaa ggc gta aaa atc gga aac aca ttg cct tca tca acg Tyr Thr Ala Lys Gly Val Lys Ile Gly Asn Thr Leu Pro Ser Ser Thr 480 485 490			1973
aac ttc ggc atc tgg tgg gac ggc gat ctc caa aga gag ctt ctg gac Asn Phe Gly Ile Trp Trp Asp Gly Asp Leu Gln Arg Glu Leu Leu Asp 495 500 505			2021
agc aac aga att gat aaa tgg gat tat caa aat tcg cga acc gtc aac Ser Asn Arg Ile Asp Lys Trp Asp Tyr Gln Asn Ser Arg Thr Val Asn 510 515 520			2069
ttg ctg aca gcg tcc gga gct tcg gca aat aac gga aca aaa gcg acg Leu Leu Thr Ala Ser Gly Ala Ser Ala Asn Asn Gly Thr Lys Ala Thr 525 530 535			2117
ccg tcc ctg cag gcg gac att ctc gga gac tgg cgc gaa gaa gtg gtc Pro Ser Leu Gln Ala Asp Ile Leu Gly Asp Trp Arg Glu Glu Val Val 540 545 550 555			2165
tgg cga gcg gag gac agc agc gaa ctg cgc atc tac acg acg aca gac Trp Arg Ala Glu Asp Ser Ser Glu Leu Arg Ile Tyr Thr Thr Thr Asp 560 565 570			2213
gtg acg gag cac cgc atg tat acg ctg atg cat gat gca gtc tat cgc Val Thr Glu His Arg Met Tyr Thr Leu Met His Asp Ala Val Tyr Arg 575 580 585			2261
ctc ggt atc gcc tgg cag aat gtc ggc tac aac cag cct ccg cac acc Leu Gly Ile Ala Trp Gln Asn Val Gly Tyr Asn Gln Pro Pro His Thr 590 595 600			2309
ggc ttt tat tta ggc gaa ggc atg cag aca ccg gag aag ccg aac att Gly Phe Tyr Leu Gly Glu Gly Met Gln Thr Pro Glu Lys Pro Asn Ile 605 610 615			2357
tat aca cgc tgatgataaa ggggagctgc ataataaagc gatatgttcg Tyr Thr Arg 620			2406
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ccgaaagccg ctgccgcgca tcacagtcag gatctttttc tggtcgattt tggaaaaggt			2526
cccgtgaga aggattatgt gaaagtgaac gagtcctccg tgtatcaaaa tgggtgctggc			2586
tacggatttt ctcaggcagg aagcgctgtg tgcaaaaaa cgcaaaaaaa agaagcgctc			2646

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 aaaatgggga cgatccccggc cggagcaaag ggaagctcag ccgaaaaagc gttcacccgtt 2826  
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Asp Gly Arg Thr Ala Ala Gln Ala Arg Gln Met Glu Ser Leu Asn Arg  
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Gly Leu Val Ala Val Lys Thr Gly Asn Gly Val Phe Val Ser Trp Arg  
 50 55 60

Leu Leu Gly Thr Glu Pro Ser Ser Val Ser Phe Asn Val Tyr Arg Asn  
 65 70 75 80

Gly Lys Lys Leu Asn Gly Ser Pro Ile Thr Ser Ser Thr Asn Tyr Gln  
 85 90 95

Asp Ala Gly Gly Asp Leu Asn Ala Val Tyr Gln Val Arg Ala Val Leu  
 100 105 110

Asn Gly Arg Glu Gln Ala Pro Ser Glu Ser Val Gly Val Leu Asn Lys  
 115 120 125

Gln Tyr Lys Ser Val Pro Leu Gln Lys Pro Ala Gly Gly Lys Thr Pro  
 130 135 140

Asp Gly Val Ser Tyr Thr Tyr Ser Ala Asn Asp Ala Ser Val Gly Asp  
 145 150 155 160

Leu Asp Gly Asp Gly Gln Tyr Glu Ile Ile Leu Lys Trp Asp Pro Ser  
 165 170 175

Asn Ser Lys Asp Asn Ser Gln Asp Gly Tyr Thr Gly Asp Val Leu Ile  
 180 185 190

Asp Ala Tyr Lys Leu Asp Gly Thr Met Met Trp Arg Ile Asn Leu Gly  
 195 200 205

Lys Asn Ile Arg Ala Gly Ala His Tyr Thr Gln Phe Leu Val Tyr Asp  
 210 215 220

Phe Asp Gly Asp Gly Lys Ala Glu Ile Ala Met Lys Thr Ala Asp Gly  
 225 230 235 240

Thr Lys Asp Gly Lys Gly Lys Val Ile Gly Asn Ala Asn Ala Asp Tyr  
 245 250 255

Arg Asn Ala Gln Gly Arg Ile Leu Ser Gly Pro Glu Tyr Leu Thr Val  
 260 265 270

Phe Lys Gly Asp Thr Gly Ala Glu Leu Thr Thr Val Asn Tyr Glu Pro  
 275 280 285

Ala Arg Gly Asn Val Ala Asp Trp Gly Asp Ser Tyr Gly Asn Arg Val  
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Asp Arg Phe Leu Ala Gly Val Ala Tyr Leu Asp Gly Glu Arg Pro Ser  
 305 310 315 320

Phe Val Met Ala Arg Gly Tyr Tyr Thr Arg Thr Val Leu Val Ala Tyr  
 325 330 335

Asn Phe Arg Gly Gly Lys Leu Thr Lys Leu Trp Thr Phe Asp Ser Asp  
 340 345 350

Ala Pro Gly Asn Gly Ala Tyr Ala Gly Gln Gly Asn His Ser Leu Ser  
 355 360 365

Val Ala Asp Val Asp Gly Asp Gly Lys Asp Glu Ile Ile Tyr Gly Ala  
 370 375 380

Met Ala Val Asp His Asp Gly Lys Gly Leu Tyr Ser Thr Gly Trp Gly

385

390

395

400

His Gly Asp Ala Met His Thr Gly Asn Leu Asp Pro Ser Arg Pro Gly  
 405 410 415

Leu Glu Val Phe Gln Val His Glu Asn Ser Asn Ser Pro Tyr Gly Leu  
 420 425 430

Ser Phe Arg Asp Ala Lys Thr Gly Lys Ile Ile Trp Gly Val His Ala  
 435 440 445

Gly Lys Asp Val Gly Arg Gly Met Ala Ala Asp Ile Asp Pro Arg Tyr  
 450 455 460

Glu Gly Ala Glu Val Trp Ala Asn Gly Ser Leu Tyr Thr Ala Lys Gly  
 465 470 475 480

Val Lys Ile Gly Asn Thr Leu Pro Ser Ser Thr Asn Phe Gly Ile Trp  
 485 490 495

Trp Asp Gly Asp Leu Gln Arg Glu Leu Leu Asp Ser Asn Arg Ile Asp  
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Lys Trp Asp Tyr Gln Asn Ser Arg Thr Val Asn Leu Leu Thr Ala Ser  
 515 520 525

Gly Ala Ser Ala Asn Asn Gly Thr Lys Ala Thr Pro Ser Leu Gln Ala  
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Asp Ile Leu Gly Asp Trp Arg Glu Glu Val Val Trp Arg Ala Glu Asp  
 545 550 555 560

Ser Ser Glu Leu Arg Ile Tyr Thr Thr Thr Asp Val Thr Glu His Arg  
 565 570 575

Met Tyr Thr Leu Met His Asp Ala Val Tyr Arg Leu Gly Ile Ala Trp  
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aaaaaacatg acatggatga tgccgctttt tttatcttta agcagtttct tttggccgaa      180
cacgttctcc catatctttt gaaggcgctc cttcgctccgc ttatcaaaat cctctttttg      240
tccgagcctg atgtaactga ttctcgttct gatcaaatag acgaacagat aaacggcgta      300
aacggttaca ctaaaaaacg caatgaaatt caacgacagc aagacattca tcagctgctc      360
cccctttcat ttccccaacc ttaaattccc ttgaactacc tttatcttaa ataatgaatg      420
agtgttcagt caatatatth tcataaatgc aggaaaatag ggggacacta ttctttacac      480
gaaaaaaggg agtgtcttca ttg gtg ccg ctt atg att atg gta tgt ttt ctc      533
                    Leu Val Pro Leu Met Ile Met Val Cys Phe Leu
                    1             5             10

atc ctg ctt ctt gcg ctc gat ttc cat ttt ggc cgc aaa gcc ttt gag      581
Ile Leu Leu Leu Ala Leu Asp Phe His Phe Gly Arg Lys Ala Phe Glu
                    15             20             25

aag aaa gcc tac gag ccc gtt ttt tca gag aag aaa agc gat att gaa      629
Lys Lys Ala Tyr Glu Pro Val Phe Ser Glu Lys Lys Ser Asp Ile Glu
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ctg att cat aat gga gaa gac ttg tgt gag cgg ctg ctg gat gac atc      677
Leu Ile His Asn Gly Glu Asp Leu Cys Glu Arg Leu Leu Asp Asp Ile
                    45             50             55

cgc cag gcc gaa tcg tcg gtg cat gtc atg ttt tat att gtg aag aac      725
Arg Gln Ala Glu Ser Ser Val His Val Met Phe Tyr Ile Val Lys Asn
                    60             65             70             75

gat gac atc agc ctt gaa ttt ttg aag gtg ctg aag gat aaa gcg aaa      773
Asp Asp Ile Ser Leu Glu Phe Leu Lys Val Leu Lys Asp Lys Ala Lys
                    80             85             90

tcc ggc gta tgc gta cga ttg ctg atc gac cgg atc ggc gcg atg aag      821
Ser Gly Val Cys Val Arg Leu Leu Ile Asp Arg Ile Gly Ala Met Lys
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Val Lys Lys Lys Thr Leu Ser Gly Leu Lys Gln Ser Gly Val His Val	
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Phe Phe Ala Asn Lys Pro Gly Phe Pro Tyr Phe Phe Tyr Arg Leu Asn	
125 130 135	
gcg agg aat cat cga aaa atc gcc gtc ata gac gga aag atc ggc tat	965
Ala Arg Asn His Arg Lys Ile Ala Val Ile Asp Gly Lys Ile Gly Tyr	
140 145 150 155	
gtg ggc gga ttt aac atc gcg aaa gaa tac ctt ggt aaa aaa gcg gaa	1013
Val Gly Gly Phe Asn Ile Ala Lys Glu Tyr Leu Gly Lys Lys Ala Glu	
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Phe Gly Pro Trp Lys Asp Tyr His Leu Arg Met Thr Gly Glu Gly Val	
175 180 185	
gcc gac ttg cag cac att ttt ata tcg gac ttc aaa aga gaa gcg ccg	1109
Ala Asp Leu Gln His Ile Phe Ile Ser Asp Phe Lys Arg Glu Ala Pro	
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Gln Ala Lys Pro Ala Asn Ser Val Phe Pro Pro Leu Gln Gln Gly Ala	
205 210 215	
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Tyr Ile Ser Phe Ile Glu Gln Ala Lys Glu Arg Ile Met Ile Cys Thr	
240 245 250	
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Pro Tyr Tyr Ile Pro Ser Pro Ala Leu Gln Gln Ala Val Leu Ser Ala	
255 260 265	
agg gaa agg ggc gtg atc gtg tcg gtt ctc gtg ccg atg aaa ccc gat	1349
Arg Glu Arg Gly Val Ile Val Ser Val Leu Val Pro Met Lys Pro Asp	
270 275 280	
cat ccg ctt gtc aaa gag gcc gcc tac acg cac ttt cca gcc ctt tta	1397
His Pro Leu Val Lys Glu Ala Ala Tyr Thr His Phe Pro Ala Leu Leu	
285 290 295	
aaa gcg ggc tgc tat att tac cgg tac tac aga ggc ttt tat cat gca	1445
Lys Ala Gly Cys Tyr Ile Tyr Arg Tyr Tyr Arg Gly Phe Tyr His Ala	
300 305 310 315	
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Lys Ala Leu Ile Val Asp Asp Arg His Val Met Ile Gly Thr Ser Asn	
320 325 330	
ttt gac aac agg agc ctg ttt ctc aat gat gaa gtg aat gtc gtc atc	1541



Phe Asp Asn Arg Ser Leu Phe Leu Asn Asp Glu Val Asn Val Val Ile  
335 340 345  
cat gat aaa gac tgg aca aag caa ttc ttc gac gtc gtc aag gaa agc 1589  
His Asp Lys Asp Trp Thr Lys Gln Phe Phe Asp Val Val Lys Glu Ser  
350 355 360  
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Ile Glu His Ala Glu Leu Leu Thr Lys Glu Arg Tyr Ala Lys Arg Pro  
365 370 375  
gtg atg cag cgg ccc gtc gaa tgg ctg gcg aaa tcg att tca ttc ttt 1685  
Val Met Gln Arg Pro Val Glu Trp Leu Ala Lys Ser Ile Ser Phe Phe  
380 385 390 395  
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Leu  
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Pro Val Phe Ser Glu Lys Lys Ser Asp Ile Glu Leu Ile His Asn Gly  
35 40 45  
Glu Asp Leu Cys Glu Arg Leu Leu Asp Asp Ile Arg Gln Ala Glu Ser  
50 55 60

Ser Val His Val Met Phe Tyr Ile Val Lys Asn Asp Asp Ile Ser Leu  
65 70 75 80

Glu Phe Leu Lys Val Leu Lys Asp Lys Ala Lys Ser Gly Val Cys Val  
85 90 95

Arg Leu Leu Ile Asp Arg Ile Gly Ala Met Lys Val Lys Lys Lys Thr  
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Leu Ser Gly Leu Lys Gln Ser Gly Val His Val Phe Phe Ala Asn Lys  
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Pro Gly Phe Pro Tyr Phe Phe Tyr Arg Leu Asn Ala Arg Asn His Arg  
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Lys Ile Ala Val Ile Asp Gly Lys Ile Gly Tyr Val Gly Gly Phe Asn  
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Ile Ala Lys Glu Tyr Leu Gly Lys Lys Ala Glu Phe Gly Pro Trp Lys  
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Asp Tyr His Leu Arg Met Thr Gly Glu Gly Val Ala Asp Leu Gln His  
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Ile Phe Ile Ser Asp Phe Lys Arg Glu Ala Pro Gln Ala Lys Pro Ala  
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Asn Ser Val Phe Pro Pro Leu Gln Gln Gly Ala Val Thr His Thr Thr  
210 215 220

His Ala Thr Lys Gly Phe Ser Leu Glu Glu Lys Tyr Ile Ser Phe Ile  
225 230 235 240

Glu Gln Ala Lys Glu Arg Ile Met Ile Cys Thr Pro Tyr Tyr Ile Pro  
245 250 255

Ser Pro Ala Leu Gln Gln Ala Val Leu Ser Ala Arg Glu Arg Gly Val  
260 265 270

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275 280 285

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 290 295 300

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 305 310 315 320

Asp Asp Arg His Val Met Ile Gly Thr Ser Asn Phe Asp Asn Arg Ser  
 325 330 335

Leu Phe Leu Asn Asp Glu Val Asn Val Val Ile His Asp Lys Asp Trp  
 340 345 350

Thr Lys Gln Phe Phe Asp Val Val Lys Glu Ser Ile Glu His Ala Glu  
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Val Leu Ile Asn Lys Ser Lys Lys Phe Phe Val  
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gaa gtt gca aaa gcc gat tcc gga aaa aac tat aaa atc atc ggc tac Glu Val Ala Lys Ala Asp Ser Gly Lys Asn Tyr Lys Ile Ile Gly Tyr	629
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tat cca tca tgg ggt gct tat gga agg gat ttt caa gtt tgg gat atg Tyr Pro Ser Trp Gly Ala Tyr Gly Arg Asp Phe Gln Val Trp Asp Met	677
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gac gtt tcg aaa gtc agc cac att aat tat gcc ttt gct gat att tgc Asp Val Ser Lys Val Ser His Ile Asn Tyr Ala Phe Ala Asp Ile Cys	725
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80 85 90	
acg tgg tca tgc cag gat gaa aac gga gtg atc gac gcg cca aat gga Thr Trp Ser Cys Gln Asp Glu Asn Gly Val Ile Asp Ala Pro Asn Gly	821
95 100 105	
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125 130 135	
aag ctg aaa aag agc cac cct cat ttg aaa acg ttc ata tcg gtc ggg Lys Leu Lys Lys Ser His Pro His Leu Lys Thr Phe Ile Ser Val Gly	965
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175 180 185	
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190 195 200	
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205 210 215	
ctc ctg caa gag gtg cgc aaa aaa ctt gac gct gca gaa gca aaa gac Leu Leu Gln Glu Val Arg Lys Lys Leu Asp Ala Ala Glu Ala Lys Asp	1205

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Gly Lys Glu Tyr Leu Leu Thr Ile Ala Ser Gly Ala Ser Pro Asp Tyr	240	245	250	
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Val Ser Asn Thr Glu Leu Asp Lys Ile Ala Gln Thr Val Asp Trp Ile	255	260	265	
aac att atg acc tat gac ttt aat ggc gga tgg caa agc ata agc gcc				1349
Asn Ile Met Thr Tyr Asp Phe Asn Gly Gly Trp Gln Ser Ile Ser Ala	270	275	280	
cat aat gca ccg ctg ttc tat gat cca aaa gcg aaa gaa gca ggc gtt				1397
His Asn Ala Pro Leu Phe Tyr Asp Pro Lys Ala Lys Glu Ala Gly Val	285	290	295	
cca aac gct gag acc tac aat att gaa aac act gtg aaa cgc tac aag				1445
Pro Asn Ala Glu Thr Tyr Asn Ile Glu Asn Thr Val Lys Arg Tyr Lys	300	305	310	315
gaa gcc ggt gtc aag ggt gac aaa tta gtg ctt gga aca ccg ttc tac				1493
Glu Ala Gly Val Lys Gly Asp Lys Leu Val Leu Gly Thr Pro Phe Tyr	320	325	330	
gga agg ggc tgg agc ggt tgt gaa cca ggg ggg cac gga gaa tat cag				1541
Gly Arg Gly Trp Ser Gly Cys Glu Pro Gly Gly His Gly Glu Tyr Gln	335	340	345	
aaa tgc gga ccg gct aaa gaa ggg aca tgg gaa aag ggc gta ttc gat				1589
Lys Cys Gly Pro Ala Lys Glu Gly Thr Trp Glu Lys Gly Val Phe Asp	350	355	360	
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Phe Ser Asp Leu Glu Arg Asn Tyr Val Asn Gln Asn Gly Tyr Lys Arg	365	370	375	
tat tgg aac gat caa gca aaa gtg ccg ttt ttg tat aat gcg gaa aat				1685
Tyr Trp Asn Asp Gln Ala Lys Val Pro Phe Leu Tyr Asn Ala Glu Asn	380	385	390	395
ggc aat ttc atc act tat gat gat gaa caa tca ttc ggc cac aaa acg				1733
Gly Asn Phe Ile Thr Tyr Asp Asp Glu Gln Ser Phe Gly His Lys Thr	400	405	410	
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Asp Phe Ile Lys Ala Asn Gly Leu Ser Gly Ala Met Phe Trp Asp Phe	415	420	425	
agc ggc gat tcc aat cgg acg ctt ctc aat aaa ttg gca gcc gat tta				1829
Ser Gly Asp Ser Asn Arg Thr Leu Leu Asn Lys Leu Ala Ala Asp Leu	430	435	440	
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Asp Phe Ala Pro Asp Gly Gly Asn Pro Glu Pro Pro Ser Ser Ala Pro	445	450	455	

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attaattatg cgtttgccca catcggggaa gatcatcgga tttcagtcgg agaagaggca	2735
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<213> Bacillus licheniformis

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Asp Ser Gly Lys Asn Tyr Lys Ile Ile Gly Tyr Tyr Pro Ser Trp Gly  
35 40 45

Ala Tyr Gly Arg Asp Phe Gln Val Trp Asp Met Asp Val Ser Lys Val  
50 55 60

Ser His Ile Asn Tyr Ala Phe Ala Asp Ile Cys Trp Glu Gly Arg His  
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Gly Asn Pro Asp Pro Thr Gly Pro Asn Pro Gln Thr Trp Ser Cys Gln  
85 90 95

Asp Glu Asn Gly Val Ile Asp Ala Pro Asn Gly Thr Ile Val Met Gly  
100 105 110

Asp Pro Trp Ile Asp Ala Gln Lys Ser Asn Pro Gly Asp Val Trp Asp  
115 120 125

Glu Pro Ile Arg Gly Asn Phe Lys Gln Leu Leu Lys Leu Lys Lys Ser  
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His Pro His Leu Lys Thr Phe Ile Ser Val Gly Gly Trp Thr Trp Ser  
145 150 155 160

Asn Arg Phe Ser Asp Val Ala Ala Asp Pro Ala Ala Arg Glu Asn Phe  
165 170 175

Ala Ala Ser Ala Val Glu Phe Leu Arg Lys Tyr Gly Phe Asp Gly Val  
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Asp Leu Asp Trp Glu Tyr Pro Val Ser Gly Gly Leu Pro Gly Asn Ser  
195 200 205

Thr Arg Pro Glu Asp Lys Arg Asn Tyr Thr Leu Leu Leu Gln Glu Val

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Arg Lys Lys Leu Asp	Ala Ala Glu Ala Lys Asp	Gly Lys Glu Tyr Leu
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Leu Asp Lys Ile Ala Gln	Thr Val Asp Trp Ile Asn	Ile Met Thr Tyr
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Asp Phe Asn Gly Gly Trp	Gln Ser Ile Ser Ala His	Asn Ala Pro Leu
	275	280 285
Phe Tyr Asp Pro Lys Ala	Lys Glu Ala Gly Val Pro	Asn Ala Glu Thr
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Tyr Asn Ile Glu Asn Thr	Val Lys Arg Tyr Lys Glu	Ala Gly Val Lys
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Gly Asp Lys Leu Val Leu	Gly Thr Pro Phe Tyr Gly	Arg Gly Trp Ser
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Gly Cys Glu Pro Gly Gly	His Gly Glu Tyr Gln Lys	Cys Gly Pro Ala
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Lys Glu Gly Thr Trp Glu	Lys Gly Val Phe Asp Phe	Ser Asp Leu Glu
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Arg Asn Tyr Val Asn Gln	Asn Gly Tyr Lys Arg Tyr	Trp Asn Asp Gln
	370	375 380
Ala Lys Val Pro Phe Leu	Tyr Asn Ala Glu Asn Gly	Asn Phe Ile Thr
385	390	395 400
Tyr Asp Asp Glu Gln Ser	Phe Gly His Lys Thr Asp	Phe Ile Lys Ala
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Asn Gly Leu Ser Gly Ala	Met Phe Trp Asp Phe Ser	Gly Asp Ser Asn
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Arg Thr Leu Leu Asn Lys	Leu Ala Ala Asp Leu Asp	Phe Ala Pro Asp
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Gly Gly Asn Pro Glu Pro Pro Ser Ser Ala Pro Val Asn Val Arg Val  
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Thr Gly Lys Thr Ala Thr Ser Val Ser Leu Ala Trp Asp Ala Pro Ser  
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Ser Gly Ala Asn Ile Ala Glu Tyr Val Val Ser Phe Glu Asn Arg Ser  
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Ile Ser Val Lys Glu Thr Ser Ala Glu Ile Gly Gly Leu Lys Pro Gly  
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Thr Ala Tyr Ser Phe Thr Val Ser Ala Lys Asp Ala Asp Gly Lys Leu  
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Ser Tyr Asp Glu Trp Lys Glu Thr Ser Ala Tyr Thr Gly Gly Glu Arg  
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Val Ala Phe Asn Gly Lys Val Tyr Glu Ala Lys Trp Trp Thr Lys Gly  
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ccgtcagcaa ttttttcttg gactatcttt attattccag acagcttcaa aatttatttt	360
catgattgag taaaagaatt tatgggaatg gacgaatatg ggtaacaccg cgttctgcaa	420
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Phe Ile Val Val Leu Phe Leu Ile Val His Val Phe Gln Ser Leu Glu	
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Ala Ala Gly Asn Thr Pro Leu Glu Gln Leu Ala Glu Gly Leu Ser Arg	
30 35 40	
cat gat gtc gag ctt gaa gag tgg acc atg cat aca aaa aaa cag ctt	677
His Asp Val Glu Leu Glu Glu Trp Thr Met His Thr Lys Lys Gln Leu	
45 50 55	
acc cta agt gaa aaa gat ttt ttt gca aaa ctg aaa cat ttc aag aaa	725
Thr Leu Ser Glu Lys Asp Phe Phe Ala Lys Leu Lys His Phe Lys Lys	
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cag cat cga caa tat gaa tgg act tta acg cgg gaa gac gac gat aca	773
Gln His Arg Gln Tyr Glu Trp Thr Leu Thr Arg Glu Asp Asp Asp Thr	
80 85 90	
gtt aaa gcg aca ggt gtt ttt cag gac aaa aaa aat cat atc aat tcc	821
Val Lys Ala Thr Gly Val Phe Gln Asp Lys Lys Asn His Ile Asn Ser	
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Leu Leu Tyr Glu Gln Lys Gly Ala Gly Pro Arg Glu Asn Trp Asn Ala	
125 130 135	
aca tat aag cag ttt gaa cgg gat gca ttc gac ata atg cga gaa aag	965
Thr Tyr Lys Gln Phe Glu Arg Asp Ala Phe Asp Ile Met Arg Glu Lys	
140 145 150 155	
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Thr Ala Ile Phe Thr Cys Leu Lys Gly His Leu Asn Gly Met Met Asn	
160 165 170	
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Lys	Ser	Val	Glu	Asp	Leu	Ile	Glu	Pro	Asn	Phe	Val	Ser	Ile	Ser	Ala	
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Tyr	Thr	Asn	Glu	Trp	Lys	Glu	Ser	Ile	Lys	Thr	Glu	Lys	His	Arg	Met	
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Asn	Leu	Gln	Val	Ser	Leu	Arg	Asn	Ala	Gly	Met	Gly	Glu	Lys	Leu	Thr	
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Val	Thr	Val	Gly	Thr	Pro	Ile	Val	Thr	Thr	Glu	Tyr					
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Pro	Leu	Glu	Gln	Leu	Ala	Glu	Gly	Leu	Ser	Arg	His	Asp	Val	Glu	Leu	
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Glu Glu Trp Thr Met His Thr Lys Lys Gln Leu Thr Leu Ser Glu Lys  
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Asp Phe Phe Ala Lys Leu Lys His Phe Lys Lys Gln His Arg Gln Tyr  
 65 70 75 80

Glu Trp Thr Leu Thr Arg Glu Asp Asp Asp Thr Val Lys Ala Thr Gly  
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Val Phe Gln Asp Lys Lys Asn His Ile Asn Ser Lys Ile His Leu Val  
 100 105 110

Ser Thr His Lys Asn Gln Arg Leu Val Ser Tyr Leu Leu Tyr Glu Gln  
 115 120 125

Lys Gly Ala Gly Pro Arg Glu Asn Trp Asn Ala Thr Tyr Lys Gln Phe  
 130 135 140

Glu Arg Asp Ala Phe Asp Ile Met Arg Glu Lys Thr Ala Ile Phe Thr  
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Cys Leu Lys Gly His Leu Asn Gly Met Met Asn Val Val Leu Gln Lys  
 165 170 175

Lys Ala Asn Glu Leu Val His Glu Phe Asp Ala Lys Ser Val Glu Asp  
 180 185 190

Leu Ile Glu Pro Asn Phe Val Ser Ile Ser Ala Tyr Thr Asn Glu Trp  
 195 200 205

Lys Glu Ser Ile Lys Thr Glu Lys His Arg Met Asn Leu Gln Val Ser  
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Pro Ile Val Thr Thr Glu Tyr  
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Ile Thr Gly Leu Ile Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro
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Ala Gln Ala Ala Pro Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser
                30         35         40

tac aaa gcg gaa aca tcg gtt act tat gac cca aac att aag agc gat      677
Tyr Lys Ala Glu Thr Ser Val Thr Tyr Asp Pro Asn Ile Lys Ser Asp
                45         50         55

caa tac ggc ttg tat tca aaa gcg ttt aca ggc acc ggc aaa gtg aat      725
Gln Tyr Gly Leu Tyr Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn
                60         65         70         75

gaa aca aag gaa aaa gcg gaa aaa aag tca ccc gcc aaa gct cct tac      773
Glu Thr Lys Glu Lys Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr
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agc att aaa tcg gtg att ggt tct gat gat cgg aca agg gtc acc aac      821
Ser Ile Lys Ser Val Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn
                95         100        105

aca acc gca tat ccg tac aga gcg atc gtt cat att tca agc agc atc      869
Thr Thr Ala Tyr Pro Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile
                110        115        120

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Gly Ser Cys Thr Gly Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala
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140 145 150 155	
act gtt tcg ccg gga cgg aac ggg aca agc tat cct tac ggc tca gtt	1013
Thr Val Ser Pro Gly Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val	
160 165 170	
aaa tcg acg cgc tac ttt att ccg tca gga tgg aga agc gga aac acc	1061
Lys Ser Thr Arg Tyr Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr	
175 180 185	
aat tac gat tac ggc gca atc gaa cta agc gaa ccg atc ggc aat act	1109
Asn Tyr Asp Tyr Gly Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr	
190 195 200	
gtc gga tac ttc gga tac tcg tac act act tca tca ctt gtt ggg aca	1157
Val Gly Tyr Phe Gly Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr	
205 210 215	
act gtt acc atc agc ggc tac cca ggc gat aaa aca gca ggc aca caa	1205
Thr Val Thr Ile Ser Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln	
220 225 230 235	
tgg cag cat tca gga ccg att gcc atc tcc gaa acg tat aaa ttg cag	1253
Trp Gln His Ser Gly Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln	
240 245 250	
tac gca atg gac acg tac gga gga caa agc ggt tca ccg gta ttc gaa	1301
Tyr Ala Met Asp Thr Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu	
255 260 265	
caa agc agc tcc aga acg aac tgc agc ggt ccg tgc tcg ctt gcc gta	1349
Gln Ser Ser Ser Arg Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val	
270 275 280	
cac aca aat gga gta tac ggc ggc tcc tcg tac aac aga ggc acc ccg	1397
His Thr Asn Gly Val Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg	
285 290 295	
att aca aaa gag gtg ttc gac aat ttg acc aac tgg aaa aac agc gca	1445
Ile Thr Lys Glu Val Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala	
300 305 310 315	
caa taatacacga agacagcccg cttccttttg gaacgggctg tcacatctaa	1498
Gln	
cggccgtata cttaatttcc tttaagcctg tacttttttg catctattga tatcgtgaaa	1558
tttgaaggac cgctgatcgg caaataatag acaagctgaa actccgcttc ctcaccaggt	1618
ttaatggttt tccagattga tagagtact ctgatgcggt ggaaatctac tgtcagtcgg	1678
ccaatgttcg gtcccgtatg cccttttagaa atcacttcaa catgatcgcc gctccagctt	1738

ctaaaccgag gggaagtgga tgtcggcgca tcaaattcga taaaagaacc tcccgtaatc 1798  
 gtgacatcgc tgttggtgat cagcttcac accgggtgga tcgggtaatt ttgatctcct 1858  
 aacggaaagt tcgtcaactc tacttctgca tctagtgatt catcaggcaa aggtgatgtg 1918  
 ctgagtcgat tatcgtatgg tggtgtatcc 1948

<210> 244  
 <211> 316  
 <212> PRT  
 <213> Bacillus licheniformis

<400> 244

Leu Val Ser Lys Lys Ser Val Lys Arg Gly Leu Ile Thr Gly Leu Ile  
 1 5 10 15

Gly Ile Ser Ile Tyr Ser Leu Gly Met His Pro Ala Gln Ala Ala Pro  
 20 25 30

Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr  
 35 40 45

Ser Val Thr Tyr Asp Pro Asn Ile Lys Ser Asp Gln Tyr Gly Leu Tyr  
 50 55 60

Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys  
 65 70 75 80

Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val  
 85 90 95

Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro  
 100 105 110

Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly  
 115 120 125

Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr  
 130 135 140

Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly  
 145 150 155 160

Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr

165

170

175

Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly  
 180 185 190

Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly  
 195 200 205

Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser  
 210 215 220

Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly  
 225 230 235 240

Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr  
 245 250 255

Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg  
 260 265 270

Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val  
 275 280 285

Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val  
 290 295 300

Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln  
 305 310 315

<210> 245

<211> 1231

<212> DNA

<213> *Bacillus licheniformis*

<220>

<221> CDS

<222> (501) .. (731)

<400> 245

attggccggg aaatttcccg gacctgtgga ggaaacctcc attattgaaa gccggccggg 60

aatgggcgctc caccttgaaa tcaccgcgc gtccggagga aggagttttt ggaggccttt 120

tctatataag gggagggagg agccaaaacg gggacctttc cgaaattatg tcaagccggt 180

ccccaaggtg ctccaggcca gacacctgaaa atggaacctc aggttatctg gggtaggacc 240



tgctaaacca tgagggagga ataaaggaat ggaccggaaa gcccgttcg tccaggaatt	300
tatgtccac cgccttggtgc cggaggacct cattcaaaaa attgatgaaa accttttcga	360
ttccaacccg cctgaaccgt cgatgccacc aaaggacctt gtccacgcat atgctgcaat	420
ctttctatac ctttgcttcg gcggcaaagg aagggaccgg agaccctttt aaaaagaagc	480
ccgaagaacc agggacaagc ttg agc gag ctt gcc aaa acg tat cca gaa aaa	533
Leu Ser Glu Leu Ala Lys Thr Tyr Pro Glu Lys	
1 5 10	
aca aaa acg ctg ctt gaa tcc ttt acg gat gaa gaa ttg gat cgt gaa	581
Thr Lys Thr Leu Leu Glu Ser Phe Thr Asp Glu Glu Leu Asp Arg Glu	
15 20 25	
gtc gat ttg acc ggc gtc ttc gga cga aaa gta gcc ggc gaa cag cta	629
Val Asp Leu Thr Gly Val Phe Gly Arg Lys Val Ala Gly Glu Gln Leu	
30 35 40	
ctg cag ctc gcg atc gga cac gaa att cac cac aaa ggc aat ctg ttt	677
Leu Gln Leu Ala Ile Gly His Glu Ile His His Lys Gly Asn Leu Phe	
45 50 55	
gtt tat gtc cgt gaa atg gga cac acg gat ctg cct ttg tat gta aag	725
Val Tyr Val Arg Glu Met Gly His Thr Asp Leu Pro Leu Tyr Val Lys	
60 65 70 75	
att cat tgatcctgag agccctcctt gaaagaaaac cggttaaaaa ggaatacgaa	781
Ile His	
agcaccggg agtacacatt atgagtaaaa gctaaaggag ggtgtcaggt gaatacgag	841
cgtgccagg aaatcgtcga atcaccgat atggttgatg ttacttataa cggcaggccg	901
atttatattc agcgtgtcga cgaacaaaat gaaaccgcaa gaatctttcc gctcggccag	961
ccggagaacg agcaggaagt gccgctcgca aatttgaaag aacattaataa agaaaccctt	1021
tctgaggaag gggttttgtt ttggatttgc ctgccacaca gccatcaaaa aaacaccgga	1081
aagaccgagt gtttaattta taattttcgc aagtcctctt actgccagcc tcagcacata	1141
aaacaatggc tcaagcaaat cgacgagata aagataatcc catttgatcat cattacgttt	1201
atTTTTTTTc ttcaacgaat gtttctcctt	1231

<210> 246

<211> 77

<212> PRT

<213> Bacillus licheniformis

<400> 246

Leu Ser Glu Leu Ala Lys Thr Tyr Pro Glu Lys Thr Lys Thr Leu Leu  
 1 5 10 15

Glu Ser Phe Thr Asp Glu Glu Leu Asp Arg Glu Val Asp Leu Thr Gly  
 20 25 30

Val Phe Gly Arg Lys Val Ala Gly Glu Gln Leu Leu Gln Leu Ala Ile  
 35 40 45

Gly His Glu Ile His His Lys Gly Asn Leu Phe Val Tyr Val Arg Glu  
 50 55 60

Met Gly His Thr Asp Leu Pro Leu Tyr Val Lys Ile His  
 65 70 75

<210> 247  
 <211> 1597  
 <212> DNA  
 <213> Bacillus licheniformis

<220>  
 <221> CDS  
 <222> (501)..(1097)

<400> 247  
 ggccattcctt ttccctccaa tctttgtgaa ttttttgtaa attgaagttc tattaatcat 60  
 agcataaact gccgccgtct gtgaataaca cggaaatgca tgtttggttg cgaaaaaatt 120  
 cattcccgaa attaaatcgt cattttccaa aaaaagtgcg cgaaaaaagc gaaaaccgcg 180  
 ccaagcggaa tacaggagat cattgcggtt ccgttgacca gcccgtcagc cccgcttatt 240  
 ttcaggggctt cccggtagcc tattaaaaag tggatgatcg ataggacata acataagagc 300  
 atcatatagt aaggattcat ttgtataccc tcctctattc gctttactat attacattca 360  
 atagaggggaa agattatgcc tgtttaagta ggaaaaagaa caaatatta tagacgaaaa 420  
 gattttcaat tacaatacat gtttttaaaa atatttccac tataatcaaa atgaaagata 480  
 aatttagggg gtcatacaaa atg aaa aaa agg ctg atg tca cta ttg gtc tgc 533  
 Met Lys Lys Arg Leu Met Ser Leu Leu Val Cys  
 1 5 10  
 atc ctg gtt tta gtg ccg gca gca gga gct ttt gcc gcg ccg aaa cag 581  
 Ile Leu Val Leu Val Pro Ala Ala Gly Ala Phe Ala Ala Pro Lys Gln  
 15 20 25  
 gcc gag ctt aaa gat tat ctt gaa gaa ata gga atg aca gaa aaa gaa 629  
 Ala Glu Leu Lys Asp Tyr Leu Glu Glu Ile Gly Met Thr Glu Lys Glu

30	35	40	
ttg gaa gcc tat ttg cag gat aca tat gat gag agt tta aaa ggt ttt			677
Leu Glu Ala Tyr Leu Gln Asp Thr Tyr Asp Glu Ser Leu Lys Gly Phe			
45	50	55	
gac tcg gtg gaa gag ttg aaa gac ttt tta ggg caa aga ctg act aaa			725
Asp Ser Val Glu Glu Leu Lys Asp Phe Leu Gly Gln Arg Leu Thr Lys			
60	65	70	75
aag ctt ttg gca tcc tat ttg aaa gaa tac gga ttg agc gaa aaa gaa			773
Lys Leu Leu Ala Ser Tyr Leu Lys Glu Tyr Gly Leu Ser Glu Lys Glu			
	80	85	90
gcg gct gac cta ttt gtt gaa aat ggc tat atg gaa agc ggc caa aac			821
Ala Ala Asp Leu Phe Val Glu Asn Gly Tyr Met Glu Ser Gly Gln Asn			
	95	100	105
att ctc gac gtg ttt atg ttt gaa tac gaa ttg gac gat gcg ctc tac			869
Ile Leu Asp Val Phe Met Phe Glu Tyr Glu Leu Asp Asp Ala Leu Tyr			
	110	115	120
acc gtg aca tat gaa gaa gac gat ttt cag atc gga aac atg ttt caa			917
Thr Val Thr Tyr Glu Glu Asp Asp Phe Gln Ile Gly Asn Met Phe Gln			
	125	130	135
gaa ttg ggt gtg gat gat cag gag tgg gaa aga ctc gtg aat cac ctc			965
Glu Leu Gly Val Asp Asp Gln Glu Trp Glu Arg Leu Val Asn His Leu			
140	145	150	155
cga aaa gtg cgc gat aac aat ccg aac ctt gaa aat gac ttg atg gct			1013
Arg Lys Val Arg Asp Asn Asn Pro Asn Leu Glu Asn Asp Leu Met Ala			
	160	165	170
ctt gga gaa cgt ctt gaa gcg gta gcc gat ttc gag tct gta tca gag			1061
Leu Gly Glu Arg Leu Glu Ala Val Ala Asp Phe Glu Ser Val Ser Glu			
	175	180	185
ctg tca gct cag gat atc gct gaa tgc tgt cca ttt taacgatctt			1107
Leu Ser Ala Gln Asp Ile Ala Glu Cys Cys Pro Phe			
	190	195	
cagaagacgc tcgaagtga aacgaatatt atcttggttaa gacggaaaga aaaaagaagt			1167
gtctttgacg acgcttgatca gtgctgaaga tctgaaggga gcaagcctcc tagtggaagt			1227
atacgatctg cagggcaatt tcattttgga tgtattgctg acgcctgaaa tgatcggatc			1287
tgatttaatt catgacacag ggtcgaaagt gaagcaaacc caaacggctg ttaaacacga			1347
cgcaaagaaa tctcatgtga aaaagacggt taaagggtgca aagcttccga aaacggccgg			1407
gcattacgca gaatggatcga tctttggcgc cgttctgatg tttggcggat tgtttatggt			1467
cagaaggctt cgaaaagcgg cttaacattt tacttcccat tctaagtctg tatagaatgg			1527
gaagttttta taaggagtga aaggaaatta aggcacatcg aaaaaagatc atctggcttg			1587

cagccattgc

1597

<210> 248  
<211> 199  
<212> PRT  
<213> Bacillus licheniformis

<400> 248

Met Lys Lys Arg Leu Met Ser Leu Leu Val Cys Ile Leu Val Leu Val  
1 5 10 15

Pro Ala Ala Gly Ala Phe Ala Ala Pro Lys Gln Ala Glu Leu Lys Asp  
20 25 30

Tyr Leu Glu Glu Ile Gly Met Thr Glu Lys Glu Leu Glu Ala Tyr Leu  
35 40 45

Gln Asp Thr Tyr Asp Glu Ser Leu Lys Gly Phe Asp Ser Val Glu Glu  
50 55 60

Leu Lys Asp Phe Leu Gly Gln Arg Leu Thr Lys Lys Leu Leu Ala Ser  
65 70 75 80

Tyr Leu Lys Glu Tyr Gly Leu Ser Glu Lys Glu Ala Ala Asp Leu Phe  
85 90 95

Val Glu Asn Gly Tyr Met Glu Ser Gly Gln Asn Ile Leu Asp Val Phe  
100 105 110

Met Phe Glu Tyr Glu Leu Asp Asp Ala Leu Tyr Thr Val Thr Tyr Glu  
115 120 125

Glu Asp Asp Phe Gln Ile Gly Asn Met Phe Gln Glu Leu Gly Val Asp  
130 135 140

Asp Gln Glu Trp Glu Arg Leu Val Asn His Leu Arg Lys Val Arg Asp  
145 150 155 160

Asn Asn Pro Asn Leu Glu Asn Asp Leu Met Ala Leu Gly Glu Arg Leu  
165 170 175

Glu Ala Val Ala Asp Phe Glu Ser Val Ser Glu Leu Ser Ala Gln Asp  
180 185 190

Ile Ala Glu Cys Cys Pro Phe  
195